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(54) Title: METHODS OF DIAGNOSIS OF BREAST CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF BREAST CANCER

(57) Abstract: Described herein are genes whose expression are up-regulated or down-regulated in breast cancer. Related methods and compositions that can be used for diagnosis and treatment of breast cancer are disclosed. Also described herein are methods that can be used to identify modulators of breast cancer.

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METHODS OF DIAGNOSIS OF BREAST CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF BREAST CANCER

CROSS-REFERENCES TO RELATED APPLICATIONS

This application claims priority to USSN 60/263,965, filed January 24, 2001; USSN 60/265,928, filed February 2, 2001; USSN 09/829,472 filed April 9, 2001; USSN 60/282,698, filed April 9, 2001; USSN 60/288,590, filed May 4, 2001; and USSN 60/294,443, filed May 29, 2001, all of which are incorporated herein by reference in their entirety.

FIELD OF THE INVENTION

The invention relates to the identification of nucleic acid and protein expression profiles and nucleic acids, products, and antibodies thereto that are involved in breast cancer; and to the use of such expression profiles and compositions in the diagnosis, prognosis and therapy of breast cancer. The invention further relates to methods for identifying and using agents and/or targets that inhibit breast cancer.

BACKGROUND OF THE INVENTION

Breast cancer is one of the most frequently diagnosed cancers and the second leading cause of female cancer death in North America and northern Europe, with lung cancer being the leading cause. Lifetime incidence of the disease in the United States is one-in-eight, with a 1-in-29 lifetime risk of dying from breast cancer. Early detection of breast cancer, using mammography, clinical breast examination, and self breast examination, has dramatically improved the treatment of the disease, although sensitivity is still major concern, as mammographic sensitivity has been estimated at only 60%–90%. Treatment of breast cancer consists largely of surgical lumpectomy or mastectomy, radiation therapy, anti-

hormone therapy, and/or chemotherapy. Although many breast cancer patients are effectively treated, the current therapies can all induce serious side effects which diminish quality of life. Deciding on a particular course of treatment is typically based on a variety of prognostic parameters and markers (Fitzgibbons et al., 2000, Arch. Pathol. Lab. Med. 124:966-978; Hamilton and Piccart, 2000, Ann. Oncol. 11:647-663), including genetic predispostion markers BRCA-1 and BRCA-2 (Robson, 2000, J. Clin. Oncol. 18:113sup-118sup).

Imaging of breast cancer for diagnosis has been problematic and limited. In addition, dissemination of tumor cells (metastases) to locoregional lymph nodes is an important prognostic factor; five year survival rates drop from 80 percent in patients with no lymph node metastases to 45 to 50 percent in those patients who do have lymph node metastases. A recent report showed that micrometastases can be detected from lymph nodes using reverse transcriptase-PCR methods based on the presence of mRNA for carcinoembryonic antigen, which has previously been shown to be present in the vast majority of breast cancers but not in normal tissues. Liefers et al., New England J. of Med. 339(4):223 (1998).

The identification of novel therapeutic targets and diagnostic markers is essential for improving the current treatment of breast cancer patients. Recent advances in molecular medicine have increased the interest in tumor-specific cell surface antigens that could serve as targets for various immunotherapeutic or small molecule strategies. Antigens suitable for immunotherapeutic strategies should be highly expressed in cancer tissues and ideally not expressed in normal adult tissues. Expression in tissues that are dispensable for life, however, may be tolerated. Examples of such antigens include Her2/neu and the B-cell antigen CD20. Humanized monclonal antibodies directed to Her2/neu (Herceptin®/trastuzumab) are currently in use for the treatment of metastatic breast cancer (Ross and Fletcher, 1998, Stem Cells 16:413-428). Similarly, anti-CD20 monoclonal antibodies (Rituxin®/rituximab) are used to effectively treat non-Hodgekin's lymphoma (Maloney et al., 1997, Blood 90:2188-2195; Leget and Czuczman, 1998, Curr. Opin. Oncol. 10:548-551).

Other potential immunotherapeutic targets have been identified for breast cancer. One such target is polymorphic epithelial mucin (MUC1). MUC1 is a transmembrane

protein, present at the apical surface of glandular epithelial cells. It is often overexpressed in breast cancer, and typically exhibits an altered glycosylation pattern, resulting in an antigenically distinct molecule, and is in early clinical trials as a vaccine target (Gilewski et al., 2000, Clin. Cancer Res. 6:1693-1701; Scholl et al., 2000, J. Immunother. 23:570-580). The tumor-expressed protein is often cleaved into the circulation, where it is detectable as the tumor marker, CA 15-3 (Bon et al., 1997, Clin. Chem. 43:585-593). However, many patients have tumors that express neither HER2 nor MUC-1; therefore, it is clear that other targets need to be identified to manage localized and metastatic disease. Many other genes have been reported to be overexpressed in breast cancer, such as EGFR (Sainsbury et al., 1987, Lancet 1(8547):1398-1402), c-erbB3 (Naidu et al., 1988, Br. J. Cancer 78:1385-1390), FGFR2 (Penault-Llorca et al., 1991, Int. J. Cancer 61:170-176), PKW (Preiherr et al., 2000, Anticancer Res. 20:2255-2264), MTA1 (Nawa et al., 2000, J. Cell Biochem. 79:202-212), breast cancer associated gene 1 (Kurt et al., 2000, Breast Cancer Res. Treat. 59:41-48). Although monoclonal antibodies to the protein products of some of these overexpressed genes have been reported (for review, see Green et al., 2000, Cancer Treat. Rev. 26:269-286), none are currently approved for breast cancer therapy in the US.

Disclosures of certain genes and ESTs described as being expressed in breast cancer are found in international patent applications WO-99/33869, WO-97/25426, WO-97/02280 and WO-00/55173, WO-98/45328 and WO-00/22130. Similarly, genes and ESTs described as being expressed in breast cancer are disclosed in US Patent Nos. 5,759,776 and 5,693,522. The utility of such genes is described in each of these publications, and their disclosures are incorporated herein in their entirety.

While industry and academia have identified novel sequences, there has not been an equal effort exerted to identify the function of these novel sequences. The elucidation of a role for novel proteins and compounds in disease states for identification of therapeutic targets and diagnostic markers is essential for improving the current treatment of breast cancer patients. Accordingly, provided herein are molecular targets for therapeutic intervention in breast and other cancers. Additionally, provided herein are methods that can be used in diagnosis and prognosis of breast cancer. Further provided are methods that can be used to screen candidate bioactive agents for the ability to modulate breast cancer.

SUMMARY OF THE INVENTION

The present invention therefore provides nucleotide sequences of genes that are up- and down-regulated in breast cancer cells. Such genes are useful for diagnostic purposes, and also as targets for screening for therapeutic compounds that modulate breast cancer, such as hormones or antibodies. Other aspects of the invention will become apparent to the skilled artisan by the following description of the invention.

In one aspect, the present invention provides a method of detecting a breast cancer-associated transcript in a cell from a patient, the method comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-25.

In one embodiment, the present invention provides a method of determining the level of a breast cancer associated transcript in a cell from a patient.

In one embodiment, the present invention provides a method of detecting a breast cancer-associated transcript in a cell from a patient, the method comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-25.

In one embodiment, the polynucleotide selectively hybridizes to a sequence at least 95% identical to a sequence as shown in Tables 1-25.

In one embodiment, the biological sample is a tissue sample. In another embodiment, the biological sample comprises isolated nucleic acids, e.g., mRNA.

In one embodiment, the polynucleotide is labeled, e.g., with a fluorescent label.

In one embodiment, the polynucleotide is immobilized on a solid surface.

In one embodiment, the patient is undergoing a therapeutic regimen to treat breast cancer. In another embodiment, the patient is suspected of having metastatic breast cancer.

In one embodiment, the patient is a human.

In one embodiment, the breast cancer associated transcript is mRNA.

In one embodiment, the method further comprises the step of amplifying nucleic acids before the step of contacting the biological sample with the polynucleotide.

In another aspect, the present invention provides a method of monitoring the efficacy of a therapeutic treatment of breast cancer, the method comprising the steps of: (i) providing a biological sample from a patient undergoing the therapeutic treatment; and (ii) determining the level of a breast cancer-associated transcript in the biological sample by contacting the biological sample with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-25, thereby monitoring the efficacy of the therapy. In a further embodiment, the patient has metastatic breast cancer. In a further embodiment, the patient has a drug resistant form of breast cancer.

In one embodiment, the method further comprises the step of: (iii) comparing the level of the breast cancer-associated transcript to a level of the breast cancer-associated transcript in a biological sample from the patient prior to, or earlier in, the therapeutic treatment.

Additionally, provided herein is a method of evaluating the effect of a candidate breast cancer drug comprising administering the drug to a patient and removing a cell sample from the patient. The expression profile of the cell is then determined. This method may further comprise comparing the expression profile to an expression profile of a healthy individual. In a preferred embodiment, said expression profile includes a gene of Tables 1-25.

In one aspect, the present invention provides an isolated nucleic acid molecule consisting of a polynucleotide sequence as shown in Tables 1-25.

In one embodiment, an expression vector or cell comprises the isolated nucleic acid.

In one aspect, the present invention provides an isolated polypeptide which is encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1-25.

In another aspect, the present invention provides an antibody that specifically binds to an isolated polypeptide which is encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1-25.

In one embodiment, the antibody is conjugated to an effector component, e.g., a fluorescent label, a radioisotope or a cytotoxic chemical.

In one embodiment, the antibody is an antibody fragment. In another embodiment, the antibody is humanized.

In one aspect, the present invention provides a method of detecting a breast cancer cell in a biological sample from a patient, the method comprising contacting the biological sample with an antibody as described herein.

In another aspect, the present invention provides a method of detecting antibodies specific to breast cancer in a patient, the method comprising contacting a biological sample from the patient with a polypeptide encoded by a nucleic acid comprising a sequence from Tables 1-25.

In another aspect, the present invention provides a method for identifying a compound that modulates a breast cancer-associated polypeptide, the method comprising the steps of: (i) contacting the compound with a breast cancer-associated polypeptide, the polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-25; and (ii) determining the functional effect of the compound upon the polypeptide.

In one embodiment, the functional effect is a physical effect, an enzymatic effect, or a chemical effect.

In one embodiment, the polypeptide is expressed in a eukaryotic host cell or cell membrane. In another embodiment, the polypeptide is recombinant.

In one embodiment, the functional effect is determined by measuring ligand binding to the polypeptide.

In another aspect, the present invention provides a method of inhibiting proliferation of a breast cancer-associated cell to treat breast cancer in a patient, the method comprising the step of administering to the subject a therapeutically effective amount of a compound identified as described herein.

In one embodiment, the compound is an antibody.

In another aspect, the present invention provides a drug screening assay comprising the steps of: (i) administering a test compound to a mammal having breast cancer

or to a cell sample isolated therefrom; (ii) comparing the level of gene expression of a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-25 in a treated cell or mammal with the level of gene expression of the polynucleotide in a control cell sample or mammal, wherein a test compound that modulates the level of expression of the polynucleotide is a candidate for the treatment of breast cancer.

In one embodiment, the control is a mammal with breast cancer or a cell sample therefrom that has not been treated with the test compound. In another embodiment, the control is a normal cell or mammal.

In one embodiment, the test compound is administered in varying amounts or concentrations. In another embodiment, the test compound is administered for varying time periods. In another embodiment, the comparison can occur after addition or removal of the drug candidate.

In one embodiment, the levels of a plurality of polynucleotides that selectively hybridize to a sequence at least 80% identical to a sequence as shown in Tables 1-25 are individually compared to their respective levels in a control cell sample or mammal. In a preferred embodiment the plurality of polynucleotides is from three to ten.

In another aspect, the present invention provides a method for treating a mammal having breast cancer comprising administering a compound identified by the assay described herein.

In another aspect, the present invention provides a pharmaceutical composition for treating a mammal having breast cancer, the composition comprising a compound identified by the assay described herein and a physiologically acceptable excipient.

In one aspect, the present invention provides a method of screening drug candidates by providing a cell expressing a gene that is up- and down-regulated as in a breast cancer. In one embodiment, a gene is selected from Tables 1-25. The method further includes adding a drug candidate to the cell and determining the effect of the drug candidate on the expression of the expression profile gene.

In one embodiment, the method of screening drug candidates includes comparing the level of expression in the absence of the drug candidate to the level of

expression in the presence of the drug candidate, wherein the concentration of the drug candidate can vary when present, and wherein the comparison can occur after addition or removal of the drug candidate. In a preferred embodiment, the cell expresses at least two expression profile genes. The profile genes may show an increase or decrease.

Also provided is a method of evaluating the effect of a candidate breast cancer drug comprising administering the drug to a transgenic animal expressing or over-expressing the breast cancer modulatory protein, or an animal lacking the breast cancer modulatory protein, for example as a result of a gene knockout.

Moreover, provided herein is a biochip comprising one or more nucleic acid segments of Tables 1-25, wherein the biochip comprises fewer than 1000 nucleic acid probes. Preferably, at least two nucleic acid segments are included. More preferably, at least three nucleic acid segments are included.

Furthermore, a method of diagnosing a disorder associated with breast cancer is provided. The method comprises determining the expression of a gene of Tables 1-25, preferably a gene of Table 25, in a first tissue type of a first individual, and comparing the distribution to the expression of the gene from a second normal tissue type from the first individual or a second unaffected individual. A difference in the expression indicates that the first individual has a disorder associated with breast cancer.

In a further embodiment, the biochip also includes a polynucleotide sequence of a gene that is not up- and down-regulated in breast cancer.

In one embodiment a method for screening for a bioactive agent capable of interfering with the binding of a breast cancer modulating protein (breast cancer modulatory protein) or a fragment thereof and an antibody which binds to said breast cancer modulatory protein or fragment thereof. In a preferred embodiment, the method comprises combining a breast cancer modulatory protein or fragment thereof, a candidate bioactive agent and an antibody which binds to said breast cancer modulatory protein or fragment thereof. The method further includes determining the binding of said breast cancer modulatory protein or fragment thereof and said antibody. Wherein there is a change in binding, an agent is identified as an interfering agent. The interfering agent can be an agonist or an antagonist. Preferably, the agent inhibits breast cancer.

Also provided herein are methods of eliciting an immune response in an individual. In one embodiment a method provided herein comprises administering to an individual a composition comprising a breast cancer modulating protein, or a fragment thereof. In another embodiment, the protein is encoded by a nucleic acid selected from those of Tables 1-25.

Further provided herein are compositions capable of eliciting an immune response in an individual. In one embodiment, a composition provided herein comprises a breast cancer modulating protein, preferably encoded by a nucleic acid of Tables 1-25, more preferably of Table 25, or a fragment thereof, and a pharmaceutically acccptable carrier. In another embodiment, said composition comprises a nucleic acid comprising a sequence encoding a breast cancer modulating protein, preferably selected from the nucleic acids of Tables 1-25, and a pharmaceutically acceptable carrier.

Also provided are methods of neutralizing the effect of a breast cancer protein, or a fragment thereof, comprising contacting an agent specific for said protein with said protein in an amount sufficient to effect neutralization. In another embodiment, the protein is encoded by a nucleic acid selected from those of Tables 1-25.

In another aspect of the invention, a method of treating an individual for breast cancer is provided. In one embodiment, the method comprises administering to said individual an inhibitor of a breast cancer modulating protein. In another embodiment, the method comprises administering to a patient having breast cancer an antibody to a breast cancer modulating protein conjugated to a therapeutic moiety. Such a therapeutic moiety can be a cytotoxic agent or a radioisotope.

DETAILED DESCRIPTION OF THE INVENTION

In accordance with the objects outlined above, the present invention provides novel methods for diagnosis and prognosis evaluation for breast cancer (PC), including metastatic breast cancer, as well as methods for screening for compositions which modulate breast cancer. Also provided are methods for treating breast cancer.

Tables 1-24B provide unigene cluster identification numbers for the nucleotide sequence of genes that exhibit increased or decreased expression in breast cancer

samples. Tables 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 18, 19, 20, 21, and 22 list those genes that are up-regulated in breast cancer cells. Table 14 lists those genes that are highly upregulated in breast cancer cells. Table 1, 2, 3, 15, and 23 list genes that are down-regulated in breast cancer cells and Table 16, lists genes that are highly down-regulated in breast cancer genes. The Tables also provide an exemplar accession number that provides a nucleotide sequence that is part of the unigene cluster.

Definitions

The term "breast cancer protein" or "breast cancer polynucleotide" or "breast cancer-associated transcript" refers to nucleic acid and polypeptide polymorphic variants, alleles, mutants, and interspecies homologues that: (1) have a nucleotide sequence that has greater than about 60% nucleotide sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% or greater nucleotide sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more nucleotides, to a nucleotide sequence of or associated with a gene of Tables 1-25; (2) bind to antibodies, e.g., polyclonal antibodies, raised against an immunogen comprising an amino acid sequence encoded by a nucleotide sequence of or associated with a gene of Tables 1-25, and conservatively modified variants thereof; (3) specifically hybridize under stringent hybridization conditions to a nucleic acid sequence, or the complement thereof of Tables 1-25 and conservatively modified variants thereof or (4) have an amino acid sequence that has greater than about 60% amino acid sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% or greater amino sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more amino acid, to an amino acid sequence encoded by a nucleotide sequence of or associated with a gene of Tables 1-25. A polynucleotide or polypeptide sequence is typically from a mammal including, but not limited to, primate, e.g., human; rodent, e.g., rat, mouse, hamster; cow, pig, horse, sheep, or other mammal. A "breast cancer polypeptide" and a "breast cancer polynucleotide," include both naturally occurring or recombinant forms.

A "full length" breast cancer protein or nucleic acid refers to a breast cancer polypeptide or polynucleotide sequence, or a variant thereof, that contains all of the elements normally contained in one or more naturally occurring, wild type breast cancer polynucleotide or polypeptide sequences. The "full length" may be prior to, or after, various stages of post-translation processing or splicing, including alternative splicing.

"Biological sample" as used herein is a sample of biological tissue or fluid that contains nucleic acids or polypeptides, e.g., of a breast cancer protein, polynucleotide or transcript. Such samples include, but are not limited to, tissue isolated from primates, e.g., humans, or rodents, e.g., mice, and rats. Biological samples may also include sections of tissues such as biopsy and autopsy samples, frozen sections taken for histologic purposes, blood, plasma, serum, sputum, stool, tears, mucus, hair, skin, etc. Biological samples also include explants and primary and/or transformed cell cultures derived from patient tissues. A biological sample is typically obtained from a eukaryotic organism, most preferably a mammal such as a primate e.g., chimpanzee or human; cow; dog; cat; a rodent, e.g., guinea pig, rat, mouse; rabbit; or a bird; reptile; or fish.

"Providing a biological sample" means to obtain a biological sample for use in methods described in this invention. Most often, this will be done by removing a sample of cells from an animal, but can also be accomplished by using previously isolated cells (*e.g.*, isolated by another person, at another time, and/or for another purpose), or by performing the methods of the invention *in vivo*. Archival tissues, having treatment or outcome history, will be particularly useful.

The terms "identical" or percent "identity," in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are the same or have a specified percentage of amino acid residues or nucleotides that are the same (i.e., about 60% identity, preferably 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or higher identity over a specified region, when compared and aligned for maximum correspondence over a comparison window or designated region) as measured using a BLAST or BLAST 2.0 sequence comparison algorithms with default parameters described below, or by manual alignment and visual inspection (*see, e.g.*, NCBI web site http://www.ncbi.nlm.nih.gov/BLAST/ or the like). Such sequences are then said to

be "substantially identical." This definition also refers to, or may be applied to, the compliment of a test sequence. The definition also includes sequences that have deletions and/or additions, as well as those that have substitutions, as well as naturally occurring, e.g., polymorphic or allelic variants, and man-made variants. As described below, the preferred algorithms can account for gaps and the like. Preferably, identity exists over a region that is at least about 25 amino acids or nucleotides in length, or more preferably over a region that is 50-100 amino acids or nucleotides in length.

For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Preferably, default program parameters can be used, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

A "comparison window", as used herein, includes reference to a segment of one of the number of contiguous positions selected from the group consisting typically of from 20 to 600, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well-known in the art. Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology algorithm of Smith & Waterman, *Adv. Appl. Math.* 2:482 (1981), by the homology alignment algorithm of Needleman & Wunsch, *J. Mol. Biol.* 48:443 (1970), by the search for similarity method of Pearson & Lipman, *Proc. Nat'l. Acad. Sci. USA* 85:2444 (1988), by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by manual alignment and visual inspection (*see, e.g., Current Protocols in Molecular Biology* (Ausubel *et al.*, eds. 1995 supplement)).

Preferred examples of algorithms that are suitable for determining percent sequence identity and sequence similarity include the BLAST and BLAST 2.0 algorithms,

which are described in Altschul *et al., Nuc. Acids Res.* 25:3389-3402 (1977) and Altschul *et al., J. Mol. Biol.* 215:403-410 (1990). BLAST and BLAST 2.0 are used, with the parameters described herein, to determine percent sequence identity for the nucleic acids and proteins of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (http://www.ncbi.nlm.nih.gov/). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul *et al., supra*). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, e.g., for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (*see* Henikoff & Henikoff, *Proc. Natl. Acad. Sci. USA* 89:10915 (1989)) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.

The BLAST algorithm also performs a statistical analysis of the similarity between two sequences (*see, e.g.*, Karlin & Altschul, *Proc. Nat'l. Acad. Sci. USA* 90:5873-5787 (1993)). One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a

nucleic acid is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.2, more preferably less than about 0.01, and most preferably less than about 0.001. Log values may be large negative numbers, e.g., 5, 10, 20, 30, 40, 40, 70, 90, 110, 150, 170, etc.

An indication that two nucleic acid sequences or polypeptides are substantially identical is that the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the antibodies raised against the polypeptide encoded by the second nucleic acid, as described below. Thus, a polypeptide is typically substantially identical to a second polypeptide, e.g., where the two peptides differ only by conservative substitutions. Another indication that two nucleic acid sequences are substantially identical is that the two molecules or their complements hybridize to each other under stringent conditions, as described below. Yet another indication that two nucleic acid sequences are substantially identical is that the same primers can be used to amplify the sequences.

A "host cell" is a naturally occurring cell or a transformed cell that contains an expression vector and supports the replication or expression of the expression vector. Host cells may be cultured cells, explants, cells *in vivo*, and the like. Host cells may be prokaryotic cells such as *E. coli*, or eukaryotic cells such as yeast, insect, amphibian, or mammalian cells such as CHO, HeLa, and the like (*see, e.g.*, the American Type Culture Collection catalog or web site, www.atcc.org).

The terms "isolated," "purified," or "biologically pure" refer to material that is substantially or essentially free from components that normally accompany it as found in its native state. Purity and homogeneity are typically determined using analytical chemistry techniques such as polyacrylamide gel electrophoresis or high performance liquid chromatography. A protein or nucleic acid that is the predominant species present in a preparation is substantially purified. In particular, an isolated nucleic acid is separated from some open reading frames that naturally flank the gene and encode proteins other than protein encoded by the gene. The term "purified" in some embodiments denotes that a nucleic acid or protein gives rise to essentially one band in an electrophoretic gel. Preferably, it means that the nucleic acid or protein is at least 85% pure, more preferably at least 95% pure, and most preferably at least 99% pure. "Purify" or "purification" in other embodiments means

removing at least one contaminant from the composition to be purified. In this sense, purification does not require that the purified compound be homogenous, e.g., 100% pure.

The terms "polypeptide," "peptide" and "protein" are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid polymers in which one or more amino acid residue is an artificial chemical mimetic of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers, those containing modified residues, and non-naturally occurring amino acid polymer.

The term "amino acid" refers to naturally occurring and synthetic amino acids, as well as amino acid analogs and amino acid mimetics that function similarly to the naturally occurring amino acids. Naturally occurring amino acids are those encoded by the genetic code, as well as those amino acids that are later modified, e.g., hydroxyproline, γ-carboxyglutamate, and O-phosphoserine. Amino acid analogs refers to compounds that have the same basic chemical structure as a naturally occurring amino acid, e.g., an α carbon that is bound to a hydrogen, a carboxyl group, an amino group, and an R group, e.g., homoserine, norleucine, methionine sulfoxide, methionine methyl sulfonium. Such analogs may have modified R groups (e.g., norleucine) or modified peptide backbones, but retain the same basic chemical structure as a naturally occurring amino acid. Amino acid mimetics refers to chemical compounds that have a structure that is different from the general chemical structure of an amino acid, but that functions similarly to a naturally occurring amino acid.

Amino acids may be referred to herein by either their commonly known three letter symbols or by the one-letter symbols recommended by the IUPAC-IUB Biochemical Nomenclature Commission. Nucleotides, likewise, may be referred to by their commonly accepted single-letter codes.

"Conservatively modified variants" applies to both amino acid and nucleic acid sequences. With respect to particular nucleic acid sequences, conservatively modified variants refers to those nucleic acids which encode identical or essentially identical amino acid sequences, or where the nucleic acid does not encode an amino acid sequence, to essentially identical or associated, e.g., naturally contiguous, sequences. Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids encode most proteins. For instance, the codons GCA, GCC, GCG and GCU all encode the amino

acid alanine. Thus, at every position where an alanine is specified by a codon, the codon can be altered to another of the corresponding codons described without altering the encoded polypeptide. Such nucleic acid variations are "silent variations," which are one species of conservatively modified variations. Every nucleic acid sequence herein which encodes a polypeptide also describes silent variations of the nucleic acid. One of skill will recognize that in certain contexts each codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine, and TGG, which is ordinarily the only codon for tryptophan) can be modified to yield a functionally identical molecule. Accordingly, often silent variations of a nucleic acid which encodes a polypeptide is implicit in a described sequence with respect to the expression product, but not with respect to actual probe sequences.

As to amino acid sequences, one of skill will recognize that individual substitutions, deletions or additions to a nucleic acid, peptide, polypeptide, or protein sequence which alters, adds or deletes a single amino acid or a small percentage of amino acids in the encoded sequence is a "conservatively modified variant" where the alteration results in the substitution of an amino acid with a chemically similar amino acid. Conservative substitution tables providing functionally similar amino acids are well known in the art. Such conservatively modified variants are in addition to and do not exclude polymorphic variants, interspecies homologs, and alleles of the invention.typically conservative substitutions for one another: 1) Alanine (A), Glycine (G); 2) Aspartic acid (D), Glutamic acid (E); 3) Asparagine (N), Glutamine (Q); 4) Arginine (R), Lysine (K); 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V); 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W); 7) Serine (S), Threonine (T); and 8) Cysteine (C), Methionine (M) (*see, e.g.*, Creighton, *Proteins* (1984)).

Macromolecular structures such as polypeptide structures can be described in terms of various levels of organization. For a general discussion of this organization, *see, e.g.*, Alberts *et al.*, *Molecular Biology of the Cell* (3rd ed., 1994) and Cantor & Schimmel, *Biophysical Chemistry Part I: The Conformation of Biological Macromolecules* (1980). "Primary structure" refers to the amino acid sequence of a particular peptide. "Secondary structure" refers to locally ordered, three dimensional structures within a polypeptide. These structures are commonly known as domains. Domains are portions of a polypeptide that

often form a compact unit of the polypeptide and are typically 25 to approximately 500 amino acids long. Typical domains are made up of sections of lesser organization such as stretches of β-sheet and α-helices. "Tertiary structure" refers to the complete three dimensional structure of a polypeptide monomer. "Quaternary structure" refers to the three dimensional structure formed, usually by the noncovalent association of independent tertiary units. Anisotropic terms are also known as energy terms.

"Nucleic acid" or "oligonucleotide" or "polynucleotide" or grammatical equivalents used herein means at least two nucleotides covalently linked together. Oligonucleotides are typically from about 5, 6, 7, 8, 9, 10, 12, 15, 25, 30, 40, 50 or more nucleotides in length, up to about 100 nucleotides in length. Nucleic acids and polynucleotides are a polymers of any length, including longer lengths, e.g., 200, 300, 500, 1000, 2000, 3000, 5000, 7000, 10,000, etc. A nucleic acid of the present invention will generally contain phosphodiester bonds, although in some cases, nucleic acid analogs are included that may have alternate backbones, comprising, e.g., phosphoramidate, phosphorothioate, phosphorodithioate, or O-methylphophoroamidite linkages (see Eckstein, Oligonucleotides and Analogues: A Practical Approach, Oxford University Press); and peptide nucleic acid backbones and linkages. Other analog nucleic acids include those with positive backbones; non-ionic backbones, and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7, ASC Symposium Series 580, *Carbohydrate Modifications in Antisense Research*, Sanghui & Cook, eds.. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of nucleic acids. Modifications of the ribose-phosphate backbone may be done for a variety of reasons, e.g. to increase the stability and half-life of such molecules in physiological environments or as probes on a biochip. Mixtures of naturally occurring nucleic acids and analogs can be made; alternatively, mixtures of different nucleic acid analogs, and mixtures of naturally occurring nucleic acids and analogs may be made.

A variety of references disclose such nucleic acid analogs, including, for example, phosphoramidate (Beaucage et al., Tetrahedron 49(10):1925 (1993) and references therein; Letsinger, J. Org. Chem. 35:3800 (1970); Sprinzl et al., Eur. J. Biochem. 81:579 (1977); Letsinger et al., Nucl. Acids Res. 14:3487 (1986); Sawai et al, Chem. Lett. 805

(1984), Letsinger et al., J. Am. Chem. Soc. 110:4470 (1988); and Pauwels et al., Chemica Scripta 26:141 91986)), phosphorothioate (Mag et al., Nucleic Acids Res. 19:1437 (1991); and U.S. Patent No. 5,644,048), phosphorodithioate (Briu et al., J. Am. Chem. Soc. 111:2321 (1989), O-methylphophoroamidite linkages (see Eckstein, Oligonucleotides and Analogues: A Practical Approach, Oxford University Press), and peptide nucleic acid backbones and linkages (see Egholm, J. Am. Chem. Soc. 114:1895 (1992); Meier et al., Chem. Int. Ed. Engl. 31:1008 (1992); Nielsen, Nature, 365:566 (1993); Carlsson et al., Nature 380:207 (1996), all of which are incorporated by reference). Other analog nucleic acids include those with positive backbones (Denpcy et al., Proc. Natl. Acad. Sci. USA 92:6097 (1995); non-ionic backbones (U.S. Patent Nos. 5,386,023, 5,637,684, 5,602,240, 5,216,141 and 4,469,863; Kiedrowshi et al., Angew. Chem. Intl. Ed. English 30:423 (1991); Letsinger et al., J. Am. Chem. Soc. 110:4470 (1988); Letsinger et al., Nucleoside & Nucleotide 13:1597 (1994); Chapters 2 and 3, ASC Symposium Series 580, "Carbohydrate Modifications in Antisense Research", Ed. Y.S. Sanghui and P. Dan Cook; Mesmaeker et al., Bioorganic & Medicinal Chem. Lett. 4:395 (1994); Jeffs et al., J. Biomolecular NMR 34:17 (1994); Tetrahedron Lett. 37:743 (1996)) and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7, ASC Symposium Series 580, "Carbohydrate Modifications in Antisense Research", Ed. Y.S. Sanghui and P. Dan Cook. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of nucleic acids (see Jenkins et al., Chem. Soc. Rev. (1995) pp 169-176). Several nucleic acid analogs are described in Rawls, C & E News June 2, 1997 page 35. All of these references are hereby expressly incorporated by reference.

Particularly preferred are peptide nucleic acids (PNA) which includes peptide nucleic acid analogs. These backbones are substantially non-ionic under neutral conditions, in contrast to the highly charged phosphodiester backbone of naturally occurring nucleic acids. This results in two advantages. First, the PNA backbone exhibits improved hybridization kinetics. PNAs have larger changes in the melting temperature (T_m) for mismatched versus perfectly matched basepairs. DNA and RNA typically exhibit a 2-4°C drop in T_m for an internal mismatch. With the non-ionic PNA backbone, the drop is closer to 7-9°C. Similarly, due to their non-ionic nature, hybridization of the bases attached to these backbones is

relatively insensitive to salt concentration. In addition, PNAs are not degraded by cellular enzymes, and thus can be more stable.

The nucleic acids may be single stranded or double stranded, as specified, or contain portions of both double stranded or single stranded sequence. As will be appreciated by those in the art, the depiction of a single strand also defines the sequence of the complementary strand; thus the sequences described herein also provide the complement of the sequence. The nucleic acid may be DNA, both genomic and cDNA, RNA or a hybrid, where the nucleic acid may contain combinations of deoxyribo- and ribo-nucleotides, and combinations of bases, including uracil, adenine, thymine, cytosine, guanine, inosine, xanthine hypoxanthine, isocytosine, isoguanine, etc. "Transcript" typically refers to a naturally occurring RNA, e.g., a pre-mRNA, hnRNA, or mRNA. As used herein, the term "nucleoside" includes nucleotides and nucleoside and nucleotide analogs, and modified nucleosides such as amino modified nucleosides. In addition, "nucleoside" includes non-naturally occurring analog structures. Thus, e.g. the individual units of a peptide nucleic acid, each containing a base, are referred to herein as a nucleoside.

A "label" or a "detectable moiety" is a composition detectable by spectroscopic, photochemical, biochemical, immunochemical, chemical, or other physical means. For example, useful labels include ^{32}P, fluorescent dyes, electron-dense reagents, enzymes (*e.g.*, as commonly used in an ELISA), biotin, digoxigenin, or haptens and proteins or other entities which can be made detectable, *e.g.*, by incorporating a radiolabel into the peptide or used to detect antibodies specifically reactive with the peptide. The labels may be incorporated into the breast cancer nucleic acids, proteins and antibodies at any position. Any method known in the art for conjugating the antibody to the label may be employed, including those methods described by Hunter et al., Nature, 144:945 (1962); David et al., Biochemistry, 13:1014 (1974); Pain et al., J. Immunol. Meth., 40:219 (1981); and Nygren, J. Histochem. and Cytochem., 30:407 (1982).

An "effector" or "effector moiety" or "effector component" is a molecule that is bound (or linked, or conjugated), either covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds, to an antibody. The "effector" can be a variety of molecules including, e.g., detection moieties including

radioactive compounds, fluorescent compounds, an enzyme or substrate, tags such as epitope tags, a toxin; activatable moieties, a chemotherapeutic agent; a lipase; an antibiotic; or a radioisotope emitting "hard" e.g., beta radiation.

A "labeled nucleic acid probe or oligonucleotide" is one that is bound, either covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds to a label such that the presence of the probe may be detected by detecting the presence of the label bound to the probe. Alternatively, method using high affinity interactions may achieve the same results where one of a pair of binding partners binds to the other, e.g., biotin, streptavidin.

As used herein a "nucleic acid probe or oligonucleotide" is defined as a nucleic acid capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, usually through hydrogen bond formation. As used herein, a probe may include natural (i.e., A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in a probe may be joined by a linkage other than a phosphodiester bond, so long as it does not functionally interfere with hybridization. Thus, e.g., probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages. It will be understood by one of skill in the art that probes may bind target sequences lacking complete complementarity with the probe sequence depending upon the stringency of the hybridization conditions. The probes are preferably directly labeled as with isotopes, chromophores, lumiphores, chromogens, or indirectly labeled such as with biotin to which a streptavidin complex may later bind. By assaying for the presence or absence of the probe, one can detect the presence or absence of the select sequence or subsequence. Diagnosis or prognosis may be based at the genomic level, or at the level of RNA or protein expression.

The term "recombinant" when used with reference, e.g., to a cell, or nucleic acid, protein, or vector, indicates that the cell, nucleic acid, protein or vector, has been modified by the introduction of a heterologous nucleic acid or protein or the alteration of a native nucleic acid or protein, or that the cell is derived from a cell so modified. Thus, e.g., recombinant cells express genes that are not found within the native (non-recombinant) form of the cell or express native genes that are otherwise abnormally expressed, under expressed

or not expressed at all. By the term "recombinant nucleic acid" herein is meant nucleic acid, originally formed *in vitro*, in general, by the manipulation of nucleic acid, e.g., using polymerases and endonucleases, in a form not normally found in nature. In this manner, operably linkage of different sequences is achieved. Thus an isolated nucleic acid, in a linear form, or an expression vector formed *in vitro* by ligating DNA molecules that are not normally joined, are both considered recombinant for the purposes of this invention. It is understood that once a recombinant nucleic acid is made and reintroduced into a host cell or organism, it will replicate non-recombinantly, i.e., using the *in vivo* cellular machinery of the host cell rather than *in vitro* manipulations; however, such nucleic acids, once produced recombinantly, although subsequently replicated non-recombinantly, are still considered recombinant for the purposes of the invention. Similarly, a "recombinant protein" is a protein made using recombinant techniques, i.e., through the expression of a recombinant nucleic acid as depicted above.

The term "heterologous" when used with reference to portions of a nucleic acid indicates that the nucleic acid comprises two or more subsequences that are not normally found in the same relationship to each other in nature. For instance, the nucleic acid is typically recombinantly produced, having two or more sequences, e.g., from unrelated genes arranged to make a new functional nucleic acid, e.g., a promoter from one source and a coding region from another source. Similarly, a heterologous protein will often refer to two or more subsequences that are not found in the same relationship to each other in nature (e.g., a fusion protein).

A "promoter" is defined as an array of nucleic acid control sequences that direct transcription of a nucleic acid. As used herein, a promoter includes necessary nucleic acid sequences near the start site of transcription, such as, in the case of a polymerase II type promoter, a TATA element. A promoter also optionally includes distal enhancer or repressor elements, which can be located as much as several thousand base pairs from the start site of transcription. A "constitutive" promoter is a promoter that is active under most environmental and developmental conditions. An "inducible" promoter is a promoter that is active under environmental or developmental regulation. The term "operably linked" refers to a functional linkage between a nucleic acid expression control sequence (such as a

promoter, or array of transcription factor binding sites) and a second nucleic acid sequence, wherein the expression control sequence directs transcription of the nucleic acid corresponding to the second sequence.

An "expression vector" is a nucleic acid construct, generated recombinantly or synthetically, with a series of specified nucleic acid elements that permit transcription of a particular nucleic acid in a host cell. The expression vector can be part of a plasmid, virus, or nucleic acid fragment. Typically, the expression vector includes a nucleic acid to be transcribed operably linked to a promoter.

The phrase "selectively (or specifically) hybridizes to" refers to the binding, duplexing, or hybridizing of a molecule only to a particular nucleotide sequence under stringent hybridization conditions when that sequence is present in a complex mixture (e.g., total cellular or library DNA or RNA).

The phrase "stringent hybridization conditions" refers to conditions under which a probe will hybridize to its target subsequence, typically in a complex mixture of nucleic acids, but to no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in Tijssen, *Techniques in Biochemistry and Molecular Biology--Hybridization with Nucleic Probes*, "Overview of principles of hybridization and the strategy of nucleic acid assays" (1993). Generally, stringent conditions are selected to be about 5-10°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength pH. The T_m is the temperature (under defined ionic strength, pH, and nucleic concentration) at which 50% of the probes complementary to the target hybridize to the target sequence at equilibrium (as the target sequences are present in excess, at T_m, 50% of the probes are occupied at equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30°C for short probes (e.g., 10 to 50 nucleotides) and at least about 60°C for long probes (e.g., greater than 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. For selective or specific hybridization, a positive signal is at least two times

background, preferably 10 times background hybridization. Exemplary stringent hybridization conditions can be as following: 50% formamide, 5x SSC, and 1% SDS, incubating at 42°C, or, 5x SSC, 1% SDS, incubating at 65°C, with wash in 0.2x SSC, and 0.1% SDS at 65°C. For PCR, a temperature of about 36°C is typical for low stringency amplification, although annealing temperatures may vary between about 32°C and 48°C depending on primer length. For high stringency PCR amplification, a temperature of about 62°C is typical, although high stringency annealing temperatures can range from about 50°C to about 65°C, depending on the primer length and specificity. Typical cycle conditions for both high and low stringency amplifications include a denaturation phase of 90°C - 95°C for 30 sec - 2 min., an annealing phase lasting 30 sec. - 2 min., and an extension phase of about 72°C for 1 - 2 min. Protocols and guidelines for low and high stringency amplification reactions are provided, e.g., in Innis *et al.* (1990) *PCR Protocols, A Guide to Methods and Applications*, Academic Press, Inc. N.Y.).

Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the polypeptides which they encode are substantially identical. This occurs, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code. In such cases, the nucleic acids typically hybridize under moderately stringent hybridization conditions. Exemplary "moderately stringent hybridization conditions" include a hybridization in a buffer of 40% formamide, 1 M NaCl, 1% SDS at 37°C, and a wash in 1X SSC at 45°C. A positive hybridization is at least twice background. Those of ordinary skill will readily recognize that alternative hybridization and wash conditions can be utilized to provide conditions of similar stringency. Additional guidelines for determining hybridization parameters are provided in numerous reference, e.g., and Current Protocols in Molecular Biology, ed. Ausubel, *et al.*

The phrase "functional effects" in the context of assays for testing compounds that modulate activity of a breast cancer protein includes the determination of a parameter that is indirectly or directly under the influence of the breast cancer protein or nucleic acid, e.g., a functional, physical, or chemical effect, such as the ability to decrease breast cancer. It includes ligand binding activity; cell growth on soft agar; anchorage dependence; contact

inhibition and density limitation of growth; cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis *in vivo*; mRNA and protein expression in cells undergoing metastasis, and other characteristics of breast cancer cells. "Functional effects" include *in vitro*, *in vivo*, and *ex vivo* activities.

By "determining the functional effect" is meant assaying for a compound that increases or decreases a parameter that is indirectly or directly under the influence of a breast cancer protein sequence, e.g., functional, enzymatic, physical and chemical effects. Such functional effects can be measured by any means known to those skilled in the art, e.g., changes in spectroscopic characteristics (e.g., fluorescence, absorbance, refractive index), hydrodynamic (e.g., shape), chromatographic, or solubility properties for the protein, measuring inducible markers or transcriptional activation of the breast cancer protein; measuring binding activity or binding assays, e.g. binding to antibodies or other ligands, and measuring cellular proliferation. Determination of the functional effect of a compound on breast cancer can also be performed using breast cancer assays known to those of skill in the art such as an *in vitro* assays, e.g., cell growth on soft agar; anchorage dependence; contact inhibition and density limitation of growth; cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis *in vivo*; mRNA and protein expression in cells undergoing metastasis, and other characteristics of breast cancer cells. The functional effects can be evaluated by many means known to those skilled in the art, e.g., microscopy for quantitative or qualitative measures of alterations in morphological features, measurement of changes in RNA or protein levels for breast cancer-associated sequences, measurement of RNA stability, identification of downstream or reporter gene expression (CAT, luciferase, β-gal, GFP and the like), e.g., via chemiluminescence, fluorescence, colorimetric reactions, antibody binding, inducible markers, and ligand binding assays.

"Inhibitors", "activators", and "modulators" of breast cancer polynucleotide and polypeptide sequences are used to refer to activating, inhibitory, or modulating molecules or compounds identified using *in vitro* and *in vivo* assays of breast cancer polynucleotide and polypeptide sequences. Inhibitors are compounds that, e.g., bind to, partially or totally block

activity, decrease, prevent, delay activation, inactivate, desensitize, or down regulate the activity or expression of breast cancer proteins, e.g., antagonists. Antisense nucleic acids may seem to inhibit expression and subsequent function of the protein. "Activators" are compounds that increase, open, activate, facilitate, enhance activation, sensitize, agonize, or up regulate breast cancer protein activity. Inhibitors, activators, or modulators also include genetically modified versions of breast cancer proteins, e.g., versions with altered activity, as well as naturally occurring and synthetic ligands, antagonists, agonists, antibodies, small chemical molecules and the like. Such assays for inhibitors and activators include, e.g., expressing the breast cancer protein *in vitro*, in cells, or cell membranes, applying putative modulator compounds, and then determining the functional effects on activity, as described above. Activators and inhibitors of breast cancer can also be identified by incubating breast cancer cells with the test compound and determining increases or decreases in the expression of 1 or more breast cancer proteins, e.g., 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 40, 50 or more breast cancer proteins, such as breast cancer proteins encoded by the sequences set out in Tables 1-25.

Samples or assays comprising breast cancer proteins that are treated with a potential activator, inhibitor, or modulator are compared to control samples without the inhibitor, activator, or modulator to examine the extent of inhibition. Control samples (untreated with inhibitors) are assigned a relative protein activity value of 100%. Inhibition of a polypeptide is achieved when the activity value relative to the control is about 80%, preferably 50%, more preferably 25-0%. Activation of a breast cancer polypeptide is achieved when the activity value relative to the control (untreated with activators) is 110%, more preferably 150%, more preferably 200-500% (i.e., two to five fold higher relative to the control), more preferably 1000-3000% higher.

The phrase "changes in cell growth" refers to any change in cell growth and proliferation characteristics *in vitro* or *in vivo*, such as formation of foci, anchorage independence, semi-solid or soft agar growth, changes in contact inhibition and density limitation of growth, loss of growth factor or serum requirements, changes in cell morphology, gaining or losing immortalization, gaining or losing tumor specific markers, ability to form or suppress tumors when injected into suitable animal hosts, and/or

immortalization of the cell. *See, e.g.,* Freshney, *Culture of Animal Cells a Manual of Basic Technique* pp. 231-241 (3rd ed. 1994).

"Tumor cell" refers to precancerous, cancerous, and normal cells in a tumor.

"Cancer cells," "transformed" cells or "transformation" in tissue culture, refers to spontaneous or induced phenotypic changes that do not necessarily involve the uptake of new genetic material. Although transformation can arise from infection with a transforming virus and incorporation of new genomic DNA, or uptake of exogenous DNA, it can also arise spontaneously or following exposure to a carcinogen, thereby mutating an endogenous gene. Transformation is associated with phenotypic changes, such as immortalization of cells, aberrant growth control, nonmorphological changes, and/or malignancy (*see*, Freshney, *Culture of Animal Cells a Manual of Basic Technique* (3rd ed. 1994)).

"Antibody" refers to a polypeptide comprising a framework region from an immunoglobulin gene or fragments thereof that specifically binds and recognizes an antigen. The recognized immunoglobulin genes include the kappa, lambda, alpha, gamma, delta, epsilon, and mu constant region genes, as well as the myriad immunoglobulin variable region genes. Light chains are classified as either kappa or lambda. Heavy chains are classified as gamma, mu, alpha, delta, or epsilon, which in turn define the immunoglobulin classes, IgG, IgM, IgA, IgD and IgE, respectively. Typically, the antigen-binding region of an antibody or its functional equivalent will be most critical in specificity and affinity of binding. See Paul, *Fundamental Immunology.*

An exemplary immunoglobulin (antibody) structural unit comprises a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair having one "light" (about 25 kD) and one "heavy" chain (about 50-70 kD). The N-terminus of each chain defines a variable region of about 100 to 110 or more amino acids primarily responsible for antigen recognition. The terms variable light chain (V_L) and variable heavy chain (V_H) refer to these light and heavy chains respectively.

Antibodies exist, e.g., as intact immunoglobulins or as a number of well-characterized fragments produced by digestion with various peptidases. Thus, e.g., pepsin digests an antibody below the disulfide linkages in the hinge region to produce $F(ab)'_2$, a dimer of Fab which itself is a light chain joined to V_H-C_H1 by a disulfide bond. The $F(ab)'_2$

may be reduced under mild conditions to break the disulfide linkage in the hinge region, thereby converting the $F(ab)'_2$ dimer into an Fab' monomer. The Fab' monomer is essentially Fab with part of the hinge region (*see Fundamental Immunology* (Paul ed., 3d ed. 1993). While various antibody fragments are defined in terms of the digestion of an intact antibody, one of skill will appreciate that such fragments may be synthesized *de novo* either chemically or by using recombinant DNA methodology. Thus, the term antibody, as used herein, also includes antibody fragments either produced by the modification of whole antibodies, or those synthesized *de novo* using recombinant DNA methodologies (e.g., single chain Fv) or those identified using phage display libraries (*see, e.g.,* McCafferty *et al., Nature* 348:552-554 (1990))

For preparation of antibodies, e.g., recombinant, monoclonal, or polyclonal antibodies, many technique known in the art can be used (*see, e.g.,* Kohler & Milstein, *Nature* 256:495-497 (1975); Kozbor *et al., Immunology Today* 4:72 (1983); Cole *et al.*, pp. 77-96 in *Monoclonal Antibodies and Cancer Therapy* (1985); Coligan, *Current Protocols in Immunology* (1991); Harlow & Lane, *Antibodies, A Laboratory Manual* (1988); and Goding, *Monoclonal Antibodies: Principles and Practice* (2d ed. 1986)). Techniques for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce antibodies to polypeptides of this invention. Also, transgenic mice, or other organisms such as other mammals, may be used to express humanized antibodies. Alternatively, phage display technology can be used to identify antibodies and heteromeric Fab fragments that specifically bind to selected antigens (*see, e.g.,* McCafferty *et al., Nature* 348:552-554 (1990); Marks *et al., Biotechnology* 10:779-783 (1992)).

A "chimeric antibody" is an antibody molecule in which (a) the constant region, or a portion thereof, is altered, replaced or exchanged so that the antigen binding site (variable region) is linked to a constant region of a different or altered class, effector function and/or species, or an entirely different molecule which confers new properties to the chimeric antibody, *e.g.*, an enzyme, toxin, hormone, growth factor, drug, etc.; or (b) the variable region, or a portion thereof, is altered, replaced or exchanged with a variable region having a different or altered antigen specificity.

Identification of breast cancer-associated sequences

In one aspect, the expression levels of genes are determined in different patient samples for which diagnosis information is desired, to provide expression profiles. An expression profile of a particular sample is essentially a "fingerprint" of the state of the sample; while two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is characteristic of the state of the cell. That is, normal tissue (e.g., normal breast or other tissue) may be distinguished from cancerous or metastatic cancerous tissue of the breast, or breast cancer tissue or metastatic breast cancerous tissue can be compared with tissue samples of breast and other tissues from surviving cancer patients. By comparing expression profiles of tissue in known different breast cancer states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained.

The identification of sequences that are differentially expressed in breast cancer versus non-breast cancer tissue allows the use of this information in a number of ways. For example, a particular treatment regime may be evaluated: does a chemotherapeutic drug act to down-regulate breast cancer, and thus tumor growth or recurrence, in a particular patient. Similarly, diagnosis and treatment outcomes may be done or confirmed by comparing patient samples with the known expression profiles. Metastatic tissue can also be analyzed to determine the stage of breast cancer in the tissue. Furthermore, these gene expression profiles (or individual genes) allow screening of drug candidates with an eye to mimicking or altering a particular expression profile; e.g., screening can be done for drugs that suppress the breast cancer expression profile. This may be done by making biochips comprising sets of the important breast cancer genes, which can then be used in these screens. These methods can also be done on the protein basis; that is, protein expression levels of the breast cancer proteins can be evaluated for diagnostic purposes or to screen candidate agents. In addition, the breast cancer nucleic acid sequences can be administered for gene therapy purposes, including the administration of antisense nucleic acids, or the breast cancer proteins (including antibodies and other modulators thereof) administered as therapeutic drugs.

Thus the present invention provides nucleic acid and protein sequences that are differentially expressed in breast cancer, herein termed "breast cancer sequences." As outlined below, breast cancer sequences include those that are up-regulated (i.e., expressed at a higher level) in breast cancer, as well as those that are down-regulated (i.e., expressed at a lower level). In a preferred embodiment, the breast cancer sequences are from humans; however, as will be appreciated by those in the art, breast cancer sequences from other organisms may be useful in animal models of disease and drug evaluation; thus, other breast cancer sequences are provided, from vertebrates, including mammals, including rodents (rats, mice, hamsters, guinea pigs, etc.), primates, farm animals (including sheep, goats, pigs, cows, horses, etc.) and pets, e.g., (dogs, cats, etc.). Breast cancer sequences from other organisms may be obtained using the techniques outlined below.

Breast cancer sequences can include both nucleic acid and amino acid sequences. As will be appreciated by those in the art and is more fully outlined below, breast cancer nucleic acid sequences are useful in a variety of applications, including diagnostic applications, which will detect naturally occurring nucleic acids, as well as screening applications; e.g., biochips comprising nucleic acid probes or PCR microtiter plates with selected probes to the breast cancer sequences can be generated.

A breast cancer sequence can be initially identified by substantial nucleic acid and/or amino acid sequence homology to the breast cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions.

For identifying breast cancer-associated sequences, the breast cancer screen typically includes comparing genes identified in different tissues, e.g., normal and cancerous tissues, or tumor tissue samples from patients who have metastatic disease vs. non metastatic tissue. Other suitable tissue comparisons include comparing breast cancer samples with metastatic cancer samples from other cancers, such as lung, breast, gastrointestinal cancers, ovarian, etc. Samples of different stages of breast cancer, e.g., survivor tissue, drug resistant states, and tissue undergoing metastasis, are applied to biochips comprising nucleic acid probes. The samples are first microdissected, if applicable, and treated as is known in the art

for the preparation of mRNA. Suitable biochips are commercially available, e.g. from Affymetrix. Gene expression profiles as described herein are generated and the data analyzed.

In one embodiment, the genes showing changes in expression as between normal and disease states are compared to genes expressed in other normal tissues, preferably normal breast, but also including, and not limited to lung, heart, brain, liver, breast, kidney, muscle, colon, small intestine, large intestine, spleen, bone and placenta. In a preferred embodiment, those genes identified during the breast cancer screen that are expressed in any significant amount in other tissues are removed from the profile, although in some embodiments, this is not necessary. That is, when screening for drugs, it is usually preferable that the target be disease specific, to minimize possible side effects.

In a preferred embodiment, breast cancer sequences are those that are up-regulated in breast cancer; that is, the expression of these genes is higher in the breast cancer tissue as compared to non-cancerous tissue. "Up-regulation" as used herein often means at least about a two-fold change, preferably at least about a three fold change, with at least about five-fold or higher being preferred. All unigene cluster identification numbers and accession numbers herein are for the GenBank sequence database and the sequences of the accession numbers are hereby expressly incorporated by reference. GenBank is known in the art, *see, e.g.*, Benson, DA, *et al.*, Nucleic Acids Research 26:1-7 (1998) and http://www.ncbi.nlm.nih.gov/. Sequences are also available in other databases, e.g., European Molecular Biology Laboratory (EMBL) and DNA Database of Japan (DDBJ). U.S. Patent Application N. 09/687,576, with the same assignee as the present application, further discloses related sequences, compositions, and methods of diagnosis and treatment of breast cancer is hereby expressly incorporated by reference.

In another preferred embodiment, breast cancer sequences are those that are down-regulated in the breast cancer; that is, the expression of these genes is lower in breast cancer tissue as compared to non-cancerous tissue (*see, e.g.*, Tables 1,2, 3, 15, 16 etc...). "Down-regulation" as used herein often means at least about a two-fold change, preferably at least about a three fold change, with at least about five-fold or higher being preferred.

Informatics

The ability to identify genes that are over or under expressed in breast cancer can additionally provide high-resolution, high-sensitivity datasets which can be used in the areas of diagnostics, therapeutics, drug development, pharmacogenetics, protein structure, biosensor development, and other related areas. For example, the expression profiles can be used in diagnostic or prognostic evaluation of patients with breast cancer. Or as another example, subcellular toxicological information can be generated to better direct drug structure and activity correlation (*see* Anderson, *Pharmaceutical Proteomics: Targets, Mechanism, and Function*, paper presented at the IBC Proteomics conference, Coronado, CA (June 11-12, 1998)). Subcellular toxicological information can also be utilized in a biological sensor device to predict the likely toxicological effect of chemical exposures and likely tolerable exposure thresholds (*see* U.S. Patent No. 5,811,231). Similar advantages accrue from datasets relevant to other biomolecules and bioactive agents (e.g., nucleic acids, saccharides, lipids, drugs, and the like).

Thus, in another embodiment, the present invention provides a database that includes at least one set of assay data. The data contained in the database is acquired, e.g., using array analysis either singly or in a library format. The database can be in substantially any form in which data can be maintained and transmitted, but is preferably an electronic database. The electronic database of the invention can be maintained on any electronic device allowing for the storage of and access to the database, such as a personal computer, but is preferably distributed on a wide area network, such as the World Wide Web.

The focus of the present section on databases that include peptide sequence data is for clarity of illustration only. It will be apparent to those of skill in the art that similar databases can be assembled for any assay data acquired using an assay of the invention.

The compositions and methods for identifying and/or quantitating the relative and/or absolute abundance of a variety of molecular and macromolecular species from a biological sample undergoing breast cancer, i.e., the identification of breast cancer-associated sequences described herein, provide an abundance of information, which can be correlated with pathological conditions, predisposition to disease, drug testing, therapeutic monitoring,

gene-disease causal linkages, identification of correlates of immunity and physiological status, among others. Although the data generated from the assays of the invention is suited for manual review and analysis, in a preferred embodiment, prior data processing using high-speed computers is utilized.

An array of methods for indexing and retrieving biomolecular information is known in the art. For example, U.S. Patents 6,023,659 and 5,966,712 disclose a relational database system for storing biomolecular sequence information in a manner that allows sequences to be catalogued and searched according to one or more protein function hierarchies. U.S. Patent 5,953,727 discloses a relational database having sequence records containing information in a format that allows a collection of partial-length DNA sequences to be catalogued and searched according to association with one or more sequencing projects for obtaining full-length sequences from the collection of partial length sequences. U.S. Patent 5,706,498 discloses a gene database retrieval system for making a retrieval of a gene sequence similar to a sequence data item in a gene database based on the degree of similarity between a key sequence and a target sequence. U.S. Patent 5,538,897 discloses a method using mass spectroscopy fragmentation patterns of peptides to identify amino acid sequences in computer databases by comparison of predicted mass spectra with experimentally-derived mass spectra using a closeness-of-fit measure. U.S. Patent 5,926,818 discloses a multi-dimensional database comprising a functionality for multi-dimensional data analysis described as on-line analytical processing (OLAP), which entails the consolidation of projected and actual data according to more than one consolidation path or dimension. U.S. Patent 5,295,261 reports a hybrid database structure in which the fields of each database record are divided into two classes, navigational and informational data, with navigational fields stored in a hierarchical topological map which can be viewed as a tree structure or as the merger of two or more such tree structures.

See also Mount *et al., Bioinformatics* (2001); *Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids* (Durbin *et al.*, eds., 1999); *Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins* (Baxevanis & Oeullette eds., 1998)); Rashidi & Buehler, *Bioinformatics: Basic Applications in Biological Science and Medicine* (1999); *Introduction to Computational Molecular Biology* (Setubal *et*

al., eds 1997); *Bioinformatics: Methods and Protocols* (Misener & Krawetz, eds, 2000); *Bioinformatics: Sequence, Structure, and Databanks: A Practical Approach* (Higgins & Taylor, eds., 2000); Brown, *Bioinformatics: A Biologist's Guide to Biocomputing and the Internet* (2001); Han & Kamber, *Data Mining: Concepts and Techniques* (2000); and Waterman, *Introduction to Computational Biology: Maps, Sequences, and Genomes* (1995).

The present invention provides a computer database comprising a computer and software for storing in computer-retrievable form assay data records cross-tabulated, e.g., with data specifying the source of the target-containing sample from which each sequence specificity record was obtained.

In an exemplary embodiment, at least one of the sources of target-containing sample is from a control tissue sample known to be free of pathological disorders. In a variation, at least one of the sources is a known pathological tissue specimen, e.g., a neoplastic lesion or another tissue specimen to be analyzed for breast cancer. In another variation, the assay records cross-tabulate one or more of the following parameters for each target species in a sample: (1) a unique identification code, which can include, e.g., a target molecular structure and/or characteristic separation coordinate (e.g., electrophoretic coordinates); (2) sample source; and (3) absolute and/or relative quantity of the target species present in the sample.

The invention also provides for the storage and retrieval of a collection of target data in a computer data storage apparatus, which can include magnetic disks, optical disks, magneto-optical disks, DRAM, SRAM, SGRAM, SDRAM, RDRAM, DDR RAM, magnetic bubble memory devices, and other data storage devices, including CPU registers and on-CPU data storage arrays. Typically, the target data records are stored as a bit pattern in an array of magnetic domains on a magnetizable medium or as an array of charge states or transistor gate states, such as an array of cells in a DRAM device (e.g., each cell comprised of a transistor and a charge storage area, which may be on the transistor). In one embodiment, the invention provides such storage devices, and computer systems built therewith, comprising a bit pattern encoding a protein expression fingerprint record comprising unique identifiers for at least 10 target data records cross-tabulated with target source.

When the target is a peptide or nucleic acid, the invention preferably provides a method for identifying related peptide or nucleic acid sequences, comprising performing a computerized comparison between a peptide or nucleic acid sequence assay record stored in or retrieved from a computer storage device or database and at least one other sequence. The comparison can include a sequence analysis or comparison algorithm or computer program embodiment thereof (e.g., FASTA, TFASTA, GAP, BESTFIT) and/or the comparison may be of the relative amount of a peptide or nucleic acid sequence in a pool of sequences determined from a polypeptide or nucleic acid sample of a specimen.

The invention also preferably provides a magnetic disk, such as an IBM-compatible (DOS, Windows, Windows95/98/2000, Windows NT, OS/2) or other format (e.g., Linux, SunOS, Solaris, AIX, SCO Unix, VMS, MV, Macintosh, etc.) floppy diskette or hard (fixed, Winchester) disk drive, comprising a bit pattern encoding data from an assay of the invention in a file format suitable for retrieval and processing in a computerized sequence analysis, comparison, or relative quantitation method.

The invention also provides a network, comprising a plurality of computing devices linked via a data link, such as an Ethernet cable (coax or 10BaseT), telephone line, ISDN line, wireless network, optical fiber, or other suitable signal transmission medium, whereby at least one network device (e.g., computer, disk array, etc.) comprises a pattern of magnetic domains (e.g., magnetic disk) and/or charge domains (e.g., an array of DRAM cells) composing a bit pattern encoding data acquired from an assay of the invention.

The invention also provides a method for transmitting assay data that includes generating an electronic signal on an electronic communications device, such as a modem, ISDN terminal adapter, DSL, cable modem, ATM switch, or the like, wherein the signal includes (in native or encrypted format) a bit pattern encoding data from an assay or a database comprising a plurality of assay results obtained by the method of the invention.

In a preferred embodiment, the invention provides a computer system for comparing a query target to a database containing an array of data structures, such as an assay result obtained by the method of the invention, and ranking database targets based on the degree of identity and gap weight to the target data. A central processor is preferably initialized to load and execute the computer program for alignment and/or comparison of the

assay results. Data for a query target is entered into the central processor via an I/O device. Execution of the computer program results in the central processor retrieving the assay data from the data file, which comprises a binary description of an assay result.

The target data or record and the computer program can be transferred to secondary memory, which is typically random access memory (e.g., DRAM, SRAM, SGRAM, or SDRAM). Targets are ranked according to the degree of correspondence between a selected assay characteristic (e.g., binding to a selected affinity moiety) and the same characteristic of the query target and results are output via an I/O device. For example, a central processor can be a conventional computer (e.g., Intel Pentium, PowerPC, Alpha, PA-8000, SPARC, MIPS 4400, MIPS 10000, VAX, etc.); a program can be a commercial or public domain molecular biology software package (e.g., UWGCG Sequence Analysis Software, Darwin); a data file can be an optical or magnetic disk, a data server, a memory device (e.g., DRAM, SRAM, SGRAM, SDRAM, EPROM, bubble memory, flash memory, *etc.*); an I/O device can be a terminal comprising a video display and a keyboard, a modem, an ISDN terminal adapter, an Ethernet port, a punched card reader, a magnetic strip reader, or other suitable I/O device.

The invention also preferably provides the use of a computer system, such as that described above, which comprises: (1) a computer; (2) a stored bit pattern encoding a collection of peptide sequence specificity records obtained by the methods of the invention, which may be stored in the computer; (3) a comparison target, such as a query target; and (4) a program for alignment and comparison, typically with rank-ordering of comparison results on the basis of computed similarity values.

Characteristics of breast cancer-associated proteins

Breast cancer proteins of the present invention may be classified as secreted proteins, transmembrane proteins or intracellular proteins. In one embodiment, the breast cancer protein is an intracellular protein. Intracellular proteins may be found in the cytoplasm and/or in the nucleus. Intracellular proteins are involved in all aspects of cellular function and replication (including, e.g., signaling pathways); aberrant expression of such proteins often results in unregulated or disregulated cellular processes (*see, e.g., Molecular*

Biology of the Cell (Alberts, ed., 3rd ed., 1994). For example, many intracellular proteins have enzymatic activity such as protein kinase activity, protein phosphatase activity, protease activity, nucleotide cyclase activity, polymerase activity and the like. Intracellular proteins also serve as docking proteins that are involved in organizing complexes of proteins, or targeting proteins to various subcellular localizations, and are involved in maintaining the structural integrity of organelles.

An increasingly appreciated concept in characterizing proteins is the presence in the proteins of one or more motifs for which defined functions have been attributed. In addition to the highly conserved sequences found in the enzymatic domain of proteins, highly conserved sequences have been identified in proteins that are involved in protein-protein interaction. For example, Src-homology-2 (SH2) domains bind tyrosine-phosphorylated targets in a sequence dependent manner. PTB domains, which are distinct from SH2 domains, also bind tyrosine phosphorylated targets. SH3 domains bind to proline-rich targets. In addition, PH domains, tetratricopeptide repeats and WD domains to name only a few, have been shown to mediate protein-protein interactions. Some of these may also be involved in binding to phospholipids or other second messengers. As will be appreciated by one of ordinary skill in the art, these motifs can be identified on the basis of primary sequence; thus, an analysis of the sequence of proteins may provide insight into both the enzymatic potential of the molecule and/or molecules with which the protein may associate. One useful database is Pfam (protein families), which is a large collection of multiple sequence alignments and hidden Markov models covering many common protein domains. Versions are available via the internet from Washington University in St. Louis, the Sanger Center in England, and the Karolinska Institute in Sweden (*see, e.g.*, Bateman *et al., Nuc. Acids Res.* 28:263-266 (2000); Sonnhammer *et al., Proteins* 28:405-420 (1997); Bateman *et al., Nuc. Acids Res.* 27:260-262 (1999); and Sonnhammer *et al., Nuc. Acids Res.* 26:320-322-(1998)).

In another embodiment, the breast cancer sequences are transmembrane proteins. Transmembrane proteins are molecules that span a phospholipid bilayer of a cell. They may have an intracellular domain, an extracellular domain, or both. The intracellular domains of such proteins may have a number of functions including those already described

for intracellular proteins. For example, the intracellular domain may have enzymatic activity and/or may serve as a binding site for additional proteins. Frequently the intracellular domain of transmembrane proteins serves both roles. For example certain receptor tyrosine kinases have both protein kinase activity and SH2 domains. In addition, autophosphorylation of tyrosines on the receptor molecule itself, creates binding sites for additional SH2 domain containing proteins.

Transmembrane proteins may contain from one to many transmembrane domains. For example, receptor tyrosine kinases, certain cytokine receptors, receptor guanylyl cyclases and receptor serine/threonine protein kinases contain a single transmembrane domain. However, various other proteins including channels and adenylyl cyclases contain numerous transmembrane domains. Many important cell surface receptors such as G protein coupled receptors (GPCRs) are classified as "seven transmembrane domain" proteins, as they contain 7 membrane spanning regions. Characteristics of transmembrane domains include approximately 20 consecutive hydrophobic amino acids that may be followed by charged amino acids. Therefore, upon analysis of the amino acid sequence of a particular protein, the localization and number of transmembrane domains within the protein may be predicted (*see, e.g.* PSORT web site http://psort.nibb.ac.jp/). Important transmembrane protein receptors include, but are not limited to the insulin receptor, insulin-like growth factor receptor, human growth hormone receptor, glucose transporters, transferrin receptor, epidermal growth factor receptor, low density lipoprotein receptor, epidermal growth factor receptor, leptin receptor, interleukin receptors, e.g. IL-1 receptor, IL-2 receptor,

The extracellular domains of transmembrane proteins are diverse; however, conserved motifs are found repeatedly among various extracellular domains. Conserved structure and/or functions have been ascribed to different extracellular motifs. Many extracellular domains are involved in binding to other molecules. In one aspect, extracellular domains are found on receptors. Factors that bind the receptor domain include circulating ligands, which may be peptides, proteins, or small molecules such as adenosine and the like. For example, growth factors such as EGF, FGF and PDGF are circulating growth factors that bind to their cognate receptors to initiate a variety of cellular responses. Other factors include

cytokines, mitogenic factors, neurotrophic factors and the like. Extracellular domains also bind to cell-associated molecules. In this respect, they mediate cell-cell interactions. Cell-associated ligands can be tethered to the cell, e.g., via a glycosylphosphatidylinositol (GPI) anchor, or may themselves be transmembrane proteins. Extracellular domains also associate with the extracellular matrix and contribute to the maintenance of the cell structure.

Breast cancer proteins that are transmembrane are particularly preferred in the present invention as they are readily accessible targets for immunotherapeutics, as are described herein. In addition, as outlined below, transmembrane proteins can be also useful in imaging modalities. Antibodies may be used to label such readily accessible proteins *in situ*. Alternatively, antibodies can also label intracellular proteins, in which case samples are typically permeablized to provide access to intracellular proteins.

It will also be appreciated by those in the art that a transmembrane protein can be made soluble by removing transmembrane sequences, e.g., through recombinant methods. Furthermore, transmembrane proteins that have been made soluble can be made to be secreted through recombinant means by adding an appropriate signal sequence.

In another embodiment, the breast cancer proteins are secreted proteins; the secretion of which can be either constitutive or regulated. These proteins have a signal peptide or signal sequence that targets the molecule to the secretory pathway. Secreted proteins are involved in numerous physiological events; by virtue of their circulating nature, they serve to transmit signals to various other cell types. The secreted protein may function in an autocrine manner (acting on the cell that secreted the factor), a paracrine manner (acting on cells in close proximity to the cell that secreted the factor) or an endocrine manner (acting on cells at a distance). Thus secreted molecules find use in modulating or altering numerous aspects of physiology. Breast cancer proteins that are secreted proteins are particularly preferred in the present invention as they serve as good targets for diagnostic markers, *e.g.*, for blood, plasma, serum, or stool tests.

Use of breast cancer nucleic acids

As described above, breast cancer sequence is initially identified by substantial nucleic acid and/or amino acid sequence homology or linkage to the breast cancer

sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions. Typically, linked sequences on a mRNA are found on the same molecule.

The breast cancer nucleic acid sequences of the invention, e.g., the sequences in Tables 1-25, can be fragments of larger genes, i.e., they are nucleic acid segments. "Genes" in this context includes coding regions, non-coding regions, and mixtures of coding and non-coding regions. Accordingly, as will be appreciated by those in the art, using the sequences provided herein, extended sequences, in either direction, of the breast cancer genes can be obtained, using techniques well known in the art for cloning either longer sequences or the full length sequences; see Ausubel, *et al.*, *supra*. Much can be done by informatics and many sequences can be clustered to include multiple sequences corresponding to a single gene, e.g., systems such as UniGene (see, http://www.ncbi.nlm.nih.gov/UniGene/).

Once the breast cancer nucleic acid is identified, it can be cloned and, if necessary, its constituent parts recombined to form the entire breast cancer nucleic acid coding regions or the entire mRNA sequence. Once isolated from its natural source, e.g., contained within a plasmid or other vector or excised therefrom as a linear nucleic acid segment, the recombinant breast cancer nucleic acid can be further-used as a probe to identify and isolate other breast cancer nucleic acids, e.g., extended coding regions. It can also be used as a "precursor" nucleic acid to make modified or variant breast cancer nucleic acids and proteins.

The breast cancer nucleic acids of the present invention are used in several ways. In a first embodiment, nucleic acid probes to the breast cancer nucleic acids are made and attached to biochips to be used in screening and diagnostic methods, as outlined below, or for administration, e.g., for gene therapy, vaccine, and/or antisense applications. Alternatively, the breast cancer nucleic acids that include coding regions of breast cancer proteins can be put into expression vectors for the expression of breast cancer proteins, again for screening purposes or for administration to a patient.

In a preferred embodiment, nucleic acid probes to breast cancer nucleic acids (both the nucleic acid sequences outlined in the figures and/or the complements thereof) are

made. The nucleic acid probes attached to the biochip are designed to be substantially complementary to the breast cancer nucleic acids, *i.e.* the target sequence (either the target sequence of the sample or to other probe sequences, e.g., in sandwich assays), such that hybridization of the target sequence and the probes of the present invention occurs. As outlined below, this complementarity need not be perfect; there may be any number of base pair mismatches which will interfere with hybridization between the target sequence and the single stranded nucleic acids of the present invention. However, if the number of mutations is so great that no hybridization can occur under even the least stringent of hybridization conditions, the sequence is not a complementary target sequence. Thus, by "substantially complementary" herein is meant that the probes are sufficiently complementary to the target sequences to hybridize under normal reaction conditions, particularly high stringency conditions, as outlined herein.

A nucleic acid probe is generally single stranded but can be partially single and partially double stranded. The strandedness of the probe is dictated by the structure, composition, and properties of the target sequence. In general, the nucleic acid probes range from about 8 to about 100 bases long, with from about 10 to about 80 bases being preferred, and from about 30 to about 50 bases being particularly preferred. That is, generally whole genes are not used. In some embodiments, much longer nucleic acids can be used, up to hundreds of bases.

In a preferred embodiment, more than one probe per sequence is used, with either overlapping probes or probes to different sections of the target being used. That is, two, three, four or more probes, with three being preferred, are used to build in a redundancy for a particular target. The probes can be overlapping (i.e., have some sequence in common), or separate. In some cases, PCR primers may be used to amplify signal for higher sensitivity.

As will be appreciated by those in the art, nucleic acids can be attached or immobilized to a solid support in a wide variety of ways. By "immobilized" and grammatical equivalents herein is meant the association or binding between the nucleic acid probe and the solid support is sufficient to be stable under the conditions of binding, washing, analysis, and removal as outlined below. The binding can typically be covalent or non-covalent. By "non-covalent binding" and grammatical equivalents herein is meant one or more of electrostatic,

hydrophilic, and hydrophobic interactions. Included in non-covalent binding is the covalent attachment of a molecule, such as, streptavidin to the support and the non-covalent binding of the biotinylated probe to the streptavidin. By "covalent binding" and grammatical equivalents herein is meant that the two moieties, the solid support and the probe, are attached by at least one bond, including sigma bonds, pi bonds and coordination bonds. Covalent bonds can be formed directly between the probe and the solid support or can be formed by a cross linker or by inclusion of a specific reactive group on either the solid support or the probe or both molecules. Immobilization may also involve a combination of covalent and non-covalent interactions.

In general, the probes are attached to the biochip in a wide variety of ways, as will be appreciated by those in the art. As described herein, the nucleic acids can either be synthesized first, with subsequent attachment to the biochip, or can be directly synthesized on the biochip.

The biochip comprises a suitable solid substrate. By "substrate" or "solid support" or other grammatical equivalents herein is meant a material that can be modified to contain discrete individual sites appropriate for the attachment or association of the nucleic acid probes and is amenable to at least one detection method. As will be appreciated by those in the art, the number of possible substrates are very large, and include, but are not limited to, glass and modified or functionalized glass, plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, TeflonJ, etc.), polysaccharides, nylon or nitrocellulose, resins, silica or silica-based materials including silicon and modified silicon, carbon, metals, inorganic glasses, plastics, etc. In general, the substrates allow optical detection and do not appreciably fluoresce. A preferred substrate is described in copending application entitled Reusable Low Fluorescent Plastic Biochip, U.S. Application Serial No. 09/270,214, filed March 15, 1999, herein incorporated by reference in its entirety.

Generally the substrate is planar, although as will be appreciated by those in the art, other configurations of substrates may be used as well. For example, the probes may be placed on the inside surface of a tube, for flow-through sample analysis to minimize

sample volume. Similarly, the substrate may be flexible, such as a flexible foam, including closed cell foams made of particular plastics.

In a preferred embodiment, the surface of the biochip and the probe may be derivatized with chemical functional groups for subsequent attachment of the two. Thus, e.g., the biochip is derivatized with a chemical functional group including, but not limited to, amino groups, carboxy groups, oxo groups and thiol groups, with amino groups being particularly preferred. Using these functional groups, the probes can be attached using functional groups on the probes. For example, nucleic acids containing amino groups can be attached to surfaces comprising amino groups, e.g. using linkers as are known in the art; e.g., homo-or hetero-bifunctional linkers as are well known (*see* 1994 Pierce Chemical Company catalog, technical section on cross-linkers, pages 155-200). In addition, in some cases, additional linkers, such as alkyl groups (including substituted and heteroalkyl groups) may be used.

In this embodiment, oligonucleotides are synthesized as is known in the art, and then attached to the surface of the solid support. As will be appreciated by those skilled in the art, either the 5' or 3' terminus may be attached to the solid support, or attachment may be via an internal nucleoside.

In another embodiment, the immobilization to the solid support may be very strong, yet non-covalent. For example, biotinylated oligonucleotides can be made, which bind to surfaces covalently coated with streptavidin, resulting in attachment.

Alternatively, the oligonucleotides may be synthesized on the surface, as is known in the art. For example, photoactivation techniques utilizing photopolymerization compounds and techniques are used. In a preferred embodiment, the nucleic acids can be synthesized in situ, using well known photolithographic techniques, such as those described in WO 95/25116; WO 95/35505; U.S. Patent Nos. 5,700,637 and 5,445,934; and references cited within, all of which are expressly incorporated by reference; these methods of attachment form the basis of the Affimetrix GeneChip™ technology.

Often, amplification-based assays are performed to measure the expression level of breast cancer-associated sequences. These assays are typically performed in conjunction with reverse transcription. In such assays, a breast cancer-associated nucleic acid

sequence acts as a template in an amplification reaction (e.g., Polymerase Chain Reaction, or PCR). In a quantitative amplification, the amount of amplification product will be proportional to the amount of template in the original sample. Comparison to appropriate controls provides a measure of the amount of breast cancer-associated RNA. Methods of quantitative amplification are well known to those of skill in the art. Detailed protocols for quantitative PCR are provided, e.g., in Innis *et al.*, *PCR Protocols, A Guide to Methods and Applications* (1990).

In some embodiments, a TaqMan based assay is used to measure expression. TaqMan based assays use a fluorogenic oligonucleotide probe that contains a 5' fluorescent dye and a 3' quenching agent. The probe hybridizes to a PCR product, but cannot itself be extended due to a blocking agent at the 3' end. When the PCR product is amplified in subsequent cycles, the 5' nuclease activity of the polymerase, *e.g.*, AmpliTaq, results in the cleavage of the TaqMan probe. This cleavage separates the 5' fluorescent dye and the 3' quenching agent, thereby resulting in an increase in fluorescence as a function of amplification (*see*, e.g., literature provided by Perkin-Elmer, *e.g.*, www2.perkin-elmer.com).

Other suitable amplification methods include, but are not limited to, ligase chain reaction (LCR) (*see* Wu & Wallace, *Genomics* 4:560 (1989), Landegren *et al.*, *Science* 241:1077 (1988), and Barringer *et al.*, *Gene* 89:117 (1990)), transcription amplification (Kwoh *et al.*, *Proc. Natl. Acad. Sci. USA* 86:1173 (1989)), self-sustained sequence replication (Guatelli *et al.*, *Proc. Nat. Acad. Sci. USA* 87:1874 (1990)), dot PCR, and linker adapter PCR, etc.

Expression of breast cancer proteins from nucleic acids

In a preferred embodiment, breast cancer nucleic acids, e.g., encoding breast cancer proteins are used to make a variety of expression vectors to express breast cancer proteins which can then be used in screening assays, as described below. Expression vectors and recombinant DNA technology are well known to those of skill in the art (*see, e.g.*, Ausubel, *supra*, and *Gene Expression Systems* (Fernandez & Hoeffler, eds, 1999)) and are used to express proteins. The expression vectors may be either self-replicating extrachromosomal vectors or vectors which integrate into a host genome. Generally, these

expression vectors include transcriptional and translational regulatory nucleic acid operably linked to the nucleic acid encoding the breast cancer protein. The term "control sequences" refers to DNA sequences used for the expression of an operably linked coding sequence in a particular host organism. Control sequences that are suitable for prokaryotes, e.g., include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is typically accomplished by ligation at convenient restriction sites. If such sites do not exist, synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice. Transcriptional and translational regulatory nucleic acid will generally be appropriate to the host cell used to express the breast cancer protein. Numerous types of appropriate expression vectors, and suitable regulatory sequences are known in the art for a variety of host cells.

In general, transcriptional and translational regulatory sequences may include, but are not limited to, promoter sequences, ribosomal binding sites, transcriptional start and stop sequences, translational start and stop sequences, and enhancer or activator sequences. In a preferred embodiment, the regulatory sequences include a promoter and transcriptional start and stop sequences.

Promoter sequences encode either constitutive or inducible promoters. The promoters may be either naturally occurring promoters or hybrid promoters. Hybrid promoters, which combine elements of more than one promoter, are also known in the art, and are useful in the present invention.

In addition, an expression vector may comprise additional elements. For example, the expression vector may have two replication systems, thus allowing it to be maintained in two organisms, e.g. in mammalian or insect cells for expression and in a procaryotic host for cloning and amplification. Furthermore, for integrating expression vectors, the expression vector contains at least one sequence homologous to the host cell genome, and preferably two homologous sequences which flank the expression construct. The integrating vector may be directed to a specific locus in the host cell by selecting the appropriate homologous sequence for inclusion in the vector. Constructs for integrating vectors are well known in the art (e.g., Fernandez & Hoeffler, *supra*).

In addition, in a preferred embodiment, the expression vector contains a selectable marker gene to allow the selection of transformed host cells. Selection genes are well known in the art and will vary with the host cell used.

The breast cancer proteins of the present invention are produced by culturing a host cell transformed with an expression vector containing nucleic acid encoding a breast cancer protein, under the appropriate conditions to induce or cause expression of the breast cancer protein. Conditions appropriate for breast cancer protein expression will vary with the choice of the expression vector and the host cell, and will be easily ascertained by one skilled in the art through routine experimentation or optimization. For example, the use of constitutive promoters in the expression vector will require optimizing the growth and proliferation of the host cell, while the use of an inducible promoter requires the appropriate growth conditions for induction. In addition, in some embodiments, the timing of the harvest is important. For example, the baculoviral systems used in insect cell expression are lytic viruses, and thus harvest time selection can be crucial for product yield.

Appropriate host cells include yeast, bacteria, archaebacteria, fungi, and insect and animal cells, including mammalian cells. Of particular interest are *Saccharomyces cerevisiae* and other yeasts, *E. coli, Bacillus subtilis*, Sf9 cells, C129 cells, 293 cells, *Neurospora*, BHK, CHO, COS, HeLa cells, HUVEC (human umbilical vein endothelial cells), THP1 cells (a macrophage cell line) and various other human cells and cell lines.

In a preferred embodiment, the breast cancer proteins are expressed in mammalian cells. Mammalian expression systems are also known in the art, and include

retroviral and adenoviral systems. One expression vector system is a retroviral vector system such as is generally described in PCT/US97/01019 and PCT/US97/01048, both of which are hereby expressly incorporated by reference. Of particular use as mammalian promoters are the promoters from mammalian viral genes, since the viral genes are often highly expressed and have a broad host range. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter, herpes simplex virus promoter, and the CMV promoter (*see, e.g.*, Fernandez & Hoeffler, *supra*). Typically, transcription termination and polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. Examples of transcription terminator and polyadenlyation signals include those derived form SV40.

The methods of introducing exogenous nucleic acid into mammalian hosts, as well as other hosts, is well known in the art, and will vary with the host cell used. Techniques include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, viral infection, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

In a preferred embodiment, breast cancer proteins are expressed in bacterial systems. Bacterial expression systems are well known in the art. Promoters from bacteriophage may also be used and are known in the art. In addition, synthetic promoters and hybrid promoters are also useful; e.g., the tac promoter is a hybrid of the trp and lac promoter sequences. Furthermore, a bacterial promoter can include naturally occurring promoters of non-bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. In addition to a functioning promoter sequence, an efficient ribosome binding site is desirable. The expression vector may also include a signal peptide sequence that provides for secretion of the breast cancer protein in bacteria. The protein is either secreted into the growth media (gram-positive bacteria) or into the periplasmic space, located between the inner and outer membrane of the cell (gram-negative bacteria). The bacterial expression vector may also include a selectable marker gene to allow for the selection of bacterial strains that have been transformed. Suitable selection genes include genes which

render the bacteria resistant to drugs such as ampicillin, chloramphenicol, erythromycin, kanamycin, neomycin and tetracycline. Selectable markers also include biosynthetic genes, such as those in the histidine, tryptophan and leucine biosynthetic pathways. These components are assembled into expression vectors. Expression vectors for bacteria are well known in the art, and include vectors for *Bacillus subtilis, E. coli, Streptococcus cremoris*, and *Streptococcus lividans*, among others (e.g., Fernandez & Hoeffler, *supra*). The bacterial expression vectors are transformed into bacterial host cells using techniques well known in the art, such as calcium chloride treatment, electroporation, and others.

In one embodiment, breast cancer proteins are produced in insect cells. Expression vectors for the transformation of insect cells, and in particular, baculovirus-based expression vectors, are well known in the art.

In a preferred embodiment, breast cancer protein is produced in yeast cells. Yeast expression systems are well known in the art, and include expression vectors for *Saccharomyces cerevisiae, Candida albicans* and *C. maltosa, Hansenula polymorpha, Kluyveromyces fragilis* and *K. lactis, Pichia guillerimondii and P. pastoris, Schizosaccharomyces pombe*, and *Yarrowia lipolytica*.

The breast cancer protein may also be made as a fusion protein, using techniques well known in the art. Thus, e.g., for the creation of monoclonal antibodies, if the desired epitope is small, the breast cancer protein may be fused to a carrier protein to form an immunogen. Alternatively, the breast cancer protein may be made as a fusion protein to increase expression, or for other reasons. For example, when the breast cancer protein is a breast cancer peptide, the nucleic acid encoding the peptide may be linked to other nucleic acid for expression purposes.

In a preferred embodiment, the breast cancer protein is purified or isolated after expression. Breast cancer proteins may be isolated or purified in a variety of ways known to those skilled in the art depending on what other components are present in the sample. Standard purification methods include electrophoretic, molecular, immunological and chromatographic techniques, including ion exchange, hydrophobic, affinity, and reverse-phase HPLC chromatography, and chromatofocusing. For example, the breast cancer protein may be purified using a standard anti-breast cancer protein antibody column. Ultrafiltration

and diafiltration techniques, in conjunction with protein concentration, are also useful. For general guidance in suitable purification techniques, see Scopes, *Protein Purification* (1982). The degree of purification necessary will vary depending on the use of the breast cancer protein. In some instances no purification will be necessary.

Once expressed and purified if necessary, the breast cancer proteins and nucleic acids are useful in a number of applications. They may be used as immunoselection reagents, as vaccine reagents, as screening agents, etc.

Variants of breast cancer proteins

In one embodiment, the breast cancer proteins are derivative or variant breast cancer proteins as compared to the wild-type sequence. That is, as outlined more fully below, the derivative breast cancer peptide will often contain at least one amino acid substitution, deletion or insertion, with amino acid substitutions being particularly preferred. The amino acid substitution, insertion or deletion may occur at any residue within the breast cancer peptide.

Also included within one embodiment of breast cancer proteins of the present invention are amino acid sequence variants. These variants typically fall into one or more of three classes: substitutional, insertional or deletional variants. These variants ordinarily are prepared by site specific mutagenesis of nucleotides in the DNA encoding the breast cancer protein, using cassette or PCR mutagenesis or other techniques well known in the art, to produce DNA encoding the variant, and thereafter expressing the DNA in recombinant cell culture as outlined above. However, variant breast cancer protein fragments having up to about 100-150 residues may be prepared by in vitro synthesis using established techniques. Amino acid sequence variants are characterized by the predetermined nature of the variation, a feature that sets them apart from naturally occurring allelic or interspecies variation of the breast cancer protein amino acid sequence. The variants typically exhibit the same qualitative biological activity as the naturally occurring analogue, although variants can also be selected which have modified characteristics as will be more fully outlined below.

While the site or region for introducing an amino acid sequence variation is predetermined, the mutation per se need not be predetermined. For example, in order to

optimize the performance of a mutation at a given site, random mutagenesis may be conducted at the target codon or region and the expressed breast cancer variants screened for the optimal combination of desired activity. Techniques for making substitution mutations at predetermined sites in DNA having a known sequence are well known, e.g., M13 primer mutagenesis and PCR mutagenesis. Screening of the mutants is done using assays of breast cancer protein activities.

Amino acid substitutions are typically of single residues; insertions usually will be on the order of from about 1 to 20 amino acids, although considerably larger insertions may be tolerated. Deletions range from about 1 to about 20 residues, although in some cases deletions may be much larger.

Substitutions, deletions, insertions or any combination thereof may be used to arrive at a final derivative. Generally these changes are done on a few amino acids to minimize the alteration of the molecule. However, larger changes may be tolerated in certain circumstances. When small alterations in the characteristics of the breast cancer protein are desired, substitutions are generally made in accordance with the amino acid substitution relationships provided in the definition section.

The variants typically exhibit the same qualitative biological activity and will elicit the same immune response as the naturally-occurring analog, although variants also are selected to modify the characteristics of the breast cancer proteins as needed. Alternatively, the variant may be designed such that the biological activity of the breast cancer protein is altered. For example, glycosylation sites may be altered or removed.

Substantial changes in function or immunological identity are made by selecting substitutions that are less conservative than those described above. For example, substitutions may be made which more significantly affect: the structure of the polypeptide backbone in the area of the alteration, for example the alpha-helical or beta-sheet structure; the charge or hydrophobicity of the molecule at the target site; or the bulk of the side chain. The substitutions which in general are expected to produce the greatest changes in the polypeptide's properties are those in which (a) a hydrophilic residue, e.g. seryl or threonyl is substituted for (or by) a hydrophobic residue, e.g. leucyl, isoleucyl, phenylalanyl, valyl or alanyl; (b) a cysteine or proline is substituted for (or by) any other residue; (c) a residue

having an electropositive side chain, e.g. lysyl, arginyl, or histidyl, is substituted for (or by) an electronegative residue, e.g. glutamyl or aspartyl; or (d) a residue having a bulky side chain, e.g. phenylalanine, is substituted for (or by) one not having a side chain, e.g. glycine.

Covalent modifications of breast cancer polypeptides are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of a breast cancer polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N-or C-terminal residues of a breast cancer polypeptide. Derivatization with bifunctional agents is useful, for instance, for crosslinking breast cancer polypeptides to a water-insoluble support matrix or surface for use in the method for purifying anti-breast cancer polypeptide antibodies or screening assays, as is more fully described below. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, e.g., esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-((p-azidophenyl)dithio)propioimidate.

Other modifications include deamidation of glutaminyl and asparaginyl residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl, threonyl or tyrosyl residues, methylation of the amino groups of the lysine, arginine, and histidine side chains (Creighton, *Proteins: Structure and Molecular Properties*, pp. 79-86 (1983)), acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.

Another type of covalent modification of the breast cancer polypeptide included within the scope of this invention comprises altering the native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native sequence breast cancer polypeptide, and/or adding one or more glycosylation sites that are not present in the native sequence breast cancer polypeptide. Glycosylation patterns can be altered in many ways. For example the use of different cell types to express breast cancer-associated sequences can result in different glycosylation patterns.

Addition of glycosylation sites to breast cancer polypeptides may also be accomplished by altering the amino acid sequence thereof. The alteration may be made, e.g., by the addition of, or substitution by, one or more serine or threonine residues to the native sequence breast cancer polypeptide (for O-linked glycosylation sites). The breast cancer amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the breast cancer polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the breast cancer polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. Such methods are described in the art, e.g., in WO 87/05330, and in Aplin & Wriston, *CRC Crit. Rev. Biochem.*, pp. 259-306 (1981).

Removal of carbohydrate moieties present on the breast cancer polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are known in the art and described, for instance, by Hakimuddin, *et al.*, *Arch. Biochem. Biophys.*, 259:52 (1987) and by Edge *et al.*, *Anal. Biochem.*, 118:131 (1981). Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo-and exo-glycosidases as described by Thotakura *et al.*, *Meth. Enzymol.*, 138:350 (1987).

Another type of covalent modification of breast cancer comprises linking the breast cancer polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol, polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192 or 4,179,337.

Breast cancer polypeptides of the present invention may also be modified in a way to form chimeric molecules comprising a breast cancer polypeptide fused to another, heterologous polypeptide or amino acid sequence. In one embodiment, such a chimeric molecule comprises a fusion of a breast cancer polypeptide with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino-or carboxyl-terminus of the breast cancer polypeptide. The presence of such epitope-tagged forms of a breast cancer polypeptide can be detected using

an antibody against the tag polypeptide. Also, provision of the epitope tag enables the breast cancer polypeptide to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. In an alternative embodiment, the chimeric molecule may comprise a fusion of a breast cancer polypeptide with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule, such a fusion could be to the Fc region of an IgG molecule.

Various tag polypeptides and their respective antibodies are well known in the art. Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; HIS6 and metal chelation tags, the flu HA tag polypeptide and its antibody 12CA5 (Field *et al., Mol. Cell. Biol.* 8:2159-2165 (1988)); the c-myc tag and the 8F9, 3C7, 6E10, G4, B7 and 9E10 antibodies thereto (Evan *et al., Molecular and Cellular Biology* 5:3610-3616 (1985)); and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody (*Paborsky et al., Protein Engineering* 3(6):547-553 (1990)). Other tag polypeptides include the Flag-peptide (*Hopp et al., BioTechnology* 6:1204-1210 (1988)); the KT3 epitope peptide (Martin *et al., Science* 255:192-194 (1992)); tubulin epitope peptide (Skinner *et al., J. Biol. Chem.* 266:15163-15166 (1991)); and the T7 gene 10 protein peptide tag (Lutz-Freyermuth *et al., Proc. Natl. Acad. Sci. USA* 87:6393-6397 (1990)).

Also included are other breast cancer proteins of the breast cancer family, and breast cancer proteins from other organisms, which are cloned and expressed as outlined below. Thus, probe or degenerate polymerase chain reaction (PCR) primer sequences may be used to find other related breast cancer proteins from humans or other organisms. As will be appreciated by those in the art, particularly useful probe and/or PCR primer sequences include the unique areas of the breast cancer nucleic acid sequence. As is generally known in the art, preferred PCR primers are from about 15 to about 35 nucleotides in length, with from about 20 to about 30 being preferred, and may contain inosine as needed. The conditions for the PCR reaction are well known in the art (e.g., Innis, PCR Protocols, *supra*).

Antibodies to breast cancer proteins

In a preferred embodiment, when the breast cancer protein is to be used to generate antibodies, e.g., for immunotherapy or immunodiagnosis, the breast cancer protein

should share at least one epitope or determinant with the full length protein. By "epitope" or "determinant" herein is typically meant a portion of a protein which will generate and/or bind an antibody or T-cell receptor in the context of MHC. Thus, in most instances, antibodies made to a smaller breast cancer protein will be able to bind to the full-length protein, particularly linear epitopes. In a preferred embodiment, the epitope is unique; that is, antibodies generated to a unique epitope show little or no cross-reactivity.

Methods of preparing polyclonal antibodies are known to the skilled artisan (e.g., Coligan, *supra*; and Harlow & Lane, *supra*). Polyclonal antibodies can be raised in a mammal, e.g., by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include a protein encoded by a nucleic acid of the figures or fragment thereof or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Examples of adjuvants which may be employed include Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). The immunization protocol may be selected by one skilled in the art without undue experimentation.

The antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler & Milstein, *Nature* 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized in vitro. The immunizing agent will typically include a polypeptide encoded by a nucleic acid of Tables 1-25 or fragment thereof, or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene

glycol, to form a hybridoma cell (Goding, *Monoclonal Antibodies: Principles and Practice*, pp. 59-103 (1986)). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

In one embodiment, the antibodies are bispecific antibodies. Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens or that have binding specificities for two epitopes on the same antigen. In one embodiment, one of the binding specificities is for a protein encoded by a nucleic acid Tables 1-25 or a fragment thereof, the other one is for any other antigen, and preferably for a cell-surface protein or receptor or receptor subunit, preferably one that is tumor specific. Alternatively, tetramer-type technology may create multivalent reagents.

In a preferred embodiment, the antibodies to breast cancer protein are capable of reducing or eliminating a biological function of a breast cancer protein, as is described below. That is, the addition of anti-breast cancer protein antibodies (either polyclonal or preferably monoclonal) to breast cancer tissue (or cells containing breast cancer) may reduce or eliminate the breast cancer. Generally, at least a 25% decrease in activity, growth, size or the like is preferred, with at least about 50% being particularly preferred and about a 95-100% decrease being especially preferred.

In a preferred embodiment the antibodies to the breast cancer proteins are humanized antibodies (e.g., Xenerex Biosciences, Mederex, Inc., Abgenix, Inc., Protein Design Labs,Inc.) Humanized forms of non-human (e.g., murine) antibodies are chimeric molecules of immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')2 or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include

human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, a humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework (FR) regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones *et al.*, *Nature* 321:522-525 (1986); Riechmann *et al.*, *Nature* 332:323-329 (1988); and Presta, *Curr. Op. Struct. Biol.* 2:593-596 (1992)). Humanization can be essentially performed following the method of Winter and co-workers (Jones *et al.*, *Nature* 321:522-525 (1986); Riechmann *et al.*, *Nature* 332:323-327 (1988); Verhoeyen *et al.*, *Science* 239:1534-1536 (1988)), by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. Accordingly, such humanized antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species.

Human antibodies can also be produced using various techniques known in the art, including phage display libraries (Hoogenboom & Winter, *J. Mol. Biol.* 227:381 (1991); Marks *et al.*, *J. Mol. Biol.* 222:581 (1991)). The techniques of Cole *et al.* and Boerner *et al.* are also available for the preparation of human monoclonal antibodies (Cole *et al.*, *Monoclonal Antibodies and Cancer Therapy*, p. 77 (1985) and Boerner *et al.*, *J. Immunol.* 147(1):86-95 (1991)). Similarly, human antibodies can be made by introducing of human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all

respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, e.g., in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in the following scientific publications: Marks *et al.*, *Bio/Technology* 10:779-783 (1992); Lonberg *et al.*, *Nature* 368:856-859 (1994); Morrison, *Nature* 368:812-13 (1994); Fishwild *et al.*, *Nature Biotechnology* 14:845-51 (1996); Neuberger, *Nature Biotechnology* 14:826 (1996); Lonberg & Huszar, *Intern. Rev. Immunol.* 13:65-93 (1995).

By immunotherapy is meant treatment of breast cancer with an antibody raised against breast cancer proteins. As used herein, immunotherapy can be passive or active. Passive immunotherapy as defined herein is the passive transfer of antibody to a recipient (patient). Active immunization is the induction of antibody and/or T-cell responses in a recipient (patient). Induction of an immune response is the result of providing the recipient with an antigen to which antibodies are raised. As appreciated by one of ordinary skill in the art, the antigen may be provided by injecting a polypeptide against which antibodies are desired to be raised into a recipient, or contacting the recipient with a nucleic acid capable of expressing the antigen and under conditions for expression of the antigen, leading to an immune response.

In a preferred embodiment the breast cancer proteins against which antibodies are raised are secreted proteins as described above. Without being bound by theory, antibodies used for treatment, bind and prevent the secreted protein from binding to its receptor, thereby inactivating the secreted breast cancer protein.

In another preferred embodiment, the breast cancer protein to which antibodies are raised is a transmembrane protein. Without being bound by theory, antibodies used for treatment, bind the extracellular domain of the breast cancer protein and prevent it from binding to other proteins, such as circulating ligands or cell-associated molecules. The antibody may cause down-regulation of the transmembrane breast cancer protein. As will be appreciated by one of ordinary skill in the art, the antibody may be a competitive, non-competitive or uncompetitive inhibitor of protein binding to the extracellular domain of the breast cancer protein. The antibody is also an antagonist of the breast cancer protein. Further, the antibody prevents activation of the transmembrane breast cancer protein. In one aspect, when the antibody prevents the binding of other molecules to the breast cancer

protein, the antibody prevents growth of the cell. The antibody may also be used to target or sensitize the cell to cytotoxic agents, including, but not limited to TNF-α, TNF-β, IL-1, INF-γ and IL-2, or chemotherapeutic agents including 5FU, vinblastine, actinomycin D, cisplatin, methotrexate, and the like. In some instances the antibody belongs to a sub-type that activates serum complement when complexed with the transmembrane protein thereby mediating cytotoxicity or antigen-dependent cytotoxicity (ADCC). Thus, breast cancer is treated by administering to a patient antibodies directed against the transmembrane breast cancer protein. Antibody-labeling may activate a co-toxin, localize a toxin payload, or otherwise provide means to locally ablate cells.

In another preferred embodiment, the antibody is conjugated to an effector moiety. The effector moiety can be any number of molecules, including labelling moieties such as radioactive labels or fluorescent labels, or can be a therapeutic moiety. In one aspect the therapeutic moiety is a small molecule that modulates the activity of the breast cancer protein. In another aspect the therapeutic moiety modulates the activity of molecules associated with or in close proximity to the breast cancer protein. The therapeutic moiety may inhibit enzymatic activity such as protease or collagenase or protein kinase activity associated with breast cancer.

In a preferred embodiment, the therapeutic moiety can also be a cytotoxic agent. In this method, targeting the cytotoxic agent to breast cancer tissue or cells, results in a reduction in the number of afflicted cells, thereby reducing symptoms associated with breast cancer. Cytotoxic agents are numerous and varied and include, but are not limited to, cytotoxic drugs or toxins or active fragments of such toxins. Suitable toxins and their corresponding fragments include diphtheria A chain, exotoxin A chain, ricin A chain, abrin A chain, curcin, crotin, phenomycin, enomycin and the like. Cytotoxic agents also include radiochemicals made by conjugating radioisotopes to antibodies raised against breast cancer proteins, or binding of a radionuclide to a chelating agent that has been covalently attached to the antibody. Targeting the therapeutic moiety to transmembrane breast cancer proteins not only serves to increase the local concentration of therapeutic moiety in the breast cancer afflicted area, but also serves to reduce deleterious side effects that may be associated with the therapeutic moiety.

In another preferred embodiment, the breast cancer protein against which the antibodies are raised is an intracellular protein. In this case, the antibody may be conjugated to a protein which facilitates entry into the cell. In one case, the antibody enters the cell by endocytosis. In another embodiment, a nucleic acid encoding the antibody is administered to the individual or cell. Moreover, wherein the breast cancer protein can be targeted within a cell, i.e., the nucleus, an antibody thereto contains a signal for that target localization, i.e., a nuclear localization signal.

The breast cancer antibodies of the invention specifically bind to breast cancer proteins. By "specifically bind" herein is meant that the antibodies bind to the protein with a K_d of at least about 0.1 mM, more usually at least about 1 μM, preferably at least about 0.1 μM or better, and most preferably, 0.01 μM or better. Selectivity of binding is also important.

Detection of breast cancer sequence for diagnostic and therapeutic applications

In one aspect, the RNA expression levels of genes are determined for different cellular states in the breast cancer phenotype. Expression levels of genes in normal tissue (i.e., not undergoing breast cancer) and in breast cancer tissue (and in some cases, for varying severities of breast cancer that relate to prognosis, as outlined below) are evaluated to provide expression profiles. An expression profile of a particular cell state or point of development is essentially a "fingerprint" of the state. While two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is reflective of the state of the cell. By comparing expression profiles of cells in different states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. Then, diagnosis may be performed or confirmed to determine whether a tissue sample has the gene expression profile of normal or cancerous tissue. This will provide for molecular diagnosis of related conditions.

"Differential expression," or grammatical equivalents as used herein, refers to qualitative or quantitative differences in the temporal and/or cellular gene expression patterns within and among cells and tissue. Thus, a differentially expressed gene can

qualitatively have its expression altered, including an activation or inactivation, in, e.g., normal versus breast cancer tissue. Genes may be turned on or turned off in a particular state, relative to another state thus permitting comparison of two or more states. A qualitatively regulated gene will exhibit an expression pattern within a state or cell type which is detectable by standard techniques. Some genes will be expressed in one state or cell type, but not in both. Alternatively, the difference in expression may be quantitative, e.g., in that expression is increased or decreased; i.e., gene expression is either upregulated, resulting in an increased amount of transcript, or downregulated, resulting in a decreased amount of transcript. The degree to which expression differs need only be large enough to quantify via standard characterization techniques as outlined below, such as by use of Affymetrix GeneChip™ expression arrays, Lockhart, *Nature Biotechnology* 14:1675-1680 (1996), hereby expressly incorporated by reference. Other techniques include, but are not limited to, quantitative reverse transcriptase PCR, northern analysis and RNase protection. As outlined above, preferably the change in expression (i.e., upregulation or downregulation) is at least about 50%, more preferably at least about 100%, more preferably at least about 150%, more preferably at least about 200%, with from 300 to at least 1000% being especially preferred.

Evaluation may be at the gene transcript, or the protein level. The amount of gene expression may be monitored using nucleic acid probes to the DNA or RNA equivalent of the gene transcript, and the quantification of gene expression levels, or, alternatively, the final gene product itself (protein) can be monitored, e.g., with antibodies to the breast cancer protein and standard immunoassays (ELISAs, etc.) or other techniques, including mass spectroscopy assays, 2D gel electrophoresis assays, etc. Proteins corresponding to breast cancer genes, i.e., those identified as being important in a breast cancer phenotype, can be evaluated in a breast cancer diagnostic test.

In a preferred embodiment, gene expression monitoring is performed simultaneously on a number of genes. Multiple protein expression monitoring can be performed as well. Similarly, these assays may be performed on an individual basis as well.

In this embodiment, the breast cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of breast cancer sequences in

a particular cell. The assays are further described below in the example. PCR techniques can be used to provide greater sensitivity.

In a preferred embodiment nucleic acids encoding the breast cancer protein are detected. Although DNA or RNA encoding the breast cancer protein may be detected, of particular interest are methods wherein an mRNA encoding a breast cancer protein is detected. Probes to detect mRNA can be a nucleotide/deoxynucleotide probe that is complementary to and hybridizes with the mRNA and includes, but is not limited to, oligonucleotides, cDNA or RNA. Probes also should contain a detectable label, as defined herein. In one method the mRNA is detected after immobilizing the nucleic acid to be examined on a solid support such as nylon membranes and hybridizing the probe with the sample. Following washing to remove the non-specifically bound probe, the label is detected. In another method detection of the mRNA is performed in situ. In this method permeabilized cells or tissue samples are contacted with a detectably labeled nucleic acid probe for sufficient time to allow the probe to hybridize with the target mRNA. Following washing to remove the non-specifically bound probe, the label is detected. For example a digoxygenin labeled riboprobe (RNA probe) that is complementary to the mRNA encoding a breast cancer protein is detected by binding the digoxygenin with an anti-digoxygenin secondary antibody and developed with nitro blue tetrazolium and 5-bromo-4-chloro-3-indoyl phosphate.

In a preferred embodiment, various proteins from the three classes of proteins as described herein (secreted, transmembrane or intracellular proteins) are used in diagnostic assays. The breast cancer proteins, antibodies, nucleic acids, modified proteins and cells containing breast cancer sequences are used in diagnostic assays. This can be performed on an individual gene or corresponding polypeptide level. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes and/or corresponding polypeptides.

As described and defined herein, breast cancer proteins, including intracellular, transmembrane or secreted proteins, find use as markers of breast cancer. Detection of these proteins in putative breast cancer tissue allows for detection or diagnosis

of breast cancer. In one embodiment, antibodies are used to detect breast cancer proteins. A preferred method separates proteins from a sample by electrophoresis on a gel (typically a denaturing and reducing protein gel, but may be another type of gel, including isoelectric focusing gels and the like). Following separation of proteins, the breast cancer protein is detected, e.g., by immunoblotting with antibodies raised against the breast cancer protein. Methods of immunoblotting are well known to those of ordinary skill in the art.

In another preferred method, antibodies to the breast cancer protein find use in *in situ* imaging techniques, e.g., in histology (e.g., *Methods in Cell Biology: Antibodies in Cell Biology*, volume 37 (Asai, ed. 1993)). In this method cells are contacted with from one to many antibodies to the breast cancer protein(s). Following washing to remove non-specific antibody binding, the presence of the antibody or antibodies is detected. In one embodiment the antibody is detected by incubating with a secondary antibody that contains a detectable label. In another method the primary antibody to the breast cancer protein(s) contains a detectable label, e.g. an enzyme marker that can act on a substrate. In another preferred embodiment each one of multiple primary antibodies contains a distinct and detectable label. This method finds particular use in simultaneous screening for a plurality of breast cancer proteins. As will be appreciated by one of ordinary skill in the art, many other histological imaging techniques are also provided by the invention.

In a preferred embodiment the label is detected in a fluorometer which has the ability to detect and distinguish emissions of different wavelengths. In addition, a fluorescence activated cell sorter (FACS) can be used in the method.

In another preferred embodiment, antibodies find use in diagnosing breast cancer from blood, serum, plasma, stool, and other samples. Such samples, therefore, are useful as samples to be probed or tested for the presence of breast cancer proteins. Antibodies can be used to detect a breast cancer protein by previously described immunoassay techniques including ELISA, immunoblotting (western blotting), immunoprecipitation, BIACORE technology and the like. Conversely, the presence of antibodies may indicate an immune response against an endogenous breast cancer protein.

In a preferred embodiment, *in situ* hybridization of labeled breast cancer nucleic acid probes to tissue arrays is done. For example, arrays of tissue samples, including

breast cancer tissue and/or normal tissue, are made. *In situ* hybridization (*see, e.g.,* Ausubel, *supra*) is then performed. When comparing the fingerprints between an individual and a standard, the skilled artisan can make a diagnosis, a prognosis, or a prediction based on the findings. It is further understood that the genes which indicate the diagnosis may differ from those which indicate the prognosis and molecular profiling of the condition of the cells may lead to distinctions between responsive or refractory conditions or may be predictive of outcomes.

In a preferred embodiment, the breast cancer proteins, antibodies, nucleic acids, modified proteins and cells containing breast cancer sequences are used in prognosis assays. As above, gene expression profiles can be generated that correlate to breast cancer, in terms of long term prognosis. Again, this may be done on either a protein or gene level, with the use of genes being preferred. As above, breast cancer probes may be attached to biochips for the detection and quantification of breast cancer sequences in a tissue or patient. The assays proceed as outlined above for diagnosis. PCR method may provide more sensitive and accurate quantification.

Assays for therapeutic compounds

In a preferred embodiment members of the proteins, nucleic acids, and antibodies as described herein are used in drug screening assays. The breast cancer proteins, antibodies, nucleic acids, modified proteins and cells containing breast cancer sequences are used in drug screening assays or by evaluating the effect of drug candidates on a "gene expression profile" or expression profile of polypeptides. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent (e.g., Zlokarnik, *et al.*, *Science* 279:84-8 (1998); Heid, *Genome Res* 6:986-94, 1996).

In a preferred embodiment, the breast cancer proteins, antibodies, nucleic acids, modified proteins and cells containing the native or modified breast cancer proteins are used in screening assays. That is, the present invention provides novel methods for screening for compositions which modulate the breast cancer phenotype or an identified physiological function of a breast cancer protein. As above, this can be done on an individual gene level or

by evaluating the effect of drug candidates on a "gene expression profile". In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent, see Zlokarnik, *supra.*

Having identified the differentially expressed genes herein, a variety of assays may be executed. In a preferred embodiment, assays may be run on an individual gene or protein level. That is, having identified a particular gene as up regulated in breast cancer, test compounds can be screened for the ability to modulate gene expression or for binding to the breast cancer protein. "Modulation" thus includes both an increase and a decrease in gene expression. The preferred amount of modulation will depend on the original change of the gene expression in normal versus tissue undergoing breast cancer, with changes of at least 10%, preferably 50%, more preferably 100-300%, and in some embodiments 300-1000% or greater. Thus, if a gene exhibits a 4-fold increase in breast cancer tissue compared to normal tissue, a decrease of about four-fold is often desired; similarly, a 10-fold decrease in breast cancer tissue compared to normal tissue often provides a target value of a 10-fold increase in expression to be induced by the test compound.

The amount of gene expression may be monitored using nucleic acid probes and the quantification of gene expression levels, or, alternatively, the gene product itself can be monitored, e.g., through the use of antibodies to the breast cancer protein and standard immunoassays. Proteomics and separation techniques may also allow quantification of expression.

In a preferred embodiment, gene expression or protein monitoring of a number of entities, i.e., an expression profile, is monitored simultaneously. Such profiles will typically involve a plurality of those entities described herein..

In this embodiment, the breast cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of breast cancer sequences in a particular cell. Alternatively, PCR may be used. Thus, a series, e.g., of microtiter plate, may be used with dispensed primers in desired wells. A PCR reaction can then be performed and analyzed for each well.

Expression monitoring can be performed to identify compounds that modify the expression of one or more breast cancer-associated sequences, e.g., a polynucleotide sequence set out inTable 17. Generally, in a preferred embodiment, a test modulator is added to the cells prior to analysis. Moreover, screens are also provided to identify agents that modulate breast cancer, modulate breast cancer proteins, bind to a breast cancer protein, or interfere with the binding of a breast cancer protein and an antibody or other binding partner.

The term "test compound" or "drug candidate" or "modulator" or grammatical equivalents as used herein describes any molecule, e.g., protein, oligopeptide, small organic molecule, polysaccharide, polynucleotide, etc., to be tested for the capacity to directly or indirectly alter the breast cancer phenotype or the expression of a breast cancer sequence, e.g., a nucleic acid or protein sequence. In preferred embodiments, modulators alter expression profiles, or expression profile nucleic acids or proteins provided herein. In one embodiment, the modulator suppresses a breast cancer phenotype, e.g. to a normal tissue fingerprint. In another embodiment, a modulator induced a breast cancer phenotype. Generally, a plurality of assay mixtures are run in parallel with different agent concentrations to obtain a differential response to the various concentrations. Typically, one of these concentrations serves as a negative control, i.e., at zero concentration or below the level of detection.

Drug candidates encompass numerous chemical classes, though typically they are organic molecules, preferably small organic compounds having a molecular weight of more than 100 and less than about 2,500 daltons. Preferred small molecules are less than 2000, or less than 1500 or less than 1000 or less than 500 D. Candidate agents comprise functional groups necessary for structural interaction with proteins, particularly hydrogen bonding, and typically include at least an amine, carbonyl, hydroxyl or carboxyl group, preferably at least two of the functional chemical groups. The candidate agents often comprise cyclical carbon or heterocyclic structures and/or aromatic or polyaromatic structures substituted with one or more of the above functional groups. Candidate agents are also found among biomolecules including peptides, saccharides, fatty acids, steroids, purines, pyrimidines, derivatives, structural analogs or combinations thereof. Particularly preferred are peptides.

In one aspect, a modulator will neutralize the effect of a breast cancer protein. By "neutralize" is meant that activity of a protein is inhibited or blocked and the consequent effect on the cell.

In certain embodiments, combinatorial libraries of potential modulators will be screened for an ability to bind to a breast cancer polypeptide or to modulate activity. Conventionally, new chemical entities with useful properties are generated by identifying a chemical compound (called a "lead compound") with some desirable property or activity, e.g., inhibiting activity, creating variants of the lead compound, and evaluating the property and activity of those variant compounds. Often, high throughput screening (HTS) methods are employed for such an analysis.

In one preferred embodiment, high throughput screening methods involve providing a library containing a large number of potential therapeutic compounds (candidate compounds). Such "combinatorial chemical libraries" are then screened in one or more assays to identify those library members (particular chemical species or subclasses) that display a desired characteristic activity. The compounds thus identified can serve as conventional "lead compounds" or can themselves be used as potential or actual therapeutics.

A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis by combining a number of chemical "building blocks" such as reagents. For example, a linear combinatorial chemical library, such as a polypeptide (e.g., mutein) library, is formed by combining a set of chemical building blocks called amino acids in every possible way for a given compound length (i.e., the number of amino acids in a polypeptide compound). Millions of chemical compounds can be synthesized through such combinatorial mixing of chemical building blocks (Gallop *et al., J. Med. Chem.* 37(9):1233-1251 (1994)).

Preparation and screening of combinatorial chemical libraries is well known to those of skill in the art. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (*see, e.g.,* U.S. Patent No. 5,010,175, Furka, *Pept. Prot. Res.* 37:487-493 (1991), Houghton *et al., Nature,* 354:84-88 (1991)), peptoids (PCT Publication No WO 91/19735), encoded peptides (PCT Publication WO 93/20242), random bio-oligomers (PCT Publication WO 92/00091), benzodiazepines (U.S. Pat. No. 5,288,514), diversomers such as

hydantoins, benzodiazepines and dipeptides (Hobbs *et al., Proc. Nat. Acad. Sci. USA* 90:6909-6913 (1993)), vinylogous polypeptides (Hagihara *et al., J. Amer. Chem. Soc.* 114:6568 (1992)), nonpeptidal peptidomimetics with a Beta-D-Glucose scaffolding (Hirschmann *et al., J. Amer. Chem. Soc.* 114:9217-9218 (1992)), analogous organic syntheses of small compound libraries (Chen *et al., J. Amer. Chem.* Soc. 116:2661 (1994)), oligocarbamates (Cho, *et al., Science* 261:1303 (1993)), and/or peptidyl phosphonates (Campbell *et al., J. Org. Chem.* 59:658 (1994)). *See, generally,* Gordon *et al., J. Med. Chem.* 37:1385 (1994), nucleic acid libraries (*see, e.g.*, Strategene, Corp.), peptide nucleic acid libraries (*see, e.g.*, U.S. Patent 5,539,083), antibody libraries (*see, e.g.*, Vaughn *et al., Nature Biotechnology* 14(3):309-314 (1996), and PCT/US96/10287), carbohydrate libraries (*see, e.g.*, Liang *et al., Science* 274:1520-1522 (1996), and U.S. Patent No. 5,593,853), and small organic molecule libraries (*see, e.g.*, benzodiazepines, Baum, C&EN, Jan 18, page 33 (1993); isoprenoids, U.S. Patent No. 5,569,588; thiazolidinones and metathiazanones, U.S. Patent No. 5,549,974; pyrrolidines, U.S. Patent Nos. 5,525,735 and 5,519,134; morpholino compounds, U.S. Patent No. 5,506,337; benzodiazepines, U.S. Patent No. 5,288,514; and the like).

Devices for the preparation of combinatorial libraries are commercially available (*see, e.g.*, 357 MPS, 390 MPS, Advanced Chem Tech, Louisville KY, Symphony, Rainin, Woburn, MA, 433A Applied Biosystems, Foster City, CA, 9050 Plus, Millipore, Bedford, MA).

A number of well known robotic systems have also been developed for solution phase chemistries. These systems include automated workstations like the automated synthesis apparatus developed by Takeda Chemical Industries, LTD. (Osaka, Japan) and many robotic systems utilizing robotic arms (Zymate II, Zymark Corporation, Hopkinton, Mass.; Orca, Hewlett-Packard, Palo Alto, Calif.), which mimic the manual synthetic operations performed by a chemist. Any of the above devices are suitable for use with the present invention. The nature and implementation of modifications to these devices (if any) so that they can operate as discussed herein will be apparent to persons skilled in the relevant art. In addition, numerous combinatorial libraries are themselves commercially available (*see, e.g.*, ComGenex, Princeton, N.J., Asinex, Moscow, Ru, Tripos, Inc., St. Louis,

MO, ChemStar, Ltd, Moscow, RU, 3D Pharmaceuticals, Exton, PA, Martek Biosciences, Columbia, MD, *etc.*).

The assays to identify modulators are amenable to high throughput screening. Preferred assays thus detect enhancement or inhibition of breast cancer gene transcription, inhibition or enhancement of polypeptide expression, and inhibition or enhancement of polypeptide activity.

High throughput assays for the presence, absence, quantification, or other properties of particular nucleic acids or protein products are well known to those of skill in the art. Similarly, binding assays and reporter gene assays are similarly well known. Thus, e.g., U.S. Patent No. 5,559,410 discloses high throughput screening methods for proteins, U.S. Patent No. 5,585,639 discloses high throughput screening methods for nucleic acid binding (i.e., in arrays), while U.S. Patent Nos. 5,576,220 and 5,541,061 disclose high throughput methods of screening for ligand/antibody binding.

In addition, high throughput screening systems are commercially available (*see, e.g.*, Zymark Corp., Hopkinton, MA; Air Technical Industries, Mentor, OH; Beckman Instruments, Inc. Fullerton, CA; Precision Systems, Inc., Natick, MA, *etc.*). These systems typically automate entire procedures, including all sample and reagent pipetting, liquid dispensing, timed incubations, and final readings of the microplate in detector(s) appropriate for the assay. These configurable systems provide high throughput and rapid start up as well as a high degree of flexibility and customization. The manufacturers of such systems provide detailed protocols for various high throughput systems. Thus, e.g., Zymark Corp. provides technical bulletins describing screening systems for detecting the modulation of gene transcription, ligand binding, and the like.

In one embodiment, modulators are proteins, often naturally occurring proteins or fragments of naturally occurring proteins. Thus, *e.g.*, cellular extracts containing proteins, or random or directed digests of proteinaceous cellular extracts, may be used. In this way libraries of proteins may be made for screening in the methods of the invention. Particularly preferred in this embodiment are libraries of bacterial, fungal, viral, and mammalian proteins, with the latter being preferred, and human proteins being especially

preferred. Particularly useful test compound will be directed to the class of proteins to which the target belongs, *e.g.*, substrates for enzymes or ligands and receptors.

In a preferred embodiment, modulators are peptides of from about 5 to about 30 amino acids, with from about 5 to about 20 amino acids being preferred, and from about 7 to about 15 being particularly preferred. The peptides may be digests of naturally occurring proteins as is outlined above, random peptides, or "biased" random peptides. By "randomized" or grammatical equivalents herein is meant that each nucleic acid and peptide consists of essentially random nucleotides and amino acids, respectively. Since generally these random peptides (or nucleic acids, discussed below) are chemically synthesized, they may incorporate any nucleotide or amino acid at any position. The synthetic process can be designed to generate randomized proteins or nucleic acids, to allow the formation of all or most of the possible combinations over the length of the sequence, thus forming a library of randomized candidate bioactive proteinaceous agents.

In one embodiment, the library is fully randomized, with no sequence preferences or constants at any position. In a preferred embodiment, the library is biased. That is, some positions within the sequence are either held constant, or are selected from a limited number of possibilities. For example, in a preferred embodiment, the nucleotides or amino acid residues are randomized within a defined class, e.g., of hydrophobic amino acids, hydrophilic residues, sterically biased (either small or large) residues, towards the creation of nucleic acid binding domains, the creation of cysteines, for cross-linking, prolines for SH-3 domains, serines, threonines, tyrosines or histidines for phosphorylation sites, etc., or to purines, etc.

Modulators of breast cancer can also be nucleic acids, as defined above.

As described above generally for proteins, nucleic acid modulating agents may be naturally occurring nucleic acids, random nucleic acids, or "biased" random nucleic acids. For example, digests of procaryotic or eucaryotic genomes may be used as is outlined above for proteins.

In a preferred embodiment, the candidate compounds are organic chemical moieties, a wide variety of which are available in the literature.

After the candidate agent has been added and the cells allowed to incubate for some period of time, the sample containing a target sequence to be analyzed is added to the biochip. If required, the target sequence is prepared using known techniques. For example, the sample may be treated to lyse the cells, using known lysis buffers, electroporation, etc., with purification and/or amplification such as PCR performed as appropriate. For example, an *in vitro* transcription with labels covalently attached to the nucleotides is performed. Generally, the nucleic acids are labeled with biotin-FITC or PE, or with cy3 or cy5.

In a preferred embodiment, the target sequence is labeled with, e.g., a fluorescent, a chemiluminescent, a chemical, or a radioactive signal, to provide a means of detecting the target sequence's specific binding to a probe. The label also can be an enzyme, such as, alkaline phosphatase or horseradish peroxidase, which when provided with an appropriate substrate produces a product that can be detected. Alternatively, the label can be a labeled compound or small molecule, such as an enzyme inhibitor, that binds but is not catalyzed or altered by the enzyme. The label also can be a moiety or compound, such as, an epitope tag or biotin which specifically binds to streptavidin. For the example of biotin, the streptavidin is labeled as described above, thereby, providing a detectable signal for the bound target sequence. Unbound labeled streptavidin is typically removed prior to analysis.

As will be appreciated by those in the art, these assays can be direct hybridization assays or can comprise "sandwich assays", which include the use of multiple probes, as is generally outlined in U.S. Patent Nos. 5,681,702, 5,597,909, 5,545,730, 5,594,117, 5,591,584, 5,571,670, 5,580,731, 5,571,670, 5,591,584, 5,624,802, 5,635,352, 5,594,118, 5,359,100, 5,124,246 and 5,681,697, all of which are hereby incorporated by reference. In this embodiment, in general, the target nucleic acid is prepared as outlined above, and then added to the biochip comprising a plurality of nucleic acid probes, under conditions that allow the formation of a hybridization complex.

A variety of hybridization conditions may be used in the present invention, including high, moderate and low stringency conditions as outlined above. The assays are generally run under stringency conditions which allows formation of the label probe hybridization complex only in the presence of target. Stringency can be controlled by altering a step parameter that is a thermodynamic variable, including, but not limited to,

temperature, formamide concentration, salt concentration, chaotropic salt concentration pH, organic solvent concentration, etc.

These parameters may also be used to control non-specific binding, as is generally outlined in U.S. Patent No. 5,681,697. Thus it may be desirable to perform certain steps at higher stringency conditions to reduce non-specific binding.

The reactions outlined herein may be accomplished in a variety of ways. Components of the reaction may be added simultaneously, or sequentially, in different orders, with preferred embodiments outlined below. In addition, the reaction may include a variety of other reagents. These include salts, buffers, neutral proteins, e.g. albumin, detergents, *etc.* which may be used to facilitate optimal hybridization and detection, and/or reduce non-specific or background interactions. Reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, *etc.*, may also be used as appropriate, depending on the sample preparation methods and purity of the target.

The assay data are analyzed to determine the expression levels, and changes in expression levels as between states, of individual genes, forming a gene expression profile.

Screens are performed to identify modulators of the breast cancer phenotype. In one embodiment, screening is performed to identify modulators that can induce or suppress a particular expression profile, thus preferably generating the associated phenotype. In another embodiment, *e.g.*, for diagnostic applications, having identified differentially expressed genes important in a particular state, screens can be performed to identify modulators that alter expression of individual genes. In an another embodiment, screening is performed to identify modulators that alter a biological function of the expression product of a differentially expressed gene. Again, having identified the importance of a gene in a particular state, screens are performed to identify agents that bind and/or modulate the biological activity of the gene product.

In addition screens can be done for genes that are induced in response to a candidate agent. After identifying a modulator based upon its ability to suppress a breast cancer expression pattern leading to a normal expression pattern, or to modulate a single breast cancer gene expression profile so as to mimic the expression of the gene from normal tissue, a screen as described above can be performed to identify genes that are specifically

modulated in response to the agent. Comparing expression profiles between normal tissue and agent treated breast cancer tissue reveals genes that are not expressed in normal tissue or breast cancer tissue, but are expressed in agent treated tissue. These agent-specific sequences can be identified and used by methods described herein for breast cancer genes or proteins. In particular these sequences and the proteins they encode find use in marking or identifying agent treated cells. In addition, antibodies can be raised against the agent induced proteins and used to target novel therapeutics to the treated breast cancer tissue sample.

Thus, in one embodiment, a test compound is administered to a population of breast cancer cells, that have an associated breast cancer expression profile. By "administration" or "contacting" herein is meant that the candidate agent is added to the cells in such a manner as to allow the agent to act upon the cell, whether by uptake and intracellular action, or by action at the cell surface. In some embodiments, nucleic acid encoding a proteinaceous candidate agent (i.e., a peptide) may be put into a viral construct such as an adenoviral or retroviral construct, and added to the cell, such that expression of the peptide agent is accomplished, e.g., PCT US97/01019. Regulatable gene therapy systems can also be used.

Once the test compound has been administered to the cells, the cells can be washed if desired and are allowed to incubate under preferably physiological conditions for some period of time. The cells are then harvested and a new gene expression profile is generated, as outlined herein.

Thus, e.g., breast cancer tissue may be screened for agents that modulate, e.g., induce or suppress the breast cancer phenotype. A change in at least one gene, preferably many, of the expression profile indicates that the agent has an effect on breast cancer activity. By defining such a signature for the breast cancer phenotype, screens for new drugs that alter the phenotype can be devised. With this approach, the drug target need not be known and need not be represented in the original expression screening platform, nor does the level of transcript for the target protein need to change.

In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of

either the expression of the gene or the gene product itself can be done. The gene products of differentially expressed genes are sometimes referred to herein as "breast cancer proteins" or a "breast cancer modulatory protein". The breast cancer modulatory protein may be a fragment, or alternatively, be the full length protein to the fragment encoded by the nucleic acids of the Tables. Preferably, the breast cancer modulatory protein is a fragment. In a preferred embodiment, the breast cancer amino acid sequence which is used to determine sequence identity or similarity is encoded by a nucleic acid of Table 25. In another embodiment, the sequences are naturally occurring allelic variants of a protein encoded by a nucleic acid of Table 25. In another embodiment, the sequences are sequence variants as further described herein.

Preferably, the breast cancer modulatory protein is a fragment of approximately 14 to 24 amino acids long. More preferably the fragment is a soluble fragment. Preferably, the fragment includes a non-transmembrane region. In a preferred embodiment, the fragment has an N-terminal Cys to aid in solubility. In one embodiment, the C-terminus of the fragment is kept as a free acid and the N-terminus is a free amine to aid in coupling, i.e., to cysteine.

In one embodiment the breast cancer proteins are conjugated to an immunogenic agent as discussed herein. In one embodiment the breast cancer protein is conjugated to BSA.

Measurements of breast cancer polypeptide activity, or of breast cancer or the breast cancer phenotype can be performed using a variety of assays. For example, the effects of the test compounds upon the function of the breast cancer polypeptides can be measured by examining parameters described above. A suitable physiological change that affects activity can be used to assess the influence of a test compound on the polypeptides of this invention. When the functional consequences are determined using intact cells or animals, one can also measure a variety of effects such as, in the case of breast cancer associated with tumors, tumor growth, tumor metastasis, neovascularization, hormone release, transcriptional changes to both known and uncharacterized genetic markers (e.g., northern blots), changes in cell metabolism such as cell growth or pH changes, and changes in intracellular second

messengers such as cGMP. In the assays of the invention, mammalian breast cancer polypeptide is typically used, e.g., mouse, preferably human.

Assays to identify compounds with modulating activity can be performed *in vitro*. For example, a breast cancer polypeptide is first contacted with a potential modulator and incubated for a suitable amount of time, e.g., from 0.5 to 48 hours. In one embodiment, the breast cancer polypeptide levels are determined *in vitro* by measuring the level of protein or mRNA. The level of protein is measured using immunoassays such as western blotting, ELISA and the like with an antibody that selectively binds to the breast cancer polypeptide or a fragment thereof. For measurement of mRNA, amplification, e.g., using PCR, LCR, or hybridization assays, e.g., northern hybridization, RNAse protection, dot blotting, are preferred. The level of protein or mRNA is detected using directly or indirectly labeled detection agents, e.g., fluorescently or radioactively labeled nucleic acids, radioactively or enzymatically labeled antibodies, and the like, as described herein.

Alternatively, a reporter gene system can be devised using the breast cancer protein promoter operably linked to a reporter gene such as luciferase, green fluorescent protein, CAT, or β-gal. The reporter construct is typically transfected into a cell. After treatment with a potential modulator, the amount of reporter gene transcription, translation, or activity is measured according to standard techniques known to those of skill in the art.

In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of the expression of the gene or the gene product itself can be done. The gene products of differentially expressed genes are sometimes referred to herein as "breast cancer proteins." The breast cancer protein may be a fragment, or alternatively, be the full length protein to a fragment shown herein.

In one embodiment, screening for modulators of expression of specific genes is performed. Typically, the expression of only one or a few genes are evaluated. In another embodiment, screens are designed to first find compounds that bind to differentially expressed proteins. These compounds are then evaluated for the ability to modulate

differentially expressed activity. Moreover, once initial candidate compounds are identified, variants can be further screened to better evaluate structure activity relationships.

In a preferred embodiment, binding assays are done. In general, purified or isolated gene product is used; that is, the gene products of one or more differentially expressed nucleic acids are made. For example, antibodies are generated to the protein gene products, and standard immunoassays are run to determine the amount of protein present. Alternatively, cells comprising the breast cancer proteins can be used in the assays.

Thus, in a preferred embodiment, the methods comprise combining a breast cancer protein and a candidate compound, and determining the binding of the compound to the breast cancer protein. Preferred embodiments utilize the human breast cancer protein, although other mammalian proteins may also be used, e.g. for the development of animal models of human disease. In some embodiments, as outlined herein, variant or derivative breast cancer proteins may be used.

Generally, in a preferred embodiment of the methods herein, the breast cancer protein or the candidate agent is non-diffusably bound to an insoluble support having isolated sample receiving areas (e.g. a microtiter plate, an array, etc.). The insoluble supports may be made of any composition to which the compositions can be bound, is readily separated from soluble material, and is otherwise compatible with the overall method of screening. The surface of such supports may be solid or porous and of any convenient shape. Examples of suitable insoluble supports include microtiter plates, arrays, membranes and beads. These are typically made of glass, plastic (e.g., polystyrene), polysaccharides, nylon or nitrocellulose, teflon™, etc. Microtiter plates and arrays are especially convenient because a large number of assays can be carried out simultaneously, using small amounts of reagents and samples. The particular manner of binding of the composition is not crucial so long as it is compatible with the reagents and overall methods of the invention, maintains the activity of the composition and is nondiffusable. Preferred methods of binding include the use of antibodies (which do not sterically block either the ligand binding site or activation sequence when the protein is bound to the support), direct binding to "sticky" or ionic supports, chemical crosslinking, the synthesis of the protein or agent on the surface, etc. Following binding of the protein or agent, excess unbound material is removed by washing. The sample receiving

areas may then be blocked through incubation with bovine serum albumin (BSA), casein or other innocuous protein or other moiety.

In a preferred embodiment, the breast cancer protein is bound to the support, and a test compound is added to the assay. Alternatively, the candidate agent is bound to the support and the breast cancer protein is added. Novel binding agents include specific antibodies, non-natural binding agents identified in screens of chemical libraries, peptide analogs, etc. Of particular interest are screening assays for agents that have a low toxicity for human cells. A wide variety of assays may be used for this purpose, including labeled in vitro protein-protein binding assays, electrophoretic mobility shift assays, immunoassays for protein binding, functional assays (phosphorylation assays, etc.) and the like.

The determination of the binding of the test modulating compound to the breast cancer protein may be done in a number of ways. In a preferred embodiment, the compound is labeled, and binding determined directly, e.g., by attaching all or a portion of the breast cancer protein to a solid support, adding a labeled candidate agent (e.g., a fluorescent label), washing off excess reagent, and determining whether the label is present on the solid support. Various blocking and washing steps may be utilized as appropriate.

In some embodiments, only one of the components is labeled, e.g., the proteins (or proteinaceous candidate compounds) can be labeled. Alternatively, more than one component can be labeled with different labels, e.g., ^{125}I for the proteins and a fluorophor for the compound. Proximity reagents, e.g., quenching or energy transfer reagents are also useful.

In one embodiment, the binding of the test compound is determined by competitive binding assay. The competitor is a binding moiety known to bind to the target molecule (i.e., a breast cancer protein), such as an antibody, peptide, binding partner, ligand, etc. Under certain circumstances, there may be competitive binding between the compound and the binding moiety, with the binding moiety displacing the compound. In one embodiment, the test compound is labeled. Either the compound, or the competitor, or both, is added first to the protein for a time sufficient to allow binding, if present. Incubations may be performed at a temperature which facilitates optimal activity, typically between 4 and 40°C. Incubation periods are typically optimized, e.g., to facilitate rapid high throughput

screening. Typically between 0.1 and 1 hour will be sufficient. Excess reagent is generally removed or washed away. The second component is then added, and the presence or absence of the labeled component is followed, to indicate binding.

In a preferred embodiment, the competitor is added first, followed by the test compound. Displacement of the competitor is an indication that the test compound is binding to the breast cancer protein and thus is capable of binding to, and potentially modulating, the activity of the breast cancer protein. In this embodiment, either component can be labeled. Thus, e.g., if the competitor is labeled, the presence of label in the wash solution indicates displacement by the agent. Alternatively, if the test compound is labeled, the presence of the label on the support indicates displacement.

In an alternative embodiment, the test compound is added first, with incubation and washing, followed by the competitor. The absence of binding by the competitor may indicate that the test compound is bound to the breast cancer protein with a higher affinity. Thus, if the test compound is labeled, the presence of the label on the support, coupled with a lack of competitor binding, may indicate that the test compound is capable of binding to the breast cancer protein.

In a preferred embodiment, the methods comprise differential screening to identity agents that are capable of modulating the activity of the breast cancer proteins. In this embodiment, the methods comprise combining a breast cancer protein and a competitor in a first sample. A second sample comprises a test compound, a breast cancer protein, and a competitor. The binding of the competitor is determined for both samples, and a change, or difference in binding between the two samples indicates the presence of an agent capable of binding to the breast cancer protein and potentially modulating its activity. That is, if the binding of the competitor is different in the second sample relative to the first sample, the agent is capable of binding to the breast cancer protein.

Alternatively, differential screening is used to identify drug candidates that bind to the native breast cancer protein, but cannot bind to modified breast cancer proteins. The structure of the breast cancer protein may be modeled, and used in rational drug design to synthesize agents that interact with that site. Drug candidates that affect the activity of a

breast cancer protein are also identified by screening drugs for the ability to either enhance or reduce the activity of the protein.

Positive controls and negative controls may be used in the assays. Preferably control and test samples are performed in at least triplicate to obtain statistically significant results. Incubation of all samples is for a time sufficient for the binding of the agent to the protein. Following incubation, samples are washed free of non-specifically bound material and the amount of bound, generally labeled agent determined. For example, where a radiolabel is employed, the samples may be counted in a scintillation counter to determine the amount of bound compound.

A variety of other reagents may be included in the screening assays. These include reagents like salts, neutral proteins, e.g. albumin, detergents, etc. which may be used to facilitate optimal protein-protein binding and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used. The mixture of components may be added in an order that provides for the requisite binding.

In a preferred embodiment, the invention provides methods for screening for a compound capable of modulating the activity of a breast cancer protein. The methods comprise adding a test compound, as defined above, to a cell comprising breast cancer proteins. Preferred cell types include almost any cell. The cells contain a recombinant nucleic acid that encodes a breast cancer protein. In a preferred embodiment, a library of candidate agents are tested on a plurality of cells.

In one aspect, the assays are evaluated in the presence or absence or previous or subsequent exposure of physiological signals, e.g. hormones, antibodies, peptides, antigens, cytokines, growth factors, action potentials, pharmacological agents including chemotherapeutics, radiation, carcinogenics, or other cells (i.e. cell-cell contacts). In another example, the determinations are determined at different stages of the cell cycle process.

In this way, compounds that modulate breast cancer agents are identified. Compounds with pharmacological activity are able to enhance or interfere with the activity of the breast cancer protein. Once identified, similar structures are evaluated to identify critical structural feature of the compound.

In one embodiment, a method of inhibiting breast cancer cell division is provided. The method comprises administration of a breast cancer inhibitor. In another embodiment, a method of inhibiting breast cancer is provided. The method comprises administration of a breast cancer inhibitor. In a further embodiment, methods of treating cells or individuals with breast cancer are provided. The method comprises administration of a breast cancer inhibitor.

In one embodiment, a breast cancer inhibitor is an antibody as discussed above. In another embodiment, the breast cancer inhibitor is an antisense molecule.

A variety of cell growth, proliferation, and metastasis assays are known to those of skill in the art, as described below.

Soft agar growth or colony formation in suspension

Normal cells require a solid substrate to attach and grow. When the cells are transformed, they lose this phenotype and grow detached from the substrate. For example, transformed cells can grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft agar. The transformed cells, when transfected with tumor suppressor genes, regenerate normal phenotype and require a solid substrate to attach and grow. Soft agar growth or colony formation in suspension assays can be used to identify modulators of breast cancer sequences, which when expressed in host cells, inhibit abnormal cellular proliferation and transformation. A therapeutic compound would reduce or eliminate the host cells' ability to grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft.

Techniques for soft agar growth or colony formation in suspension assays are described in Freshney, *Culture of Animal Cells a Manual of Basic Technique* (3rd ed., 1994), herein incorporated by reference. *See also*, the methods section of Garkavtsev *et al.* (1996), *supra*, herein incorporated by reference.

Contact inhibition and density limitation of growth

Normal cells typically grow in a flat and organized pattern in a petri dish until they touch other cells. When the cells touch one another, they are contact inhibited and stop growing. When cells are transformed, however, the cells are not contact inhibited and continue to grow to high densities in disorganized foci. Thus, the transformed cells grow to a

higher saturation density than normal cells. This can be detected morphologically by the formation of a disoriented monolayer of cells or rounded cells in foci within the regular pattern of normal surrounding cells. Alternatively, labeling index with (^{3}H)-thymidine at saturation density can be used to measure density limitation of growth. *See* Freshney (1994), *supra*. The transformed cells, when transfected with tumor suppressor genes, regenerate a normal phenotype and become contact inhibited and would grow to a lower density.

In this assay, labeling index with (^{3}H)-thymidine at saturation density is a preferred method of measuring density limitation of growth. Transformed host cells are transfected with a breast cancer-associated sequence and are grown for 24 hours at saturation density in non-limiting medium conditions. The percentage of cells labeling with (^{3}H)-thymidine is determined autoradiographically. *See*, Freshney (1994), *supra*.

Growth factor or serum dependence

Transformed cells have a lower serum dependence than their normal counterparts (*see, e.g.*, Temin, *J. Natl. Cancer Insti.* 37:167-175 (1966); Eagle *et al.*, *J. Exp. Med.* 131:836-879 (1970)); Freshney, *supra*. This is in part due to release of various growth factors by the transformed cells. Growth factor or serum dependence of transformed host cells can be compared with that of control.

Tumor specific markers levels

Tumor cells release an increased amount of certain factors (hereinafter "tumor specific markers") than their normal counterparts. For example, plasminogen activator (PA) is released from human glioma at a higher level than from normal brain cells (*see, e.g.*, Gullino, *Angiogenesis, tumor vascularization, and potential interference with tumor growth.* in *Biological Responses in Cancer*, pp. 178-184 (Mihich (ed.) 1985)). Similarly, Tumor angiogenesis factor (TAF) is released at a higher level in tumor cells than their normal counterparts. *See, e.g.*, Folkman, *Angiogenesis and Cancer, Sem Cancer Biol.* (1992)).

Various techniques which measure the release of these factors are described in Freshney (1994), *supra*. Also, *see*, Unkless *et al.* , *J. Biol. Chem.* 249:4295-4305 (1974); Strickland & Beers, *J. Biol. Chem.* 251:5694-5702 (1976); Whur *et al.*, *Br. J. Cancer* 42:305-

312 (1980); Gullino, *Angiogenesis, tumor vascularization, and potential interference with tumor growth.* in *Biological Responses in Cancer*, pp. 178-184 (Mihich (ed.) 1985); Freshney *Anticancer Res.* 5:111-130 (1985).

Invasiveness into Matrigel

The degree of invasiveness into Matrigel or some other extracellular matrix constituent can be used as an assay to identify compounds that modulate breast cancer-associated sequences. Tumor cells exhibit a good correlation between malignancy and invasiveness of cells into Matrigel or some other extracellular matrix constituent. In this assay, tumorigenic cells are typically used as host cells. Expression of a tumor suppressor gene in these host cells would decrease invasiveness of the host cells.

Techniques described in Freshney (1994), *supra*, can be used. Briefly, the level of invasion of host cells can be measured by using filters coated with Matrigel or some other extracellular matrix constituent. Penetration into the gel, or through to the distal side of the filter, is rated as invasiveness, and rated histologically by number of cells and distance moved, or by prelabeling the cells with ^{125}I and counting the radioactivity on the distal side of the filter or bottom of the dish. *See, e.g.*, Freshney (1984), *supra*.

Tumor growth in vivo

Effects of breast cancer-associated sequences on cell growth can be tested in transgenic or immune-suppressed mice. Knock-out transgenic mice can be made, in which the breast cancer gene is disrupted or in which a breast cancer gene is inserted. Knock-out transgenic mice can be made by insertion of a marker gene or other heterologous gene into the endogenous breast cancer gene site in the mouse genome via homologous recombination. Such mice can also be made by substituting the endogenous breast cancer gene with a mutated version of the breast cancer gene, or by mutating the endogenous breast cancer gene, e.g., by exposure to carcinogens.

A DNA construct is introduced into the nuclei of embryonic stem cells. Cells containing the newly engineered genetic lesion are injected into a host mouse embryo, which is re-implanted into a recipient female. Some of these embryos develop into chimeric mice

that possess germ cells partially derived from the mutant cell line. Therefore, by breeding the chimeric mice it is possible to obtain a new line of mice containing the introduced genetic lesion (*see, e.g.*, Capecchi *et al., Science* 244:1288 (1989)). Chimeric targeted mice can be derived according to Hogan *et al., Manipulating the Mouse Embryo: A Laboratory Manual*, Cold Spring Harbor Laboratory (1988) and *Teratocarcinomas and Embryonic Stem Cells: A Practical Approach*, Robertson, ed., IRL Press, Washington, D.C., (1987).

Alternatively, various immune-suppressed or immune-deficient host animals can be used. For example, genetically athymic "nude" mouse (*see, e.g.*, Giovanella *et al., J. Natl. Cancer Inst.* 52:921 (1974)), a SCID mouse, a thymectomized mouse, or an irradiated mouse (*see, e.g.*, Bradley *et al., Br. J. Cancer* 38:263 (1978); Selby *et al., Br. J. Cancer* 41:52 (1980)) can be used as a host. Transplantable tumor cells (typically about 10^6 cells) injected into isogenic hosts will produce invasive tumors in a high proportions of cases, while normal cells of similar origin will not. In hosts which developed invasive tumors, cells expressing a breast cancer-associated sequences are injected subcutaneously. After a suitable length of time, preferably 4-8 weeks, tumor growth is measured (e.g., by volume or by its two largest dimensions) and compared to the control. Tumors that have statistically significant reduction (using, e.g., Student's T test) are said to have inhibited growth.

Polynucleotide modulators of breast cancer

Antisense Polynucleotides

In certain embodiments, the activity of a breast cancer-associated protein is down-regulated, or entirely inhibited, by the use of antisense polynucleotide, *i.e.*, a nucleic acid complementary to, and which can preferably hybridize specifically to, a coding mRNA nucleic acid sequence, e.g., a breast cancer protein mRNA, or a subsequence thereof. Binding of the antisense polynucleotide to the mRNA reduces the translation and/or stability of the mRNA.

In the context of this invention, antisense polynucleotides can comprise naturally-occurring nucleotides, or synthetic species formed from naturally-occurring subunits or their close homologs. Antisense polynucleotides may also have altered sugar moieties or inter-sugar linkages. Exemplary among these are the phosphorothioate and other

sulfur containing species which are known for use in the art. Analogs are comprehended by this invention so long as they function effectively to hybridize with the breast cancer protein mRNA. *See, e.g.,* Isis Pharmaceuticals, Carlsbad, CA; Sequitor, Inc., Natick, MA.

Such antisense polynucleotides can readily be synthesized using recombinant means, or can be synthesized *in vitro*. Equipment for such synthesis is sold by several vendors, including Applied Biosystems. The preparation of other oligonucleotides such as phosphorothioates and alkylated derivatives is also well known to those of skill in the art.

Antisense molecules as used herein include antisense or sense oligonucleotides. Sense oligonucleotides can, e.g., be employed to block transcription by binding to the anti-sense strand. The antisense and sense oligonucleotide comprise a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target mRNA (sense) or DNA (antisense) sequences for breast cancer molecules. A preferred antisense molecule is for a breast cancer sequences in Tables 1-25, or for a ligand or activator thereof. Antisense or sense oligonucleotides, according to the present invention, comprise a fragment generally at least about 14 nucleotides, preferably from about 14 to 30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein is described in, e.g., Stein & Cohen (*Cancer Res.* 48:2659 (1988 and van der Krol *et al.* (*BioTechniques* 6:958 (1988)).

Ribozymes

In addition to antisense polynucleotides, ribozymes can be used to target and inhibit transcription of breast cancer-associated nucleotide sequences. A ribozyme is an RNA molecule that catalytically cleaves other RNA molecules. Different kinds of ribozymes have been described, including group I ribozymes, hammerhead ribozymes, hairpin ribozymes, RNase P, and axhead ribozymes (*see, e.g.,* Castanotto *et al., Adv. in Pharmacology* 25: 289-317 (1994) for a general review of the properties of different ribozymes).

The general features of hairpin ribozymes are described, e.g., in Hampel *et al., Nucl. Acids Res.* 18:299-304 (1990); European Patent Publication No. 0 360 257; U.S. Patent No. 5,254,678. Methods of preparing are well known to those of skill in the art (*see, e.g.,*

WO 94/26877; Ojwang *et al., Proc. Natl. Acad. Sci.* USA 90:6340-6344 (1993); Yamada *et al., Human Gene Therapy* 1:39-45 (1994); Leavitt *et al., Proc. Natl. Acad. Sci. USA* 92:699-703 (1995); Leavitt *et al., Human Gene Therapy* 5:1151-120 (1994); and Yamada *et al., Virology* 205: 121-126 (1994)).

Polynucleotide modulators of breast cancer may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell. Alternatively, a polynucleotide modulator of breast cancer may be introduced into a cell containing the target nucleic acid sequence, e.g., by formation of an polynucleotide-lipid complex, as described in WO 90/10448. It is understood that the use of antisense molecules or knock out and knock in models may also be used in screening assays as discussed above, in addition to methods of treatment.

Thus, in one embodiment, methods of modulating breast cancer in cells or organisms are provided. In one embodiment, the methods comprise administering to a cell an anti-breast cancer antibody that reduces or eliminates the biological activity of an endogenous breast cancer protein. Alternatively, the methods comprise administering to a cell or organism a recombinant nucleic acid encoding a breast cancer protein. This may be accomplished in any number of ways. In a preferred embodiment, e.g. when the breast cancer sequence is down-regulated in breast cancer, such state may be reversed by increasing the amount of breast cancer gene product in the cell. This can be accomplished, e.g., by overexpressing the endogenous breast cancer gene or administering a gene encoding the breast cancer sequence, using known gene-therapy techniques, e.g.. In a preferred embodiment, the gene therapy techniques include the incorporation of the exogenous gene using enhanced homologous recombination (EHR), e.g. as described in PCT/US93/03868, hereby incorporated by reference in its entirety. Alternatively, e.g. when the breast cancer

sequence is up-regulated in breast cancer, the activity of the endogenous breast cancer gene is decreased, e.g. by the administration of a breast cancer antisense nucleic acid.

In one embodiment, the breast cancer proteins of the present invention may be used to generate polyclonal and monoclonal antibodies to breast cancer proteins. Similarly, the breast cancer proteins can be coupled, using standard technology, to affinity chromatography columns. These columns may then be used to purify breast cancer antibodies useful for production, diagnostic, or therapeutic purposes. In a preferred embodiment, the antibodies are generated to epitopes unique to a breast cancer protein; that is, the antibodies show little or no cross-reactivity to other proteins. The breast cancer antibodies may be coupled to standard affinity chromatography columns and used to purify breast cancer proteins. The antibodies may also be used as blocking polypeptides, as outlined above, since they will specifically bind to the breast cancer protein.

Methods of identifying variant breast cancer-associated sequences

Without being bound by theory, expression of various breast cancer sequences is correlated with breast cancer. Accordingly, disorders based on mutant or variant breast cancer genes may be determined. In one embodiment, the invention provides methods for identifying cells containing variant breast cancer genes, e.g., determining all or part of the sequence of at least one endogenous breast cancer genes in a cell. This may be accomplished using any number of sequencing techniques. In a preferred embodiment, the invention provides methods of identifying the breast cancer genotype of an individual, e.g., determining all or part of the sequence of at least one breast cancer gene of the individual. This is generally done in at least one tissue of the individual, and may include the evaluation of a number of tissues or different samples of the same tissue. The method may include comparing the sequence of the sequenced breast cancer gene to a known breast cancer gene, i.e., a wild-type gene.

The sequence of all or part of the breast cancer gene can then be compared to the sequence of a known breast cancer gene to determine if any differences exist. This can be done using any number of known homology programs, such as Bestfit, etc. In a preferred embodiment, the presence of a difference in the sequence between the breast cancer gene of

the patient and the known breast cancer gene correlates with a disease state or a propensity for a disease state, as outlined herein.

In a preferred embodiment, the breast cancer genes are used as probes to determine the number of copies of the breast cancer gene in the genome.

In another preferred embodiment, the breast cancer genes are used as probes to determine the chromosomal localization of the breast cancer genes. Information such as chromosomal localization finds use in providing a diagnosis or prognosis in particular when chromosomal abnormalities such as translocations, and the like are identified in the breast cancer gene locus.

Administration of pharmaceutical and vaccine compositions

In one embodiment, a therapeutically effective dose of a breast cancer protein or modulator thereof, is administered to a patient. By "therapeutically effective dose" herein is meant a dose that produces effects for which it is administered. The exact dose will depend on the purpose of the treatment, and will be ascertainable by one skilled in the art using known techniques (e.g., Ansel *et al.*, *Pharmaceutical Dosage Forms and Drug Delivery*; Lieberman, *Pharmaceutical Dosage Forms* (vols. 1-3, 1992), Dekker, ISBN 0824770846, 082476918X, 0824712692, 0824716981; Lloyd, *The Art, Science and Technology of Pharmaceutical Compounding* (1999); and Pickar, *Dosage Calculations* (1999)). As is known in the art, adjustments for breast cancer degradation, systemic versus localized delivery, and rate of new protease synthesis, as well as the age, body weight, general health, sex, diet, time of administration, drug interaction and the severity of the condition may be necessary, and will be ascertainable with routine experimentation by those skilled in the art. U.S. Patent Application N. 09/687,576, further discloses the use of compositions and methods of diagnosis and treatment in breast cancer is hereby expressly incorporated by reference.

A "patient" for the purposes of the present invention includes both humans and other animals, particularly mammals. Thus the methods are applicable to both human therapy and veterinary applications. In the preferred embodiment the patient is a mammal, preferably a primate, and in the most preferred embodiment the patient is human.

The administration of the breast cancer proteins and modulators thereof of the present invention can be done in a variety of ways as discussed above, including, but not limited to, orally, subcutaneously, intravenously, intranasally, transdermally, intraperitoneally, intramuscularly, intrapulmonary, vaginally, rectally, or intraocularly. In some instances, e.g., in the treatment of wounds and inflammation, the breast cancer proteins and modulators may be directly applied as a solution or spray.

The pharmaceutical compositions of the present invention comprise a breast cancer protein in a form suitable for administration to a patient. In the preferred embodiment, the pharmaceutical compositions are in a water soluble form, such as being present as pharmaceutically acceptable salts, which is meant to include both acid and base addition salts. "Pharmaceutically acceptable acid addition salt" refers to those salts that retain the biological effectiveness of the free bases and that are not biologically or otherwise undesirable, formed with inorganic acids such as hydrochloric acid, hydrobromic acid, sulfuric acid, nitric acid, phosphoric acid and the like, and organic acids such as acetic acid, propionic acid, glycolic acid, pyruvic acid, oxalic acid, maleic acid, malonic acid, succinic acid, fumaric acid, tartaric acid, citric acid, benzoic acid, cinnamic acid, mandelic acid, methanesulfonic acid, ethanesulfonic acid, p-toluenesulfonic acid, salicylic acid and the like. "Pharmaceutically acceptable base addition salts" include those derived from inorganic bases such as sodium, potassium, lithium, ammonium, calcium, magnesium, iron, zinc, copper, manganese, aluminum salts and the like. Particularly preferred are the ammonium, potassium, sodium, calcium, and magnesium salts. Salts derived from pharmaceutically acceptable organic non-toxic bases include salts of primary, secondary, and tertiary amines, substituted amines including naturally occurring substituted amines, cyclic amines and basic ion exchange resins, such as isopropylamine, trimethylamine, diethylamine, triethylamine, tripropylamine, and ethanolamine.

The pharmaceutical compositions may also include one or more of the following: carrier proteins such as serum albumin; buffers; fillers such as microcrystalline cellulose, lactose, corn and other starches; binding agents; sweeteners and other flavoring agents; coloring agents; and polyethylene glycol.

The pharmaceutical compositions can be administered in a variety of unit dosage forms depending upon the method of administration. For example, unit dosage forms suitable for oral administration include, but are not limited to, powder, tablets, pills, capsules and lozenges. It is recognized that breast cancer protein modulators (e.g., antibodies, antisense constructs, ribozymes, small organic molecules, *etc.*) when administered orally, should be protected from digestion. This is typically accomplished either by complexing the molecule(s) with a composition to render it resistant to acidic and enzymatic hydrolysis, or by packaging the molecule(s) in an appropriately resistant carrier, such as a liposome or a protection barrier. Means of protecting agents from digestion are well known in the art.

The compositions for administration will commonly comprise a breast cancer protein modulator dissolved in a pharmaceutically acceptable carrier, preferably an aqueous carrier. A variety of aqueous carriers can be used, e.g., buffered saline and the like. These solutions are sterile and generally free of undesirable matter. These compositions may be sterilized by conventional, well known sterilization techniques. The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions such as pH adjusting and buffering agents, toxicity adjusting agents and the like, e.g., sodium acetate, sodium chloride, potassium chloride, calcium chloride, sodium lactate and the like. The concentration of active agent in these formulations can vary widely, and will be selected primarily based on fluid volumes, viscosities, body weight and the like in accordance with the particular mode of administration selected and the patient's needs (e.g., *Remington's Pharmaceutical Science* (15th ed., 1980) and Goodman & Gillman, *The Pharmacologial Basis of Therapeutics* (Hardman *et al.*,eds., 1996)).

Thus, a typical pharmaceutical composition for intravenous administration would be about 0.1 to 10 mg per patient per day. Dosages from 0.1 up to about 100 mg per patient per day may be used, particularly when the drug is administered to a secluded site and not into the blood stream, such as into a body cavity or into a lumen of an organ. Substantially higher dosages are possible in topical administration. Actual methods for preparing parenterally administrable compositions will be known or apparent to those skilled in the art, *e.g.*, *Remington's Pharmaceutical Science* and Goodman and Gillman, *The Pharmacologial Basis of Therapeutics*, *supra*.

The compositions containing modulators of breast cancer proteins can be administered for therapeutic or prophylactic treatments. In therapeutic applications, compositions are administered to a patient suffering from a disease (e.g., a cancer) in an amount sufficient to cure or at least partially arrest the disease and its complications. An amount adequate to accomplish this is defined as a "therapeutically effective dose." Amounts effective for this use will depend upon the severity of the disease and the general state of the patient's health. Single or multiple administrations of the compositions may be administered depending on the dosage and frequency as required and tolerated by the patient. In any event, the composition should provide a sufficient quantity of the agents of this invention to effectively treat the patient. An amount of modulator that is capable of preventing or slowing the development of cancer in a mammal is referred to as a "prophylactically effective dose." The particular dose required for a prophylactic treatment will depend upon the medical condition and history of the mammal, the particular cancer being prevented, as well as other factors such as age, weight, gender, administration route, efficiency, *etc.* Such prophylactic treatments may be used, *e.g.*, in a mammal who has previously had cancer to prevent a recurrence of the cancer, or in a mammal who is suspected of having a significant likelihood of developing cancer.

It will be appreciated that the present breast cancer protein-modulating compounds can be administered alone or in combination with additional breast cancer modulating compounds or with other therapeutic agent, *e.g.*, other anti-cancer agents or treatments.

In numerous embodiments, one or more nucleic acids, *e.g.*, polynucleotides comprising nucleic acid sequences set forth in Tables 1-25, such as antisense polynucleotides or ribozymes, will be introduced into cells, *in vitro* or *in vivo*. The present invention provides methods, reagents, vectors, and cells useful for expression of breast cancer-associated polypeptides and nucleic acids using *in vitro* (cell-free), *ex vivo* or *in vivo* (cell or organism-based) recombinant expression systems.

The particular procedure used to introduce the nucleic acids into a host cell for expression of a protein or nucleic acid is application specific. Many procedures for introducing foreign nucleotide sequences into host cells may be used. These include the use

of calcium phosphate transfection, spheroplasts, electroporation, liposomes, microinjection, plasma vectors, viral vectors and any of the other well known methods for introducing cloned genomic DNA, cDNA, synthetic DNA or other foreign genetic material into a host cell (*see, e.g.*, Berger & Kimmel, *Guide to Molecular Cloning Techniques, Methods in Enzymology* volume 152 (Berger), Ausubel *et al.*, eds., *Current Protocols* (supplemented through 1999), and Sambrook *et al.*, *Molecular Cloning - A Laboratory Manual* (2nd ed., Vol. 1-3, 1989.

In a preferred embodiment, breast cancer proteins and modulators are administered as therapeutic agents, and can be formulated as outlined above. Similarly, breast cancer genes (including both the full-length sequence, partial sequences, or regulatory sequences of the breast cancer coding regions) can be administered in a gene therapy application. These breast cancer genes can include antisense applications, either as gene therapy (i.e. for incorporation into the genome) or as antisense compositions, as will be appreciated by those in the art.

Breast cancer polypeptides and polynucleotides can also be administered as vaccine compositions to stimulate HTL, CTL and antibody responses.. Such vaccine compositions can include, e.g., lipidated peptides (*see, e.g.*,Vitiello, A. *et al.*, *J. Clin. Invest.* 95:341 (1995)), peptide compositions encapsulated in poly(DL-lactide-co-glycolide) ("PLG") microspheres (*see, e.g.*, Eldridge, *et al.*, *Molec. Immunol.* 28:287-294, (1991); Alonso *et al.*, *Vaccine* 12:299-306 (1994); Jones *et al.*, *Vaccine* 13:675-681 (1995)), peptide compositions contained in immune stimulating complexes (ISCOMS) (*see, e.g.*, Takahashi *et al.*, *Nature* 344:873-875 (1990); Hu *et al.*, *Clin Exp Immunol.* 113:235-243 (1998)), multiple antigen peptide systems (MAPs) (*see, e.g.*, Tam, *Proc. Natl. Acad. Sci. U.S.A.* 85:5409-5413 (1988); Tam, *J. Immunol. Methods* 196:17-32 (1996)), peptides formulated as multivalent peptides; peptides for use in ballistic delivery systems, typically crystallized peptides, viral delivery vectors (Perkus, *et al.*, In: *Concepts in vaccine development* (Kaufmann, ed., p. 379, 1996); Chakrabarti, *et al.*, *Nature* 320:535 (1986); Hu *et al.*, *Nature* 320:537 (1986); Kieny, *et al.*, *AIDS Bio/Technology* 4:790 (1986); Top *et al.*, *J. Infect. Dis.* 124:148 (1971); Chanda *et al.*, *Virology* 175:535 (1990)), particles of viral or synthetic origin (*see, e.g.*, Kofler *et al.*, *J. Immunol. Methods.* 192:25 (1996); Eldridge *et al.*, *Sem. Hematol.* 30:16 (1993); Falo *et al.*, *Nature Med.* 7:649 (1995)), adjuvants (Warren *et al.*, *Annu. Rev. Immunol.* 4:369 (1986);

Gupta *et al.*, *Vaccine* 11:293 (1993)), liposomes (Reddy *et al.*, *J. Immunol.* 148:1585 (1992); Rock, *Immunol. Today* 17:131 (1996)), or, naked or particle absorbed cDNA (Ulmer, *et al.*, *Science* 259:1745 (1993); Robinson *et al.*, *Vaccine* 11:957 (1993); Shiver *et al.*, In: *Concepts in vaccine development* (Kaufmann, ed., p. 423, 1996); Cease & Berzofsky, *Annu. Rev. Immunol.* 12:923 (1994) and Eldridge *et al.*, *Sem. Hematol.* 30:16 (1993)). Toxin-targeted delivery technologies, also known as receptor mediated targeting, such as those of Avant Immunotherapeutics, Inc. (Needham, Massachusetts) may also be used.

Vaccine compositions often include adjuvants. Many adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, *Bortadella pertussis* or *Mycobacterium tuberculosis* derived proteins. Certain adjuvants are commercially available as, e.g., Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); AS-2 (SmithKline Beecham, Philadelphia, PA); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes; biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF, interleukin-2, -7, -12, and other like growth factors, may also be used as adjuvants.

Vaccines can be administered as nucleic acid compositions wherein DNA or RNA encoding one or more of the polypeptides, or a fragment thereof, is administered to a patient. This approach is described, for instance, in Wolff *et. al.*, *Science* 247:1465 (1990) as well as U.S. Patent Nos. 5,580,859; 5,589,466; 5,804,566; 5,739,118; 5,736,524; 5,679,647; WO 98/04720; and in more detail below. Examples of DNA-based delivery technologies include "naked DNA", facilitated (bupivicaine, polymers, peptide-mediated) delivery, cationic lipid complexes, and particle-mediated ("gene gun") or pressure-mediated delivery (*see, e.g.*, U.S. Patent No. 5,922,687).

For therapeutic or prophylactic immunization purposes, the peptides of the invention can be expressed by viral or bacterial vectors. Examples of expression vectors include attenuated viral hosts, such as vaccinia or fowlpox. This approach involves the use of

vaccinia virus, e.g., as a vector to express nucleotide sequences that encode breast cancer polypeptides or polypeptide fragments. Upon introduction into a host, the recombinant vaccinia virus expresses the immunogenic peptide, and thereby elicits an immune response. Vaccinia vectors and methods useful in immunization protocols are described in, *e.g.*, U.S. Patent No. 4,722,848. Another vector is BCG (Bacille Calmette Guerin). BCG vectors are described in Stover *et al.*, *Nature* 351:456-460 (1991). A wide variety of other vectors useful for therapeutic administration or immunization e.g. adeno and adeno-associated virus vectors, retroviral vectors, *Salmonella typhi* vectors, detoxified anthrax toxin vectors, and the like, will be apparent to those skilled in the art from the description herein (*see, e.g.*, Shata *et al.*, *Mol Med Today* 6:66-71 (2000); Shedlock *et al.*, *J Leukoc Biol* 68:793-806 (2000); Hipp *et al.*, *In Vivo* 14:571-85 (2000)).

Methods for the use of genes as DNA vaccines are well known, and include placing a breast cancer gene or portion of a breast cancer gene under the control of a regulatable promoter or a tissue-specific promoter for expression in a breast cancer patient. The breast cancer gene used for DNA vaccines can encode full-length breast cancer proteins, but more preferably encodes portions of the breast cancer proteins including peptides derived from the breast cancer protein. In one embodiment, a patient is immunized with a DNA vaccine comprising a plurality of nucleotide sequences derived from a breast cancer gene. For example, breast cancer-associated genes or sequence encoding subfragments of a breast cancer protein are introduced into expression vectors and tested for their immunogenicity in the context of Class I MHC and an ability to generate cytotoxic T cell responses. This procedure provides for production of cytotoxic T cell responses against cells which present antigen, including intracellular epitopes.

In a preferred embodiment, the DNA vaccines include a gene encoding an adjuvant molecule with the DNA vaccine. Such adjuvant molecules include cytokines that increase the immunogenic response to the breast cancer polypeptide encoded by the DNA vaccine. Additional or alternative adjuvants are available.

In another preferred embodiment breast cancer genes find use in generating animal models of breast cancer. When the breast cancer gene identified is repressed or diminished in cancer tissue, gene therapy technology, e.g., wherein antisense RNA directed

to the breast cancer gene will also diminish or repress expression of the gene. Animal models of breast cancer find use in screening for modulators of a breast cancer-associated sequence or modulators of breast cancer. Similarly, transgenic animal technology including gene knockout technology, e.g. as a result of homologous recombination with an appropriate gene targeting vector, will result in the absence or increased expression of the breast cancer protein. When desired, tissue-specific expression or knockout of the breast cancer protein may be necessary.

It is also possible that the breast cancer protein is overexpressed in breast cancer. As such, transgenic animals can be generated that overexpress the breast cancer protein. Depending on the desired expression level, promoters of various strengths can be employed to express the transgene. Also, the number of copies of the integrated transgene can be determined and compared for a determination of the expression level of the transgene. Animals generated by such methods find use as animal models of breast cancer and are additionally useful in screening for modulators to treat breast cancer.

Kits for Use in Diagnostic and/or Prognostic Applications

For use in diagnostic, research, and therapeutic applications suggested above, kits are also provided by the invention. In the diagnostic and research applications such kits may include any or all of the following: assay reagents, buffers, breast cancer-specific nucleic acids or antibodies, hybridization probes and/or primers, antisense polynucleotides, ribozymes, dominant negative breast cancer polypeptides or polynucleotides, small molecules inhibitors of breast cancer-associated sequences *etc.* A therapeutic product may include sterile saline or another pharmaceutically acceptable emulsion and suspension base.

In addition, the kits may include instructional materials containing directions (i.e., protocols) for the practice of the methods of this invention. While the instructional materials typically comprise written or printed materials they are not limited to such. Any medium capable of storing such instructions and communicating them to an end user is contemplated by this invention. Such media include, but are not limited to electronic storage media (e.g., magnetic discs, tapes, cartridges, chips), optical media (e.g., CD ROM), and the

like. Such media may include addresses to internet sites that provide such instructional materials.

The present invention also provides for kits for screening for modulators of breast cancer-associated sequences. Such kits can be prepared from readily available materials and reagents. For example, such kits can comprise one or more of the following materials: a breast cancer-associated polypeptide or polynucleotide, reaction tubes, and instructions for testing breast cancer-associated activity. Optionally, the kit contains biologically active breast cancer protein. A wide variety of kits and components can be prepared according to the present invention, depending upon the intended user of the kit and the particular needs of the user. Diagnosis would typically involve evaluation of a plurality of genes or products. The genes will be selected based on correlations with important parameters in disease which may be identified in historical or outcome data.

EXAMPLES

Example 1: Tissue Preparation, Labeling Chips, and Fingerprints

Purifying total RNA from tissue sample using TRIzol Reagent

The sample weight is first estimated. The tissue samples are homogenized in 1 ml of TRIzol per 50 mg of tissue using a homogenizer (e.g., Polytron 3100). The size of the generator/probe used depends upon the sample amount. A generator that is too large for the amount of tissue to be homogenized will cause a loss of sample and lower RNA yield. A larger generator (e.g., 20 mm) is suitable for tissue samples weighing more than 0.6 g. Fill tubes should not be overfilled. If the working volume is greater than 2 ml and no greater than 10 ml, a 15 ml polypropylene tube (Falcon 2059) is suitable for homogenization.

Tissues should be kept frozen until homogenized. The TRIzol is added directly to the frozen tissue before homogenization. Following homogenization, the insoluble material is removed from the homogenate by centrifugation at 7500 x g for 15 min. in a Sorvall superspeed or 12,000 x g for 10 min. in an Eppendorf centrifuge at 4°C. The cleared

homogenate is then transferred to a new tube(s). Samples may be frozen and stored at -60 to -70°C for at least one month or else continue with the purification.

The next process is phase separation. The homogenized samples are incubated for 5 minutes at room temperature. Then, 0.2 ml of chloroform per 1ml of TRIzol reagent is added to the homogenization mixture. The tubes are securely capped and shaken vigorously by hand (do not vortex) for 15 seconds. The samples are then incubated at room temp. for 2-3 minutes and next centrifuged at 6500 rpm in a Sorvall superspeed for 30 min. at 4oC.

The next process is RNA Precipitation. The aqueous phase is transferred to a fresh tube. The organic phase can be saved if isolation of DNA or protein is desired. Then 0.5 ml of isopropyl alcohol is added per 1ml of TRIzol reagent used in the original homogenization. Then, the tubes are securely capped and inverted to mix. The samples are then incubated at room temp. for 10 minutes an centrifuged at 6500 rpm in Sorvall for 20 min. at 4°C.

The RNA is then washed. The supernatant is poured off and the pellet washed with cold 75% ethanol. 1 ml of 75% ethanol is used per 1 ml of the TRIzol reagent used in the initial homogenization. The tubes are capped securely and inverted several times to loosen pellet without vortexing . They are next centrifuged at <8000 rpm (<7500 x g) for 5 minutes at 4°C.

The RNA wash is decanted. The pellet is carefully transferred to an Eppendorf tube (sliding down the tube into the new tube by use of a pipet tip to help guide it in if necessary). Tube(s) sizes for precipitating the RNA depending on the working volumes. Larger tubes may take too long to dry. Dry pellet. The RNA is then resuspended in an appropriate volume (e.g., 2 -5 ug/ul) of DEPC H_2O. The absorbance is then measured.

The poly A+ mRNA may next be purified from total RNA by other methods such as Qiagen' s RNeasy kit. The poly A^+ mRNA is purified from total RNA by adding the oligotex suspension which has been heated to 37°C and mixing prior to adding to RNA. The Elution Buffer is incubated at 70°C. If there is precipitate in the buffer, warm up the 2 x Binding Buffer at 65°C. The the total RNA is mixed with DEPC-treated water, 2 x Binding

Buffer, and Oligotex according to Table 2 on page 16 of the Oligotex Handbook and next incubated for 3 minutes at 65°C and 10 minutes at room temperature.

The preparation is centrifuged for 2 minutes at 14,000 to 18,000 g, preferably, at a "soft setting," The supernatant is removed without disturbing Oligotex pellet. A little bit of solution can be left behind to reduce the loss of Oligotex. The supernatant is saved until satisfactory binding and elution of poly A^+ mRNA has been found.

Then, the preparation is gently resuspended in Wash Buffer OW2 and pipetted onto the spin column and centrifuged at full speed (soft setting if possible) for 1 minute.

Next, the spin column is transferred to a new collection tube and gently resuspended in Wash Buffer OW2 and centrifuged as described herein.

Then, the spin column is transferred to a new tube and eluted with 20 to 100 ul of preheated (70°C) Elution Buffer. The Oligotex resin is gently resuspended by pipetting up and down. The centrifugation is repeated as above and the elution repeated with fresh elution buffer or first eluate to keep the elution volume low.

The absorbance is next read to determine the yield, using diluted Elution Buffer as the blank.

Before proceeding with cDNA synthesis, the mRNA is precipitated before proceeding with cDNA synthesis, as components leftover or in the Elution Buffer from the Oligotex purification procedure will inhibit downstream enzymatic reactions of the mRNA. 0.4 vol. of 7.5 M NH4OAc + 2.5 vol. of cold 100% ethanol is added and the preparation precipitated at -20°C 1 hour to overnight (or 20-30 min. at -70°C), and centrifuged at 14,000-16,000 x g for 30 minutes at 4°C. Next, the pellet is washed with 0.5 ml of 80% ethanol (-20°C) and then centrifuged at 14,000-16,000 x g for 5 minutes at room temperature. The80% ethanol wash is then repeated. The last bit of ethanol from the pellet is then dried without use of a speed vacuum and the pellet is then resuspended in DEPC H_2O at 1ug/ul concentration.

Alternatively the RNA may be purified using other methods (e.g., Qiagen's RNeasy kit).

No more than 100 ug is added to the RNeasy column. The sample volume is adjusted to 100 ul with RNase-free water. 350 ul Buffer RLT and then 250 ul ethanol (100%) are added to the sample. The preparation is then mixed by pipetting and applied to an RNeasy mini spin column for centrifugation (15 sec at >10,000 rpm). If yield is low, reapply the flowthrough to the column and centrifuge again.

Then, transfer column to a new 2 ml collection tube and add 500 ul Buffer RPE and centrifuge for 15 sec at >10,000 rpm. The flowthrough is discarded. 500 ul Buffer RPE and is then added and the preparation is centriuged for 15 sec at >10,000 rpm. The flowthrough is discarded. and the column membrane dried by centrifuging for 2 min at maximum speed. The column is transferred to a new 1.5-ml collection tube. 30-50 ul of RNase-free water is applied directly onto column membrane. The column is then centrifuged for 1 min at >10,000 rpm and the elution step repeated.

The absorbance is then read to determine yield. If necessary, the material may be ethanol precipitated with ammonium acetate and 2.5X volume 100% ethanol.

First Strand cDNA Synthesis

The first strand can be make using using Gibco's "SuperScript Choice System for cDNA Synthesis" kit. The starting material is 5 ug of total RNA or 1 ug of polyA+ mRNAl. For total RNA, 2 ul of SuperScript RT is used; for polyA+ mRNA, 1 ul of SuperScript RT is used. The final volume of first strand synthesis mix is 20 ul. The RNA should be in a volume no greater than 10 ul. The RNA is incubated with 1 ul of 100 pmol T7-T24 oligo for 10 min at 70°C followed by addition on ice of 7 ul of: 4ul 5X 1st Strand Buffer, 2 ul of 0.1M DTT, and 1 ul of 10mM dNTP mix. The preparation is then incubated at 37°C for 2 min before addition of the SuperScript RT followed by incubation at 37°C for 1 hour.

Second Strand Synthesis

For the second strand synthesis, place 1st strand reactions on ice and add: 91 ul DEPC H_20; 30 ul 5X 2nd Strand Buffer; 3 ul 10mM dNTP mix; 1 ul 10 U/ul E.coli DNA Ligase; 4 ul 10 U/ul E.coli DNA Polymerase; and 1 ul 2 U/ul RNase H. Mix and incubate 2

hours at 16°C. Add 2 ul T4 DNA Polymerase. Incubate 5 min at 16°C. Add 10 ul of 0.5M EDTA.

Cleaning up cDNA

The cDNA is purified using Phenol:Chloroform:Isoamyl Alcohol (25:24:1) and Phase-Lock gel tubes. The PLG tubes are centrifuged for 30 sec at maximum speed. The cDNA mix is then transferred to PLG tube. An equal volume of phenol:chloroform:isamyl alcohol is then added, the preparation shaken vigorously (no vortexing), and centrifuged for 5 minutes at maximum speed. The top aqueous solution is transferred to a new tube and ethanol precipitated by adding 7.5X 5M NH4OAc and 2.5X volume of 100% ethanol. Next, it is centrifuged immediately at room temperature for 20 min, maximum speed. The supernatant is removed, and the pellet washed with 2X with cold 80% ethanol. As much ethanol wash as possible should be removed before air drying the pellet; and resuspending it in 3 ul RNase-free water.

In vitro Transcription (IVT) and labeling with biotin

In vitro Transcription (IVT) and labeling with biotin is performed as follows: Pipet 1.5 ul of cDNA into a thin-wall PCR tube. Make NTP labeling mix by combining 2 ul T7 10xATP (75 mM) (Ambion); 2 ul T7 10xGTP (75 mM) (Ambion); 1.5 ul T7 10xCTP (75 mM) (Ambion); 1.5 ul T7 10xUTP (75 mM) (Ambion); 3.75 ul 10 mM Bio-11-UTP (Boehringer-Mannheim/Roche or Enzo); 3.75 ul 10 mM Bio-16-CTP (Enzo); 2 ul 10x T7 transcription buffer (Ambion); and 2 ul 10x T7 enzyme mix (Ambion). The final volume is 20 ul. Incubate 6 hours at 37°C in a PCR machine. The RNA can be furthered cleaned. Clean-up follows the previous instructions for RNeasy columns or Qiagen's RNeasy protocol handbook. The cRNA often needs to be ethanol precipitated by resuspension in a volume compatible with the fragmentation step.

Fragmentation is performed as follows. 15 ug of labeled RNA is usually fragmented. Try to minimize the fragmentation reaction volume; a 10 ul volume is recommended but 20 ul is all right. Do not go higher than 20 ul because the magnesium in the fragmentation buffer contributes to precipitation in the hybridization buffer. Fragment

RNA by incubation at 94 C for 35 minutes in 1 x Fragmentation buffer (5 x Fragmentation buffer is 200 mM Tris-acetate, pH 8.1; 500 mM KOAc; 150 mM MgOAc). The labeled RNA transcript can be analyzed before and after fragmentation. Samples can be heated to 65°C for 15 minutes and electrophoresed on 1% agarose/TBE gels to get an approximate idea of the transcript size range.

For hybridization, 200 ul (10 ug cRNA) of a hybridization mix is put on the chip. If multiple hybridizations are to be done (such as cycling through a 5 chip set), then it is recommended that an initial hybridization mix of 300 ul or more be made. The hybridization mix is: fragment labeled RNA (50 ng/ul final conc.); 50 pM 948-b control oligo; 1.5 pM BioB; 5 pM BioC; 25 pM BioD; 100 pM CRE; 0.1 mg/ml herring sperm DNA; 0.5 mg/ml acetylated BSA; and 300 ul with 1xMES hyb buffer.

The hybridization reaction is conducted with non-biotinylated IVT (purified by RNcasy columns) (see example 1 for steps from tissue to IVT): The following mixture is prepared:

IVT antisense RNA; 4 µg:	µl
Random Hexamers (1 µg/µl):	4 µl
H_2O:	µl
	14 µl

Incubate the above 14 µl mixture at 70°C for 10 min.; then put on ice.

The Reverse transcription procedure uses the following mixture:

0.1 M DTT:	3 µl
50X dNTP mix:	0.6 µl
H_2O:	2.4 µl
Cy3 or Cy5 dUTP (1mM):	3 µl
SS RT II (BRL):	1 µl
	16 µl

The above solution is added to the hybridization reaction and incubated for 30 min., 42°C. Then, 1 µl SSII is added and incubated for another hour before being placed on ice.

The 50X dNTP mix contains 25mM of cold dATP, dCTP, and dGTP, 10mM of dTTP and is made by adding 25 µl each of 100mM dATP, dCTP, and dGTP; 10 µl of 100mM dTTP to 15 µl H_2O.]

RNA degradation is performed as follows. Add 86 µl H_2O, 1.5 µl 1M NaOH/ 2 mM EDTA and incubate at 65°C, 10 min.. For U-Con 30, 500 µl TE/sample spin at 7000 g for 10 min, save flow through for purification. For Qiagen purification, suspend u-con recovered material in 500 µl buffer PB and proceed using Qiagen protocol. For DNAse digestion, add 1 ul of 1/100 dilution of DNAse/30 ul Rx and incubate at 37°C for 15 min. Incubate at 5 min 95°C to denature the DNAse.

Sample preparation

For sample preparation, add Cot-1 DNA, 10 µl; 50X dNTPs, 1 µl; 20X SSC, 2.3 µl; Na pyro phosphate, 7.5 µl; 10 mg/ml Herring sperm DNA; 1 ul of 1/10 dilution to 21.8 final vol. Dry in speed vac. Resuspend in 15 µl H_20. Add 0.38 µl 10% SDS. Heat 95°C, 2 min and slow cool at room temp. for 20 min. Put on slide and hybridize overnight at 64°C. Washing after the hybridization: 3X SSC/0.03% SDS: 2 min., 37.5 ml 20X SSC+0.75ml 10% SDS in 250ml H_2O; 1X SSC: 5 min., 12.5 ml 20X SSC in 250ml H_2O; 0.2X SSC: 5 min., 2.5 ml 20X SSC in 250ml H_2O. Dry slides and scan at appropiate PMT's and channels.

TABLE 1: Figure 1 from BRCA 001 US

Table 1 shows genes, (incorporated in their entirety here and throughout the application where primekeys are provided), downregulated in tumor tissue compared to normal breast tissue.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of normal breast tissue to tumor

Pkey	ExAccn	UnigeneID	UnigeneTitle	R1
100472	D90084	Hs.1023	pyruvate dehydrogenase (lipoamide) alpha	5
100499	T51986	Hs.283108	hemoglobin, gamma G	10
100545	M55405		gb:Homo sapiens mucin (MUC-3) mRNA, part	5
100549	BE142019	Hs.222056	Homo sapiens cDNA FLJ11572 fis, clone HE	10
100613	X52078	Hs.101047	transcription factor 3 (E2A immunoglobul	5
100635	BE259039	Hs.129953	Ewing sarcoma breakpoint region 1	5
100645	X16841	Hs.167988	neural cell adhesion molecule 1	5
100654	A03758		NM_000477*:Homo sapiens albumin (ALB), m	10
100702	L27065		gb:Human neurofibromatosis 2 (NF2) mRNA,	5
100915	M60832	Hs.249239	collagen, type VIII, alpha 2	5
100971	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte	10
101125	AJ250562	Hs.82749	transmembrane 4 superfamily member 2	5
101168	M90424	Hs.2099	lipocalin 1 (protein migrating faster th	5
101184	NM_001674	Hs.460	activating transcription factor 3	10
101336	NM_006732	Hs.75678	FBJ murine osteosarcoma viral oncogene h	10
101387	X03350	Hs.4	alcohol dehydrogenase 1B (class I), beta	10
101447	M21305		gb:Human alpha satellite and satellite 3	10
101481	N98569	Hs.78422	phospholipase A2, group IIA (platelets,	10
101511	M27826	Hs.267319	endogenous retroviral protease	10
101634	AV650262	Hs.75765	GRO2 oncogene	5
101736	M74447	Hs.502	transporter 2, ATP-binding cassette, sub	10
102208	U22961		gb:Human mRNA clone with similarity to L	10
102297	NM_001504	Hs.198252	G protein-coupled receptor 9	5
102450	U48251	Hs.75871	protein kinase C binding protein 1	10
102515	U89337	Hs.169888	tenascin XB	10
102571	U60115	Hs.239069	four and a half LIM domains 1	5
102800	AA313538		gb:EST185419 Colon carcinoma (HCC) cell	10
102857	NM_006744	Hs.76461	retinol-binding protein 4, interstitial	10
102990	AA829288	Hs.332053	serum amyloid A1	10
103434	X98085	Hs.54433	tenascin R (restrictin, janusin)	5
103747	AA081995		gb:zn26d06.r1 Stratagene neuroepithelium	10
103750	AA126129		gb:zm78c07.r1 Stratagene neuroepithelium	5
103812	AA137107	Hs.326391	Homo sapiens, clone MGC:16638, mRNA, com	10
103851	AA326216	Hs.8719	hypothetical protein MGC1136	5
104080	AB041036	Hs.57771	kallikrein 11 (KLK11; TLSP; PRSS20; hipp	5
104093	R50727	Hs.336970	ESTs	10
104108	AA422123		gb:zv26h12.r1 Soares_NhHMPu_S1 Homo sapi	5
104109	AL353957	Hs.284181	hypothetical protein DKFZp434P0531	10
104250	F06638	Hs.12440	Homo sapiens clone 24734 mRNA sequence	10
104340	AA426189		gb:zw11e09.r1 Soares_NhHMPu_S1 Homo sapi	5
104492	N73185	Hs.94285	EST	10
104506	N91071	Hs.109650	ESTs	10
104511	N99542	Hs.572	orosomucoid 1	5
104532	AI498763	Hs.203013	hypothetical protein FLJ12748	10

104536	R24024	Hs.158101	Homo sapiens cDNA FLJ14673 fis, clone NT	5
104572	Y11312	Hs.132463	phosphoinositide-3-kinase, class 2, beta	5
104659	AW969769	Hs.105201	ESTs	5
104677	AA009764	Hs.190380	ESTs	10
104711	AA017245	Hs.32794	ESTs	10
104731	AA019300	Hs.125070	ESTs, Moderately similar to I54374 gene	10
104764	AI039243	Hs.278585	ESTs	5
105005	AI298208	Hs.28805	ESTs	10
105038	AA130390	Hs.25549	hypothetical protein FLJ20698	10
105105	R61532	Hs.87016	hypothetical protein FLJ22938	5
105231	AW970043	Hs.238039	hypothetical protein FLJ11090	5
105239	AA221038		gb:zr03f12.r1 Stratagene NT2 neuronal pr	10
105921	AA421973	Hs.169119	ESTs, Weakly similar to T25731 hypotheti	5
105957	BE242857	Hs.27021	hypothetical protein FLJ11159	5
106052	N79885	Hs.6382	ESTs, Highly similar to T00391 hypotheti	10
106119	AL359624	Hs.11387	KIAA1453 protein	5
106181	AI803651	Hs.191608	ESTs	10
106194	AW976171	Hs.286194	hypothetical protein FLJ22233	5
106283	AI085846	Hs.25522	KIAA1808 protein	10
106379	AL042069	Hs.119021	DKFZP434N061 protein	10
106451	AW235928	Hs.313182	ESTs	10
106491	AA135668	Hs.10083	Homo sapiens, clone IMAGE:4139786, mRNA,	10
106700	AA906434	Hs.3776	zinc finger protein 216	5
106782	AW054886	Hs.25682	Homo sapiens mRNA for KIAA1863 protein,	10
106851	AI458823		gb:tb04g09.x1 NCI_CGAP_Lu24 Homo sapiens	5
106870	AI983730	Hs.26530	serum deprivation response (phosphatidyl	5
106892	AI347578	Hs.124015	hypothetical protein MGC2605	5
106954	AF126847	Hs.204038	indolethylamine N-methyltransferase	5
106991	AJ223811	Hs.30127	hypothetical protein	5
107103	AI446183	Hs.9572	ESTs, Highly similar to CYA5_HUMAN ADENY	5
107124	AB006532	Hs.31442	RecQ protein-like 4	10
107148	AI005036	Hs.334305	GS1999full	10
107214	AF127026	Hs.5394	myosin IA	10
107242	AB020672	Hs.175411	KIAA0865 protein	10
107331	AI905985	Hs.111805	ESTs	10
107351	U51704	Hs.323428	ESTs, Moderately similar to ALU8_HUMAN A	5
107423	W26652	Hs.6163	PTEN induced putative kinase 1	5
107447	W28516	Hs.19210	hypothetical protein MGC11308	10
107451	AL042425	Hs.283976	hypothetical protein PRO2389	10
107453	AI092790	Hs.334703	hypothetical protein FLJ14529	5
107459	W38002		Empirically selected from AFFX single pr	10
107683	N53167	Hs.47623	ESTs	10
107711	W96141	Hs.220687	ESTs	10
107754	AA017462	Hs.269244	ESTs	10
107757	BE621721	Hs.280792	hypothetical protein FLJ12387 similar to	10
107864	AA025060	Hs.61246	ESTs	10
107872	BE271708	Hs.95110	ESTs, Weakly similar to A55943 1-phospha	10
107888	AA025838	Hs.191637	ESTs	5
107997	AL049176	Hs.82223	chordin-like	10
108056	AA043675	Hs.62633	ESTs	10
108081	AA093658	Hs.28576	muscleblind (Drosophila)-like	5
108113	AA012881	Hs.72531	hypothetical protein FLJ11836	10
108238	AA059473	Hs.66783	EST	10
108257	AA677927	Hs.144269	ESTs	5
108335	AA070500		gb:zm70h03.s1 Stratagene neuroepithelium	5
108351	AA071193		gb:zf79b12.s1 Soares_pineal_gland_N3HPG	10
108382	NM_006770	Hs.67726	macrophage receptor with collagenous str	5
108392	AA075124		gb:zm86a01.s1 Stratagene ovarian cancer	10
108441	AA079079		gb:zm97c09.s1 Stratagene colon HT29 (937	10
108446	AA085383		gb:zm13g03.s1 Stratagene hNT neuron (937	10
108497	AA074897		gb:zm85e05.r1 Stratagene ovarian cancer	10
108604	AA934589	Hs.49696	ESTs	5
108662	AF117646	Hs.156637	Cas-Br-M (murine) ectropic retroviral tr	5
108706	AA121820	Hs.74569	KIAA0842 protein	10
108738	AA126583	Hs.158725	ESTs	10
108827	AI273892	Hs.110470	ESTs	10
109123	AI026376	Hs.73232	ESTs	10

109389	AA101325	Hs.86154	hypothetical protein FLJ12457	10
109548	F01449	Hs.26954	Homo sapiens mRNA; cDNA DKFZp762G123 (fr	5
109919	R40604	Hs.129539	ESTs, Weakly similar to MCAT_HUMAN MITOC	10
110006	AI094674	Hs.30524	ring finger protein 24	10
110141	H46749	Hs.31540	ESTs	10
110354	W22165	Hs.22588	ESTs	5
110433	AW294162	Hs.301062	UDP-N-acetyl-alpha-D-galactosamine:polyp	10
110448	H51276	Hs.13526	hypothetical protein FLJ12688	10
110455	H52576		gb:yl85e08.r1 Soares_pineal_gland_N3HPG	5
110540	H72639	Hs.167608	ESTs	5
110553	H60593	Hs.124990	ESTs	10
110976	AL044174	Hs.159526	patched (Drosophila) homolog	10
110987	AI753316	Hs.26034	ESTs	5
111158	N66616	Hs.138629	H.sapiens mRNA for subtelomeric repeat s	5
111168	AI798376		gb:tr34b07.x1 NCI_CGAP_Ov23 Homo sapiens	10
111187	AJ224864	Hs.9688	leukocyte membrane antigen	5
111307	AA641636	Hs.37477	ESTs, Weakly similar to T46908 hypotheti	5
111400	R00144	Hs.189771	ESTs	10
111498	AI168511		gb:ow90h09.s1 Soares_fetal_liver_spleen_	10
111651	R16733	Hs.20499	ESTs	10
111738	R26065		gb:yh39d03.s1 Soares placenta Nb2HP Homo	5
111803	AA593731	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	10
111995	R42333	Hs.302292	ESTs	10
112071	AL117490	Hs.47225	Ras-associated protein Rap1	10
112204	NM_006668	Hs.25121	cytochrome P450, subfamily 46 (cholester	10
112258	R51889	Hs.24990	ESTs	5
112490	R31094	Hs.24378	ESTs	10
112588	R77302		gb:yl75h08.s1 Soares placenta Nb2HP Homo	10
112654	BE618629	Hs.268809	ESTs	5
112784	T98628	Hs.191290	ESTs	5
112817	AI057205	Hs.14584	ESTs	5
112885	AA581428	Hs.5021	EST	10
112913	T16837	Hs.4241	ESTs	5
113149	T51588		gb:yb27e06.s1 Stratagene fetal spleen (9	10
113174	T54659	Hs.301755	Homo sapiens cDNA FLJ11465 fis, clone HE	5
113203	AA743563	Hs.10305	ESTs	5
113299	AW207424	Hs.332594	ESTs	10
113367	N92359	Hs.14516	ESTs, Moderately similar to A48752 B-cel	10
113457	R16763	Hs.268679	ESTs	5
113563	AA913635	Hs.326413	Homo sapiens cDNA FLJ20812 fis, clone AD	10
113574	R06874	Hs.268628	ESTs, Moderately similar to ALU1_HUMAN A	5
113776	AI791905	Hs.95549	hypothetical protein	10
113790	AI244311	Hs.26912	ESTs	10
113807	W07586	Hs.8045	ESTs	3
113958	W86195		gb:zh54e05.s1 Soares_fetal_liver_spleen_	10
114211	Z39319	Hs.27347	EST	10
114254	AB018263	Hs.180338	tumor necrosis factor receptor superfami	5
114349	AA745978	Hs.28273	ESTs	5
114449	AA020736		gb:ze63b11.s1 Soares retina N2b4HR Homo	5
114484	AA034378	Hs.267319	endogenous retroviral protease	5
114576	AA055096		gb:zm50a02.s1 Stratagene fibroblast (937	5
114624	AA081507		gb:zm05b10.r1 Stratagene hNT neuron (937	5
114844	AA234826	Hs.87386	EST	5
114906	AA234462	Hs.87350	ESTs	5
115624	AK000725	Hs.50579	hypothetical protein FLJ20718	3
115668	AF173081	Hs.178215	Vertebrate LIN7 homolog 1, Tax interacti	5
115712	AB020649	Hs.74569	KIAA0842 protein	5
115889	AA398841	Hs.39850	hypothetical protein FLJ20517	10
115949	AI478427	Hs.43125	esophageal cancer related gene 4 protein	10
116107	AL133916	Hs.172572	hypothetical protein FLJ20093	10
116180	AA463902	Hs.13522	ESTs, Weakly similar to I38022 hypotheti	5
116267	AW968703	Hs.30085	hypothetical protein FLJ23186	5
116291	AW410377	Hs.41502	hypothetical protein FLJ21276	5
116527	AW194253	Hs.68807	ESTs	10
116659	BE314852	Hs.168694	Homo sapiens clone 23763 unknown mRNA, p	5
116708	F10528	Hs.70001	ESTs, Moderately similar to JC6169 nucle	5
117058	AW801806		gb:IL5-UM0070-110400-062-g07 UM0070 Homo	5

117151	AI803656	Hs.42373	ESTs	5
117226	N20468		gb:yx39b10.s1 Soares melanocyte 2NbHM Ho	10
117323	AI472863	Hs.43387	ESTs	5
117571	N34417	Hs.44584	ESTs	3
117624	N26827	Hs.82364	ESTs, Weakly similar to JC4124 pregnancy	5
117673	N40551	Hs.184043	Homo sapiens Ets-1 binding protein (E1B)	10
117847	N49285	Hs.182391	ESTs	10
117877	AW263476	Hs.44268	myelin gene expression factor 2	10
117919	BE222341	Hs.279472	ESTs	5
118049	N53145		gb:yv55f09.s1 Soares fetal liver spleen	3
118413	AW955696	Hs.90960	ESTs	10
118613	AI078236	Hs.49688	ESTs	5
118684	N70907	Hs.230619	EST	10
118858	AL122040	Hs.102981	Homo sapiens mRNA; cDNA DKFZp434G1972 (f	3
118902	AA993527	Hs.293907	hypothetical protein FLJ23403	5
119039	AI160570	Hs.252097	pregnancy specific beta-1-glycoprotein 6	3
119159	AF142419	Hs.15020	homolog of mouse quaking QKI (KH domain	5
119218	AA514422	Hs.221849	ESTs	5
119317	AK002001	Hs.51305	v-maf musculoaponeurotic fibrosarcoma (a	10
119366	T77892		gb:yd20f04.s1 Soares fetal liver spleen	5
119378	TB1824	Hs.90949	EST	5
119528	W38051		Empirically selected from AFFX single pr	10
119792	AL049798	Hs.80552	dermatopontin	3
119800	AF086332	Hs.58314	ESTs	10
119817	AF088061	Hs.159690	ESTs	5
119835	AF086429	Hs.58429	ESTs	5
119923	AW803308	Hs.62954	ferritin, heavy polypeptide 1	5
119961	U34249	Hs.337461	Human putative zinc finger protein (ZNFB	5
120379	AL042725		gb:DKFZp434B1822_r1 434 (synonym: htes3)	10
120931	AW136934	Hs.97162	ESTs	5
121037	AA907743	Hs.142373	ESTs	5
121282	AA401695	Hs.97334	ESTs	5
121382	AA405763	Hs.111939	Homo sapiens cDNA FLJ20470 fis, clone KA	5
121764	AA421452	Hs.164851	ESTs, Weakly similar to KIAA0926 protein	5
122034	AK000229	Hs.98017	Homo sapiens cDNA FLJ20222 fis, clone CO	10
122441	AA447555	Hs.99116	EST	10
122756	AA458945	Hs.95898	ESTs	10
122771	AW135093	Hs.97282	ESTs, Highly similar to G100_HUMAN 110 K	5
123601	AA609122	Hs.112845	Homo sapiens mRNA; cDNA DKFZp434D2472 (f	5
123823	AI024595	Hs.97508	a disintegrin and metalloproteinase dome	5
123941	AA521529		gb:af47a02.s1 Soares_total_fetus_Nb2HF8_	10
124215	H62570		gb:yr44a01.r1 Soares fetal liver spleen	5
124276	H83465		gb:ys91a11.s1 Soares retina N2b5HR Homo	5
124680	AK001527	Hs.163953	hypothetical protein FLJ10685	5
125099	NM_014312	Hs.112377	cortic al thymocyte receptor (X. laevis	10
125121	T98199	Hs.48403	hypothetical protein FLJ10847	10
125188	BE299567	Hs.271749	ESTs, Moderately similar to ALU8_HUMAN A	5
125284	NM_002666	Hs.103253	perilipin	10
125906	BE256206	Hs.17775	p75NTR-associated cell death executor; o	5
128484	AA485421	Hs.270503	ESTs, Weakly similar to ALU7_HUMAN ALU S	10
128511	NM_002250	Hs.10082	potassium intermediate/small conductance	10
128538	R44214	Hs.101189	ESTs	5
128608	C16161	Hs.283040	hypothetical protein PRO2543	5
128850	AA193106	Hs.180817	chromosome 11 open reading frame 23	10
128870	H39537	Hs.75309	eukaryotic translation elongation factor	10
128903	AW150717	Hs.296176	STAT induced STAT inhibitor 3	10
128931	N62889	Hs.107242	Homo sapiens cDNA FLJ12965 fis, clone NT	10
129001	AA443323	Hs.107812	BPOZ protein	5
129091	AA056483	Hs.301463	Human Chromosome 16 BAC clone CIT987SK-A	5
129101	NM_013403	Hs.108665	zinedin	10
129146	AL117472	Hs.108924	SH3-domain protein 5 (ponsin)	5
129213	AI146494	Hs.109525	ESTs, Weakly similar to IRX2_HUMAN IROQU	3
129228	U40714	Hs.239307	tyrosyl-tRNA synthetase	5
129265	AA530892	Hs.171695	dual specificity phosphatase 1	5
129285	BE617015	Hs.11008	ESTs, Moderately similar to T17372 plasm	10
129348	AF110141	Hs.288908	WAS protein family, member 2	10
129368	NM_003877	Hs.110776	STAT induced STAT inhibitor-2	5

129371	X06828	Hs.110802	von Willebrand factor	5
129381	AW245805	Hs.110903	claudin 5 (transmembrane protein deleted	10
129440	W37944	Hs.4007	Sarcolemmal-associated protein	5
129441	BE061069	Hs.301943	KIAA0467 protein	10
129516	AF020038	Hs.11223	Isocitrate dehydrogenase 1 (NADP+), solu	10
129554	BE222078	Hs.113069	ESTs	10
129684	BE822468	Hs.11924	ESTs, Weakly similar to I38022 hypothetl	5
129702	AI304966	Hs.12035	ESTs, Weakly similar to I38022 hypothetl	5
129778	AK001676	Hs.12457	hypothetical protein FLJ10814	10
129893	AK000956	Hs.13209	hypothetical protein FLJ10094	5
129928	AI338993	Hs.134535	ESTs	5
129973	AJ251760	Hs.273385	guanine nucleotide binding protein (G pr	5
129977	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	5
130014	NM_001158	Hs.143102	amine oxidase, copper containing 2 (reti	5
130085	M62402	Hs.274313	Insulin-like growth factor binding prote	10
130089	AA452006	Hs.333199	ESTs	5
130162	W80711	Hs.319946	Homo sapiens mRNA for KIAA1727 protein,	5
130243	D88435	Hs.153227	cyclin G associated kinase	10
130315	AI241084	Hs.154353	nonselective sodium potassium/proton exc	5
130339	AA435746		gb:zt79e03.s1 Soares_testis_NHT Homo sap	5
130400	V00517	Hs.283108	hemoglobin, gamma G	10
130436	NM_001928	Hs.155597	D component of complement (adipsin)	10
130478	X72308	Hs.251526	small inducible cytokine A7 (monocyte ch	5
130480	BE222978	Hs.15760	MYG1 protein	10
130494	AW390834	Hs.75874	pregnancy-associated plasma protein A	5
130583	BE270472	Hs.279900	HSPC015 protein	10
130589	AL110226	Hs.16441	DKFZP434H204 protein	10
130606	AI652143	Hs.288382	hypothetical protein FLJ13111	5
130634	AI769067	Hs.127824	ESTs, Weakly similar to T28770 hypothetl	3
130683	AA993269	Hs.17872	Homo sapiens, clone IMAGE:3875012, mRNA	10
130689	NM_006691	Hs.17917	extracellular link domain-containing 1	10
130716	AA232075	Hs.18259	XPA binding protein 1; putative ATP(GTP)	5
130718	AF283462	Hs.18376	KIAA1319 protein	10
130722	N41322	Hs.18441	ESTs	5
130798	M81349	Hs.1955	serum amyloid A4, constitutive	10
130840	BE048821	Hs.20144	small inducible cytokine subfamily A (Cy	10
131184	AB040935	Hs.23954	cerebral cell adhesion molecule	10
131281	AA360419	Hs.171776	inositol(myo)-1(or 4)-monophosphatase 1	10
131282	X03350	Hs.4	alcohol dehydrogenase 1B (class I), beta	10
131328	AW939251	Hs.25647	v-fos FBJ murine osteosarcoma viral onco	10
131340	AK000393	Hs.25817	BTB (POZ) domain containing 2	5
131341	AF110908	Hs.297660	TNF receptor-associated factor 3	5
131408	H83294	Hs.284122	Wnt inhibitory factor-1	5
131489	BE394648	Hs.27414	hypothetical protein	5
131543	AW968881	Hs.41839	programmed cell death 2	10
131692	BE559681	Hs.30736	KIAA0124 protein	5
131753	AA829288	Hs.332053	serum amyloid A1	10
131756	AA443966	Hs.31595	ESTs	10
131785	H59342	Hs.26320	TRABID protein	10
131815	AA021258	Hs.32753	ESTs	5
131819	BE244961	Hs.173103	FE65-LIKE 2	5
131828	AJ000263	Hs.278658	keratin, hair, basic, 6 (monilethrix)	10
131888	AW294659	Hs.34054	Homo sapiens cDNA: FLJ22488 fis, clone H	5
131927	AJ003112	Hs.34780	doublecortex; lissencephaly, X-linked (d	5
131949	AK000010	Hs.258798	hypothetical protein FLJ20003	10
132115	H81604	Hs.178471	KIAA0798 gene product	5
132177	X80818	Hs.178078	glutamate receptor, metabotropic 4	5
132296	AA467752	Hs.195161	ESTs	5
132426	AW118072	Hs.89981	diacylglycerol kinase, zeta (104kD)	10
132477	S68874	Hs.170917	prostaglandin E receptor 3 (subtype EP3)	5
132675	AI291498	Hs.5476	Homo sapiens, clone IMAGE:3530123, mRNA,	10
132796	NM_006283	Hs.173159	transforming, acidic coiled-coil contain	10
132898	W28548	Hs.224829	ESTs	10
132905	NM_004235	Hs.7934	Kruppel-like factor 4 (gut)	10
132953	BE175845	Hs.321264	LBP protein 32	5
133116	BE563966	Hs.6529	ESTs, Weakly similar to I78885 serine/th	5
133120	NM_003278	Hs.65424	tetranectin (plasminogen-binding protein	10

133139	AF052138	Hs.6580	Homo sapiens cDNA: FLJ23227 fis, clone C	5
133163	AA668224	Hs.6634	Homo sapiens cDNA: FLJ22547 fis, clone H	5
133268	AW956781	Hs.293937	ESTs, Weakly similar to FXD2_HUMAN FORKH	5
133272	NM_002776	Hs.69423	kallikrein 10 (KLK10) (PRSSL1) (nes1)	5
133379	AA207059		gb:zq80h09.s1 Stratagene hNT neuron (937	5
133407	AF017987	Hs.7306	secreted frizzled-related protein 1	5
133552	H21497	Hs.7471	BBP-like protein 1	5
133702	L02321	Hs.75652	glutathione S-transferase M5	5
133719	H26904	Hs.75736	apolipoprotein D	5
133731	N71725	Hs.272572	hemoglobin, alpha 2	10
133789	T85626	Hs.76239	hypothetical protein FLJ20608	5
134007	AF072441	Hs.7840	calcineurin binding protein 1	10
134055	D88082	Hs.182423	ES1 (zebrafish) protein, human homolog o	10
134111	AI372588	Hs.8022	TU3A protein	10
134117	AA081846	Hs.7921	Homo sapiens mRNA; cDNA DKFZp566E183 (fr	10
134177	BE243319	Hs.79572	KIAA0652 gene product	5
134308	AW905827	Hs.81454	ketohexokinase (fructokinase)	10
134381	BE549343	Hs.62208	acyl-Coenzyme A dehydrogenase, very long	5
134369	AF207664	Hs.8230	a disintegrin-like and metalloprotease (	5
134449	L34155	Hs.83450	laminin, alpha 3 (nicein (150kD), kalnl	5
134457	AI190413	Hs.8373	ESTs	10
134496	M64936		gb:Homo sapiens retinoic acid-inducible	10
134510	NM_002757	Hs.250870	mitogen-activated protein kinase kinase	10
134550	M26315	Hs.85258	CD8 antigen, alpha polypeptide (p32)	10
134577	BE244323	Hs.85951	exportin, tRNA (nuclear export receptor	5
134591	U73394	Hs.166085	killer cell immunoglobulin-like receptor	5
134678	AL008583	Hs.182595	dynein, axonemal, light polypeptide 4	5
134728	D10216	Hs.89394	POU domain, class 1, transcription facto	5
134758	NM_000078	Hs.89538	cholesteryl ester transfer protein, plas	10
134788	T29618	Hs.89640	TEK tyrosine kinase, endothelial (venous	10
134912	T87521	Hs.261457	ESTs	5
134963	NM_003394	Hs.91985	wingless-type MMTV integration site fami	10
134969	H22570	Hs.172572	hypothetical protein FLJ20093	5
135001	AA302517	Hs.92732	KIAA1444 protein	5
135066	X04430	Hs.93913	interleukin 6 (interferon, beta 2)	10
135173	AL036557	Hs.95910	putative lymphocyte G0/G1 switch gene	10
135197	U76456	Hs.190787	tissue inhibitor of metalloproteinase 4	5
135219	AB002361	Hs.96633	KIAA0363 protein	5
135250	U83171	Hs.97203	small inducible cytokine subfamily A (Cy	5
135304	AA416829	Hs.191597	ESTs	5
135337	AA905406	Hs.9905	ESTs, Weakly similar to unnamed protein	3
135417	X55019	Hs.99975	cholinergic receptor, nicotinic, delta p	10
101367	X03350	Hs.4	alcohol dehydrogenase 1B (class I), beta	5
128870	H39537	Hs.75309	eukaryotic translation elongation factor	5
129381	AW245805	Hs.110903	claudin 5 (transmembrane protein deleted	5
130085	M62402	Hs.274313	Insulin-like growth factor binding prote	5
130689	NM_006691	Hs.17917	extracellular link domain-containing 1	10
133120	NM_003278	Hs.65424	tetranectin (plasminogen-binding protein	3
133407	AF017987	Hs.7306	secreted frizzled-related protein 1	5
133731	N71725	Hs.272572	hemoglobin, alpha 2	5
134369	AF207664	Hs.8230	a disintegrin-like and metalloprotease (	5
135066	X04430	Hs.93913	interleukin 6 (interferon, beta 2)	10
135173	AL036557	Hs.95910	putative lymphocyte G0/G1 switch gene	5
322580	AK001852	Hs.274151	ligatin	5
408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor, type 2	10
418043	AW377752	Hs.83341	AXL receptor tyrosine kinase	5
427458	BE208364	Hs.29283	ESTs, Weakly similar to LKHU proteoglycan link	5
446874	AA563892	Hs.306000	solute carrier family 4 (anion exchanger), memb	10
449826	U85642	Hs.138506	ESTs	5
	RC_H15814_s		Human apM1 mRNA for GS3109 (novel adipose specific collagen	10
	YEL024w/RIP1		EST - YEL024w/RIP1	3

TABLE 1A

Table 1 A shows the accession numbers for those pkeys lacking unigeneID's for Table 1. For each probeset, we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accessions
108446	112224_1	AA085383 AA126091 AA074174 AA075373 AA079120 AA070831 AA075978 AA075372 AA128503
108497	110079_2	AA074897 AA113914 AA064871 AA078329 AA071309 AA084710 AA129030 AA075042 AA074794 AA071453 AA078803 AA148628 AA122204 AA074159 AA126185 AA079117 AA127089 AA070912 AA079280 AA131372 AA078833 AA071087 AA076131 AA071047 AA079401 AA083070 AA102076 AA115163 AA074198 AA134725 AA113889 AA121103 AA075041 AA065148 AA071310 AA101144 AA079859 AA078931 AA079209 AA070928 AA068994 AA069817 AA076187 AA069053 AA131489 AA071308 AA063317 AA070156 AA071430 AA076056 AA075684 AA070053 AA126283 AA126078 AA075895 AA079208 AA074583 AA071086 AA079823 AA070627 AA078802 AA076622 AA065051 AA079143 AA071110 AA079434 AA148748 AA079230 AA085188 AA074485 AA070580 AA076151 AA083166 AA085118 AA079450 AA085044 AA120938 AA079200 AA100188 AA081472 AA122355 AA129031 AA085382 AA069220 AA070940 AA075968 AA074563 AA084027 AA115929
124215	1597154_1	H62570 H59063
117058	1219924_1	AW801806 H90434 BE085530
110455	46874_1	H52578 AF085971 H52172
111168	38585_1	AI798376 646400 AW811617 AW811616 W00557 BE142245 AW858232 AW861851 AW856362 AA232351 AA218567 AA055556 AW858231 AW857541 AW814172 H66214 AW814398 AF134164 AA243093 AA173345 AA199942 AA223384 AA227092 AA227080 T12379 AA092174 T61139 AA149776 AA699829 AW879188 AW813567 AW813538 AI267168 AA157718 AA157719 AA100472 AA100774 AA130758 AA157705 AA157730 AA157715 AA053524 AW849581 AW854568 C05254 AW882836 T92637 AW812621 AA206583 AA209204 BE156909 AA226824 AI829309 AW991957 N66951 AA527374 H66215 AA045564 AI594265 H60808 AA149726 AW195820 BE081333 BE073424 AW817662 AW817705 AW817703 AW817659 BE081531 H59570
111498	411008_1	AI168511 AI022712 AA700366 R07371 R07324
104340	46289_10	AA426189 F15201
103747	117944_1	AA081995 AA101099
134496	46501_1	M64938 AI025512 AI382987 BE061777 AA089988 BE169930 T41176 AW594624 BE502415 AA121893 AI269283 T40311 AI684569 AA257011 AI079277 AI241318 BE327710 AW975215 AW898268 AA884990 BE327514
103750	118365_1	AA126129 AA126033 AA082561
105239	34824_1	AA221036 R87170 BE537068 BE544757 C18935 AW812058 T92565 AA227415 AA233942 AA223237 AA668403 AA601627 AW869639 BE061833 BE000620 AW961170 AW847519 AA308542 AW821833 AW945688 C04699 AA205504 AA377241 AW821657 AA055720 AW817981 AW856468 AA155719 AA179928 T03007 AW754288 AA227407 AA113928 AA307904 C16859
120379	34624_3	AL042725 BE063316 AW975610 AA457591 BE062092 AI655202 AA714296 AI267264 AI075321 AA223286 AA071122 AA227849 AA218700 AI696002 AA101887 AA099426 AA135997 AL041698 T02815 T51824 AA207189 T59230 T51868 AA663341 BE165757 AW818104 AW392886 AA584918 AA099408 AW856396 AW861859 AA053045
114624	111686_1	AA081507 AA070071 AA070840 AA084362
106851	322947_1	AI458623 AA639708 AA485409 R22065 AA485570
108392	113549_1	AA075124 AA075208
100545	22955_11	M55405 AW752552
100654	tigr_HT2969	A03758 A06977 A15293 D17029 D17107 D17171 L00132 L00133 M12523 M13075 M13076 M92816 U22961 V00494 V00495 X51363 X51364 X51365
100702	tigr_HT3413	L27065
102208	6735_9	U22961 AA203823 AA503337 AI174733 AI192802 C06092 AA035357 AI190619 AI199244 AI828450 AA602296 AI378195 AI209170 AI186853 AI127795 AI183848 H77389 AI589465 AA629390 H94306 AI018388 R68584 AA027196 AI745413 AI685092 AI093426 AI823873 AI074570 N50098 AA047486 N25060 AA327614 AI042512 AI383957 AA156873 AI333101 N70806 AI141254 AI383191 AI401237 AI080709 AI093400 W84549 T90806 R00012 W01413 AA630557 AI378348 AI559265 AA877103 W84484 AA625146 R68379 AI133207 AI132980 AI133214 AI084826 AI061616 AI133473 AI174852 AI133404 AI133272 V00494 M12523 M12523 AI207526 AI133120 AI084802 AI174993 AI114729 AI061845 AI084716 AI084959 H77388 T85706 AF075298 AI110799 D17107 NM_000477 AF190168 R50724 AI248416 AI207432 AI133684 AI133345 AI174710 AI133290 AI133304 AI174948 AI207484 AI110717 AF074624 AI114515 AF063516 AI110842 AI114559 AI114498 AI114759 AI207568 AI084960 AI174753 AI114668 R69184 R00011 AI084997 T60501 AI207701 T71735 AA385318 H73569 T60496 H94399 AI133158 T74675 AA484750 T73413 T55909 R50261 T72061 N80533 T51189 T74938 AI207490 AI132925 AI084701 AI174748 AI114663 AI133104 AI132999 AI133100 AI084925 AI084979 AI133063 AA343347 T69091 AA233989 T39772 AI444620 T52290 D16931 T40012 T48403 T58926 T69195 AI133061 T50850 AI400677 AI091138 AA334608 T57411 Z20979 N56507 T87485 AI133622 AA343370 T40075 T69671 T53849 T74820 AF075316 AI110818 T40121 T57381 AI114468 AA332728 T51362 AI114589 R06691 AI110629 AF063503 AI140543 AA334661 AA332720 AA343262 T73513 T86549 AI114840 T57284 T39961 T61407 T72757 T51749 T56630 AA343125 T72126 R94135 T83028 T39972 T39896 AI174788 AI132926 R09237 AI084838 AI133680 T60398 T88753 T55930 T92126 AI444602 T60998 AI114792 H93911 AI133106 R10779 AI065020 T90925 T50889 D17029 AI133703 AA333805 AI133040 AI133017 AI084857 AI110730 AF074637 AI207567 H71080 T73217 AA343950 AI174743 AA334224 AA334281 R06692 T64739 T40183 T60826 T61681 T73179 R01842 AA501730 T39931 T39662 T40136 AA334904 T71425 H77784 R00874 AI065049 T84512 T55918 AI207595 T39951 AA005018 T60381 T69178 T73356 T58795 T61233 T39955 T60612 AI114676 AI064778 AA035710 W52763 AI114788 T83564 AA341859 T61684 T55769 AI114710 T51776 AA343213 AI114714 T58102 AI110809 R28984 AI174854 AA305875 AA343592 T53838 T48669 T84721 T55508 W05241 T54019 T57945 T60513 T48364 AF075308 W88731 T82851 T48269 H54053 T73211 AI114590 T48317 T55965 T74857 R84226 T56552 T52231 T74946 T76976 R02576 T95668 AI203974 AI189471 AA005147 AI478102 AI207662 AI192792 AI768421 AI064737 AW051713 AA936693 AI133117 AI768232 AI913648 T83962 AI065112 AI207689 AI174684 AI207702 T81475 AI133325 AI032512 AA701169 AI938354 AI114720 AI433289 AA046980 AI823482 AI114536 AA860851 AW242644 R07469 AW300438 AI133416 AW271670 AI991363 T78943 AI823481 AA845518 AA719124 AA883454 T68850 T69115 AI935509 AI150977 T82890 T71374 T68294 AI174774 T67411 T68318 AI064589 T56624 T69010 T68982 T68302 AI332829 T72908 AI064819 AI205680 T62895 T69430 T95111 AA025050 T73330 W52657 T71984 T69118 W92684 AI114860 T62093 T81797 AI522333 T73322 H92981 T56018 T61811 T57232 AI336158 T61821 T69457 T62900 T62912 T72917 T46885 AI702448 T57212 T57203 R94581 T71311 T61819 T69358 T67708 T70918 T59166 AI187111 T64308 T62071 T69427 AI114750 T60430 R09734 T69033 T69141 T69453 T87908 R16809 T69394 AI207729 T55839 T90273 T73339 AW194909 T75486 T71850 T71305 T71287 T53877 T73452 T68852 N75290 AI312890 T67751 AI174983 T51879 T54851 H69880 N73734 AA443453 T73466 H69672 N53869 T68447 D11809 D12412 T64300 T28321 T55864
123941	genbank_AA621529	AA621529
118049	genbank_N53145	N53145
102800	14782_20	AA313538 U88895 U88902
104106	AA422123_I_atAA422123_I	
111738	genbank_R26065	R26065
113149	genbank_T51588	T51588
113958	genbank_W86195	W86195
108335	genbank_AA070500	AA070500
108351	genbank_AA071193	AA071193
108441	genbank_AA079079	AA079079
124276	genbank_H83465	H83465
101447	entrez_M21305	M21305
117226	genbank_N20468	N20468
133379	genbank_AA207059	AA207059,AA207241
119366	genbank_T77892	T77892
119528	NOT_FOUND_entrez_W38051	W38051
112588	genbank_R77302	R77302
114449	genbank_AA020736	AA020736
114576	genbank_AA065096	AA065096
107459	W38002_s_at	W38002_s
130339	genbank_AA435746	AA435746

TABLE 2: Figure 2 from BRCA 001 US

Table 2 shows genes downregulated in tumor tissue compared to normal breast tissue.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of normal breast tissue to tumor

Pkey	ExAccn	UnigeneID	Unigene Title	R1
100499	T51988	Hs.283108	hemoglobin, gamma G	10
100549	BE142019	Hs.222056	Homo sapiens cDNA FLJ11572 fis, clone HE	10
100654	A03758		NM_000477:Homo sapiens albumin (ALB), m	10
100971	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte	10
101184	NM_001874	Hs.460	activating transcription factor 3	10
101336	NM_006732	Hs.75678	FBJ murine osteosarcoma viral oncogene h	10
101367	X03350	Hs.4	alcohol dehydrogenase 1B (class I), beta	10
101447	M21305		gb:Human alpha satellite and satellite 3	10
101461	N98569	Hs.76422	phospholipase A2, group IIA (platelets,	10
101511	M27826	Hs.267319	endogenous retroviral protease	10
101736	M74447	Hs.502	transporter 2, ATP-binding cassette, sub-famil	10
102208	U22961		gb:Human mRNA clone with similarity to L	10
102450	U48251	Hs.75871	protein kinase C binding protein 1	10
102800	AA313538		gb:EST185419 Colon carcinoma (HCC) cell	10
102857	NM_006744	Hs.76461	retinol-binding protein 4, interstitial	10
102990	AA829288	Hs.332053	serum amyloid A1	10
103747	AA091995		gb:zn26d06.r1 Stratagene neuroepithelium	10
103812	AA137107	Hs.326391	Homo sapiens, clone MGC:16638, mRNA, com	10
104093	R50727	Hs.336970	ESTs	10
104109	AL353957	Hs.284181	hypothetical protein DKFZp434P0531	10
104250	F06638	Hs.12440	Homo sapiens clone 24734 mRNA sequence	10
104492	N73185	Hs.94285	EST	10
104506	N91071	Hs.109650	ESTs	10
104532	AI498783	Hs.203013	hypothetical protein FLJ12748	10
104677	AA009764	Hs.190380	ESTs	10
104711	AA017245	Hs.32794	ESTs	10
104731	AA018300	Hs.125070	ESTs, Moderately similar to I54374 gene	10
105005	AI298208	Hs.28805	ESTs	10
105038	AA130390	Hs.25549	hypothetical protein FLJ20698	10
105239	AA221036		gb:zr03f12.r1 Stratagene NT2 neuronal pr	10
106052	N79885	Hs.6382	ESTs, Highly similar to T00391 hypothet	10
106181	AI803651	Hs.191608	ESTs	10
106283	AI085848	Hs.25522	KIAA1808 protein	10
106379	AL042069	Hs.119021	DKFZP434N061 protein	10
106451	AW235928	Hs.313182	ESTs	10
106491	AA135688	Hs.10083	Homo sapiens, clone IMAGE:4139786, mRNA,	10
106782	AW054886	Hs.25682	Homo sapiens mRNA for KIAA1863 protein,	10
107124	AB006532	Hs.31442	RecQ protein-like 4	10
107148	AI005038	Hs.334305	GS1999full	10
107214	AF127026	Hs.5394	myosin IA	10
107242	AB020672	Hs.175411	KIAA0865 protein	10
107331	AI905985	Hs.111805	ESTs	10
107447	W28516	Hs.19210	hypothetical protein MGC11308	10
107451	AL042425	Hs.283976	hypothetical protein PRO2389	10
107872	BE271708	Hs.95110	ESTs, Weakly similar to A55943 1-phospha	10
108351	AA071193		gb:zf79b12.s1 Soares_pineal_gland_N3HPG	10
109546	F01449	Hs.26954	Homo sapiens mRNA; cDNA DKFZp762G123 (fr	10
110433	AW294162	Hs.301062	UDP-N-acetyl-alpha-D-galactosamine:polyp	10
110976	AL044174	Hs.159526	patched (Drosophila) homolog	5

111168	AI798376		gb:t34b07.x1 NCI_CGAP_Ov23 Homo sapiens	10
111851	R16733	Hs.20489	ESTs	10
111903	AA593731	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	10
114484	AA034378	Hs.267319	endogenous retroviral protease	10
125284	NM_002666	Hs.103253	perilipin	10
128850	AA193108	Hs.180817	chromosome 11 open reading frame 23	5
128903	AW150717	Hs.296176	STAT induced STAT inhibitor 3	10
129348	AF110141	Hs.288908	WAS protein family, member 2	10
129381	AW245805	Hs.110903	claudin 5 (transmembrane protein deleted	10
129518	AF020038	Hs.11223	isocitrate dehydrogenase 1 (NADP+), solu	10
129554	BE222078	Hs.113069	ESTs	10
130065	M62402	Hs.274313	insulin-like growth factor binding prote	10
130243	D88435	Hs.153227	cyclin G associated kinase	10
130400	V00517	Hs.283108	hemoglobin, gamma G	10
130438	NM_001928	Hs.155597	D component of complement (adipsin)	10
130563	BE270472	Hs.279900	HSPC015 protein	10
130589	AL110226	Hs.18441	DKFZP434H204 protein	10
130683	AA993269	Hs.17872	Homo sapiens, clone IMAGE:3875012, mRNA	10
130689	NM_006691	Hs.17917	extracellular link domain-containing 1	10
130689	AA046747	Hs.17917	extracellular link domain-containing 1	10
130718	N70198	Hs.18378	KIAA1319 protein	10
130768	M81349	Hs.1955	serum amyloid A4, constitutive	10
130840	BE048821	Hs.20144	small inducible cytokine subfamily A (Cy	10
131184	AB040935	Hs.23954	cerebral cell adhesion molecule	10
131262	X03350	Hs.4	alcohol dehydrogenase 1B (class I), beta	10
131328	AW939251	Hs.25647	v-fos FBJ murine osteosarcoma viral onco	10
131543	AW966881	Hs.41839	programmed cell death 2	10
131753	AA829286	Hs.332053	serum amyloid A1	10
131785	H59342	Hs.26320	TRABID protein	10
131828	AJ000263	Hs.278658	keratin, hair, basic, 6 (monilethrix)	10
132426	AW118072	Hs.89981	diacylglycerol kinase, zeta (104kD)	10
132675	AI291496	Hs.5476	Homo sapiens, clone IMAGE:3530123, mRNA,	10
132898	W28548	Hs.224829	ESTs	10
132905	NM_004235	Hs.7934	Kruppel-like factor 4 (gut)	10
133120	NM_003278	Hs.65424	tetranectin (plasminogen-binding protein	10
133407	AF017987	Hs.7308	secreted frizzled-related protein 1	10
133719	H26904	Hs.75736	apolipoprotein D	10
134007	AF072441	Hs.7840	calcineurin binding protein 1	10
134055	D86062	Hs.182423	ES1 (zebrafish) protein, human homolog o	10
134111	AI372588	Hs.8022	TU3A protein	5
134117	AA081846	Hs.7921	Homo sapiens mRNA; cDNA DKFZp566E183 (fr	5
134177	BE243319	Hs.79872	KIAA0652 gene product	10
134369	AF207664	Hs.8230	a disintegrin-like and metalloprotease (	10
134496	M64936		gb:Homo sapiens retinoic acid-inducible	10
134510	NM_002757	Hs.250870	mitogen-activated protein kinase kinase	10
134550	M26315	Hs.85258	CD8 antigen, alpha polypeptide (p32)	5
134758	NM_000078	Hs.89538	cholesteryl ester transfer protein, plas	5
134963	NM_003394	Hs.91985	wingless-type MMTV integration site fami	10
135068	X04430	Hs.93913	interleukin 6 (interferon, beta 2)	10
408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor, type 2	10
446674	AA563892	Hs.306000	solute carrier family 4 (anion exchanger), memb	10

TABLE 2A

Table 2A shows the accession numbers for those pkeys lacking unigeneID's for Table 2. For each probeset, we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT number	Accessions
111168	38585_1	AI798376 S46400 AW811617 AW811618 W00557 BE142245 AW858232 AW861851 AW858362 AA232351 AA218567 AA055558 AW858231 AW857541 AW814172 H66214 AW814398 AF134184 AA243093 AA173345 AA199942 AA223384 AA227092 AA227080 T12379 AA092174 T61139 AA149776 AA699829 AW879188 AW813567 AW813538 AI267168 AA157718 AA157719 AA100472 AA100774 AA130756 AA157705 AA157730 AA157715 AA053524 AW849581 AW854588 C05254 AW882838 T92637 AW812621 AA206583 AA209204 BE156909 AA226824 AI829309 AW991957 N66951 AA527374 H66215 AA045564 AI694265 H60808 AA149726 AW195620 BE081333 BE073424 AW817662 AW817705 AW817703 AW817659 BE081531 H59570
103747	117944_1	AA081995 AA101099
134496	46501_1	M64936 AI025512 AI382987 BE081777 AA089968 BE169930 T41176 AW594624 BE502415 AA121893 AI269283 T40311 AI684569 AA257011 AI078277 AI241318 BE327710 AW975215 AW896268 AA884990 BE327514
105239	34624_1	AA221036 R87170 BE537068 BE544757 C18935 AW812058 T92565 AA227415 AA233942 AA223237 AA668403 AA601627 AW869639 BE061833 BE000620 AW961170 AW847519 AA308542 AW821833 AW945688 C04699 AA205504 AA377241 AW821687 AA055720 AW817981 AW856468 AA155719 AA179928 T03007 AW754298 AA227407 AA113928 AA307904 C16859
100654	tigr_HT2969	A03758 A06977 A15293 D17029 D17107 D17171 L00132 L00133 M12523 M13075 M13076 M92816 U22961 V00494 V00495 X51363 X51364 X51365
102208	6735_9	U22961 AA203623 AA503337 AI174733 AI192802 C06092 AA035357 AI190619 AI199244 AI828450 AA602296 AI378195 AI209170 AI186653 AI127795 AI183846 H77389 AI589465 AA629390 H94306 AI018388 R68584 AA027196 AI745413 AI685092 AI093428 AI623873 AI074570 N50096 AA047486 N25060 AA327814 AI042512 AI383957 AA156873 AI333101 N70808 AI141254 AI383191 AI401237 AI080709 AI093400 W84549 T90806 R00012 W01413 AA630557 AI378348 AI559265 AA877103 W84464 AA625146 R68379 AI133207 AI132980 AI133214 AI064826 AI081615 AI133473 AI174852 AI133404 AI133272 V00494 M12523 M12523 AI207526 AI133120 AI064802 AI174993 AI114729 AI081645 AI064716 AI064959 H77388 T85706 AF075298 AI110799 D17107 NM_000477 AF190168 R50724 AI248418 AI207432 AI133684 AI133345 AI174710 AI133290 AI133304 AI174948 AI207484 AI110717 AF074624 AI114515 AF083516 AI110642 AI114559 AI114498 AI114759 AI207568 AI064960 AI174753 AI114666 R69184 R00011 AI064997 T60501 AI207701 T71735 AA385318 H73569 T60496 H94399 AI133158 T74675 AA484750 T73413 T55909 R50261 T72081 N80533 T51189 T74936 AI207490 AI132925 AI064701 AI174748 AI114663 AI133104 AI132999 AI133100 AI064925 AI064979 AI133063 AA343347 T69091 AA233989 T39772 AI444620 T52290 D16931 T40012 T48403 T58926 T69195 AI133061 T50850 AI400677 AI091136 AA334608 T57411 Z20979 N56507 T87485 AI133622 AA343370 T40075 T69671 T53849 T74820 AF075316 AI110818 T40121 T57381 AI114468 AA332728 T51382 AI114589 R06691 AI110629 AF083503 AI140543 AA334681 AA332720 AA343262 T73513 T86549 AI114840 T57284 T39981 T61407 T72757 T51749 T56630 AA343125 T72126 R94135 T83028 T39972 T39896 AI174786 AI132926 R09237 AI064838 AI133660 T60398 T88753 T55930 T92126 AI444602 T60996 AI114792 H93911 AI133105 R10779 AI065020 T90925 T50889 D17029 AI133703 AA333805 AI133040 AI133017 AI064857 AI110730 AF074637 AI207567 H71080 T73217 AA343950 AI174743 AA334224 AA334281 R06692 T64739 T40183 T60628 T81681 T73179 R01842 AA501730 T39931 T39662 T40138 AA334904 T71425 H77784 R00874 AI065049 T84512 T55918 AI207595 T39951 AA005018 T60361 T69178 T73356 T58795 T61233 T39955 T60612 AI114676 AI064778 AA035710 W52763 AI114786 T83584 AA341859 T81684 T55769 AI114710 T51776 AA343213 AI114714 T58102 AI110809 R28984 AI174854 AA305675 AA343592 T53836 T46869 T64721 T55508 W05241 T34019 T57945 T60513 T48364 AF075308 W86731 T82851 T46269 H54053 T73211 AI114590 T48317 T55965 T74657 R84226 T56552 T52231 T74946 T76976 R02576 T95666 AI203974 AI189471 AA005147 AI478102 AI207662 AI192792 AI768421 AI064737 AW051713 AA936693 AI133117 AI766232 AI913646 T63962 AI065112 AI207689 AI174684 AI207702 T81475 AI133325 AI032512 AA701169 AI936354 AI114720 AI433289 AA046980 AI823482 AI114536 AA860651 AW242644 R07469 AW300438 AI133416 AW271670 AI991363 T78943 AI823461 AA845518 AA719124 AA883454 T68850 T69115 AI935509 AI150977 T62890 T71374 T68294 AI174774 T67411 T68318 AI064689 T56624 T69010 T68982 T68302 AI332829 T72908 AI064819 AI205680 T62895 T69430 T95111 AA025050 T73330 W52657 T71984 T69118 W92684 AI114860 T62093 T61797 AI522333 T73322 H92981 T56018 T61811 T57232 AI336158

		T61821 T69457 T62900 T62912 T72917 T46885 AI702448 T57212 T57203 R84581 T71311 T61819 T69358 T67708 T70918 T59168 AI187111 T64308 T62071 T69427 AI114750 T60430 R09734 T69033 T69141 T69453 T67908 R16809 T69394 AI207729 T55839 T90273 T73339 AW194909 T75486 T71850 T71305 T71287 T53877 T73452 T68852 N75290 AI312890 T67751 AI174983 T51679 T54851 H69880 N73734 AA443453 T73468 H69872 N53869 T68447 D11809 D12412 T64300 T28321 T55864
102800	14782_20	AA313538 U88895 U88902
108351	genbank_AA071193	AA071193
101447	entrez_M21305	M21305

TABLE 3: Figure 3 from BRCA 001 US

Table 3 shows genes downregulated in tumor tissue compared to normal breast tissue.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of normal breast tissue to tumor

Pkey	ExAccn	UnigeneID	UnigeneTitle	R1
101336	NM_006732	Hs.75678	FBJ murine osteosarcoma viral oncogene h	10.0
102208	U22961		gb:Human mRNA clone with similarity to L	10.0
102990	AA829288	Hs.332053	serum amyloid A1	10.0
111168	AI798376		gb:tr34b07.x1 NCI_CGAP_Ov23 Homo sapiens	10.0
111803	AA593731	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	10.0
130085	M62402	Hs.274313	insulin-like growth factor binding prote	10.0
130840	BE046821	Hs.20144	small inducible cytokine subfamily A (Cy	10.0
131543	AW966881	Hs.41639	programmed cell death 2	10.0
133120	NM_003278	Hs.65424	tetranectin (plasminogen-binding protein	10.0
134758	NM_000078	Hs.89538	cholesteryl ester transfer protein, plas	10.0

TABLE 3A

Table 3A shows the accession numbers for those pkeys lacking unigeneID's for Table 3. For each probeset, we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

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Accession: Genbank accession numbers

Pkey	CAT number	Accessions
111168	38585_1	AI798376 S46400 AW811617 AW811616 W00557 BE142245 AW858232 AW861851 AW858362 AA232351 AA218567 AA055556 AW858231 AW857541 AW814172 H66214 AW814398 AF134164 AA243093 AA173345 AA199942 AA223384 AA227092 AA227080 T12379 AA092174 T61139 AA149776 AA699829 AW879188 AW813567 AW813538 AI267168 AA157718 AA157719 AA100472 AA100774 AA130756 AA157705 AA157730 AA157715 AA053524 AW849581 AW854566 C05254 AW882836 T92637 AW812621 AA206583 AA209204 BE156909 AA226824 AI829309 AW991957 N66951 AA527374 H66215 AA045564 AI694265 H60808 AA149726 AW195620 BE081333 BE073424 AW817662 AW817705 AW817703 AW817659 BE081531 H59570
1022086735_9		U22961 AA203623 AA503337 AI174733 AI192802 C06092 AA035357 AI190619 AI199244 AI828450 AA602296 AI378195 AI209170 AI186653 AI127795 AI183846 H77389 AI589465 AA829390 H94306 AI018388 R68584 AA027196 AI745413 AI685092 AI093426 AI623873 AI074570 N50096 AA047486 N25060 AA327814 AI042512 AI383957 AA156873 AI333101 N70806 AI141254 AI383191 AI401237 AI080709 AI093400 W84549 T90806 R00012 W01413 AA630557 AI378348 AI559265 AA877103 W84484 AA625148 R68379 AI133207 AI132980 AI133214 AI084828 AI061615 AI133473 AI174852 AI133404 AI133272 V00494 M12523 M12523 AI207526 AI133120 AI084802 AI174993 AI114729 AI061645 AI084716 AI084959 H77388 T85706 AF075298 AI110799 D17107 NM_000477 AF190168 R50724 AI248416 AI207432 AI133684 AI133345 AI174710 AI133290 AI133304 AI174948 AI207484 AI110717 AF074624 AI114515 AF063516 AI110642 AI114559 AI114498 AI114759 AI207568 AI084960 AI174753 AI114868 R69184 R00011 AI084997 T60501 AI207701 T71735 AA385316 H73569 T60496 H94399 AI133158 T74875 AA484750 T73413 T55909 R50261 T72081 N80533 T51189 T74936 AI207490 AI132925 AI084701 AI174748 AI114663 AI133104 AI132999 AI133100 AI084825 AI084979 AI133083 AA343347 T69091 AA233989 T39772 AI444620 T52290 D16931 T40012 T48403 T58926 T69195 AI133061 T50850 AI400677 AI091136 AA334508 T57411 Z20979 N56507 T87485 AI133622 AA343370 T40075 T69671 T53849 T74820 AF075316 AI110818 T40121 T57381 AI114468 AA332728 T51382 AI114589 R06691 AI110629 AF063503 AI140543 AA334661 AA332720 AA343282 T73513 T86549 AI114840 T67284 T39981 T61407 T72757 T31749 T56630 AA343125 T72126 R94135 T83028 T39972 T39896 AI174788 AI132926 R09237 AI084838 AI133660 T60398 T68753 T55930 T92126 AI444602 T60996 AI114792 H93911 AI133106 R10779 AI085020 T90925 T50889 D17029 AI133703 AA333805 AI133040 AI133017 AI084857 AI110730 AF074637 AI207567 H71080 T73217 AA343850 AI174743 AA334224 AA334281 R06692 T64739 T40183 T60828 T81661 T73179 R01842 AA501730 T39931 T39662 T40136 AA334904 T71425 H77784 R00874 AI065049 T84512 T55918 AI207595 T39951 AA005016 T60381 T69176 T73356 T58795 T61233 T39955 T60612 AI114676 AI084778 AA035710 W52783 AI114788 T83584 AA341859 T81684 T55769 AI114710 T51776 AA343213 AI114714 T58102 AI110809 R28984 AI174854 AA305675 AA343592 T53836 T46869 T84721 T55508 W05241 T54019 T57945 T60513 T48364 AF075308 W86731 T82851 T49269 H54053 T73211 AI114590 T48317 T55965 T74857 R84228 T56552 T52231 T74946 T76976 R02576 T95666 AI203974 AI189471 AA005147 AI478102 AI207662 AI192792 AI768421 AI084737 AW051713 AA936693 AI133117 AI766232 AI913646 T83962 AI065112 AI207689 AI174584 AI207702 T81475 AI133325 AI032512 AA701169 AI938354 AI114720 AI433289 AA046980 AI823482 AI114536 AA850651 AW242644 R07469 AW300438 AI133418 AW271670 AI991363 T78943 AI823481 AA845518 AA719124 AA883454 T68850 T69115 AI935509 AI150977 T82890 T71374 T68294 AI174774 T67411 T68318 AI084689 T56624 T69010 T68982 T68302 AI332829 T72908 AI084819 AI205880 T82895 T69430 T95111 AA025050 T73330 W52657 T71984 T69118 W92684 AI114860 T82093 T61797 AI522333 T73322 H92981 T56018 T81811 T57232 AI336158 T61821 T69457 T62900 T62912 T72917 T46885 AI702448 T57212 T57203 R94581 T71311 T61819 T89358 T67708 T70918 T59166 AI187111 T64308 T62071 T69427 AI114750 T60430 R09734 T69033 T69141 T69453 T67908 R16809 T69394 AI207729 T55839 T90273 T73339 AW194909 T75486 T71850 T71305 T71287 T53877 T73452 T68852 N75290 AI312890 T67751 AI174983 T51679 T54851 H69880 N73734 AA443453 T73468 H69672 N53869 T68447 D11809 D12412 T64300 T28321 T55864

TABLE 4: Figure 4 from BRCA 001 US

Table 4 shows genes upregulated in tumor tissue compared to normal breast tissue.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of tumor to normal breast tissue

Pkey	ExAccn	UnigeneID	Unigene Title	R1
100113	NM_001269	Hs.84746	chromosome condensation 1	2.3
100114	X02308	Hs.82962	thymidylate synthetase	2.9
100131	D12485	Hs.11951	ectonucleotide pyrophosphatase/phosphodiesterase 1	1.9
100146	BE185499	Hs.2471	KIAA0020 gene product	1.9
100147	D13666	Hs.136348	osteoblast specific factor 2 (fasciclin I-like) (periostin)	7.5
100154	H60720	Hs.81892	KIAA0101 gene product	9.2
100163	W44671	Hs.124	gene predicted from cDNA with a complete coding sequence	1.6
100220	AW015534	Hs.217493	annexin A2	2.0
100265	D38521	Hs.112396	KIAA0077 protein	1.5
100271	BE160081	Hs.256290	S100 calcium-binding protein A11 (calgizzarin)	13.5
100275	BE242802	Hs.154797	KIAA0090 protein	5.1
100323	D50920	Hs.23106	KIAA0130 gene product	1.9
100335	AW247529	Hs.6793	platelet-activating factor acetylhydrolase, isoform Ib, gamma subunit (29kD)	2.7
100364	NM_004341	Hs.154868	carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase	2.0
100372	NM_014791	Hs.184339	KIAA0175 gene product	2.6
100393	D84145	Hs.39913	novel RGD-containing protein	3.2
100400	AW954324	Hs.75790	phosphatidylinositol glycan, class C	1.5
100418	D86978	Hs.84790	KIAA0225 protein	2.0
100482	M65028	Hs.81361	heterogeneous nuclear ribonucleoprotein A/B	2.9
100518	NM_004415	Hs.74316	desmoplakin (DPI, DPII)	1.9
100668	L05424	Hs.169610	CD44 antigen (homing function and Indian blood group system)	5.7
100667	L05424	Hs.169610	CD44 antigen (homing function and Indian blood group system)	9.0
100668	L05424	Hs.169610	CD44 antigen (homing function and Indian blood group system)	7.6
100678	AW502935	Hs.740	PTK2 protein tyrosine kinase 2	53.2
100685	AA328229	Hs.184582	ribosomal protein L24	1.8
100690	AA383256	Hs.1657	estrogen receptor 1	1.6
100783	AF078847	Hs.191358	general transcription factor IIH, polypeptide 2 (44kD subunit)	5.9
100850	AA836472	Hs.297939	cathepsin B	1.7
100892	BE245294	Hs.180789	S164 protein	1.7
100945	AF002225	Hs.180686	ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome)	1.5
100969	AA157634	Hs.79172	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5	6.3
100988	AK000405	Hs.76480	ubiquitin-like 4	11.4
100999	H38765	Hs.80706	diaphorase (NADH/NADPH) (cytochrome b-5 reductase)	1.6
101031	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B, 92kD gelatinase, 92kD type IV collagenase)	8.2
101045	J05614		gb:Human proliferating cell nuclear antigen (PCNA) gene, promoter region.	5.0
101077	N99692	Hs.75227	Empirically selected from AFFX single probeset	2.6
101093	L06419	Hs.75093	procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI)	1.4
101161	NM_006262	Hs.37044	periphertn	16.9
101186	AA020958	Hs.179881	core-binding factor, beta subunit	2.0
101216	AA284168	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK2-associated dual specificity phosphatase)	1.8
101228	AA333387	Hs.82916	chaperonin containing TCP1, subunit 6A (zeta 1)	1.7
101247	AA132668	Hs.78802	glycogen synthase kinase 3 beta	1.9
101249	L18964	Hs.1904	protein kinase C, iota	1.5
101332	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	5.2
101332	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	3.4
101352	AI494299	Hs.18297	COX17 (yeast) homolog, cytochrome c oxidase assembly protein	6.3
101396	BE267931	Hs.78996	proliferating cell nuclear antigen	4.2
101445	M21259		gb:Human Alu repeats in the region 5' to the small nuclear rib	1.9
101470	NM_000546	Hs.1846	tumor protein p53 (Li-Fraumeni syndrome)	1.6

101478	NM_002890	Hs.758	RAS p21 protein activator (GTPase activating protein) 1	2.5
101483	M24486	Hs.76768	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide I	5.5
101540	J04977	Hs.84981	X-ray repair complementing defective repair in Chinese hamster cells 5 (double-strand-break rejoining	2.1
101573	AW248421	Hs.250758	proteasome (prosome, macropain) 26S subunit, ATPase, 3	1.6
101580	NM_012151	Hs.83363	coagulation factor VIII-associated (intronic transcript)	5.7
101592	AF064853	Hs.91299	guanine nucleotide binding protein (G protein), beta polypeptide 2	1.8
101592	AF064853	Hs.91299	guanine nucleotide binding protein (G pr	5.8
101621	BE391804	Hs.62661	guanylate binding protein 1, interferon-inducible, 67kD	2.4
101702	AW504089	Hs.179574	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), alpha isoform	1.3
101734	M74099	Hs.147049	cut (Drosophila)-like 1 (CCAAT displacement protein)	2.1
101759	M80244	Hs.184601	solute carrier family 7 (cationic amino acid transporter, y+ system), member 5	5.0
101767	M81057	Hs.180884	carboxypeptidase B1 (tissue)	14.4
101782	AA306495	Hs.1869	phosphoglucomutase 1	5.2
101805	AW409747	Hs.75612	stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein)	6.6
101806	AA586894	Hs.112408	S100 calcium-binding protein A7 (psoriasin 1)	8.9
101810	NM_000318	Hs.180612	peroxisomal membrane protein 3 (35kD, Zellweger syndrome)	3.2
101879	AA176374	Hs.243886	nuclear autoantigenic sperm protein (histone-binding)	1.6
101911	AA441787	Hs.119689	glycoprotein hormones, alpha polypeptide	31.3
101920	AF182845	Hs.8024	IK cytokine, down-regulator of HLA II	1.8
101973	U41514	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1 (GalNAc-T1)	2.4
101983	AI904232	Hs.75323	prohibitin	6.4
102009	BE245149	Hs.82643	protein tyrosine kinase 9	1.3
102036	BE250127	Hs.82906	CDC20 (cell division cycle 20, S. cerevisiae, homolog)	2.0
102083	T35901	Hs.75117	interleukin enhancer binding factor 2, 45kD	1.6
102083	T35901	Hs.75117	interleukin enhancer binding factor 2, 4	1.3
102107	BE258602	Hs.182366	heat shock protein 75	1.4
102123	NM_001809	Hs.1594	centromere protein A (17kD)	1.8
102165	BE313260	Hs.159627	death associated protein 3	4.6
102198	AW950852	Hs.74598	polymerase (DNA directed), delta 2, regulatory subunit (50kD)	4.3
102217	AA829978	Hs.301613	JTV1 gene	6.7
102220	U24389	Hs.85436	lysosomal	4.3
102234	AW163390	Hs.278554	heterochromatin-like protein 1	1.9
102260	AL039104	Hs.159557	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)	4.4
102302	AA306342	Hs.69171	protein kinase C-like 2	2.7
102330	BE298063	Hs.77254	chromobox homolog 1 (Drosophila HP1 beta)	1.5
102339	BE378432	Hs.95577	cyclin-dependent kinase 4	2.3
102348	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member B2	2.0
102349	AU077055	Hs.289107	baculoviral IAP repeat-containing 2	3.2
102369	U39840	Hs.299867	hepatocyte nuclear factor 3, alpha	2.0
102374	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	6.2
102391	AA296874	Hs.77494	deoxyguanosine kinase	1.5
102455	U48705	Hs.75562	discoidin domain receptor family, member 1	6.9
102465	NM_001359	Hs.81548	2,4-dienoyl CoA reductase 1, mitochondrial	1.8
102488	U50939	Hs.61828	amyloid beta precursor protein-binding protein 1, 59kD	1.5
102489	AL080116	Hs.74420	origin recognition complex, subunit 3 (yeast homolog)-like	3.3
102494	AI188137	Hs.75193	COP9 homolog	2.1
102501	AF217197	Hs.74562	alah binding protein 1; FBP interacting repressor; pyrimidine tract binding splicing	3.2
102522	BE250944	Hs.183556	solute carrier family 1 (neutral amino acid transporter), member 5	2.8
102532	AF040253	Hs.70186	suppressor of Ty (S.cerevisiae) 5 homolog	5.7
102564	U59423	Hs.79067	MAD (mothers against decapentaplegic, Drosophila) homolog 1	2.3
102568	W81489	Hs.223025	RAB31, member RAS oncogene family	5.3
102580	U60808	Hs.152881	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 1	2.1
102581	AU077228	Hs.77258	enhancer of zeste (Drosophila) homolog 2	1.6
102582	U61232	Hs.32675	tubulin-specific chaperone e	2.1
102617	AW161453	Hs.198767	COP9 (constitutive photomorphogenic, Arabidopsis, homolog) subunit 5	1.8
102618	AL037672	Hs.81071	extracellular matrix protein 1	5.8
102627	AL021918	Hs.158174	zinc finger protein 184 (Kruppel-like)	1.3
102663	NM_002270	Hs.168075	karyopherin (importin) beta 2	1.8
102676	BE262989	Hs.12045	putative protein	2.3
102687	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	4.3
102689	U96132	Hs.171280	hydroxyacyl-Coenzyme A dehydrogenase, type II	6.0
102696	BE540274	Hs.239	forkhead box M1	4.2
102704	AU077058	Hs.54089	BRCA1 associated RING domain 1	1.9
102705	T97490	Hs.50002	small inducible cytokine subfamily A (Cys-Cys), member 19	2.3
102750	AB014460	Hs.86196	nth (E.coli endonuclease III)-like 1	1.2
102801	BE252241	Hs.38041	pyridoxal (pyridoxine, vitamin B6) kinase	6.4
102812	U90549	Hs.236774	high-mobility group (nonhistone chromosomal) protein 17-like 3	1.6

102827	BE244588	Hs.6458	chaperonin containing TCP1, subunit 2 (beta)	5.6
102831	AA262170	Hs.80917	adaptor-related protein complex 3, sigma 1 subunit	2.0
102844	AV653790	Hs.324275	WW domain-containing protein 1	1.3
102868	X02419	Hs.77274	plasminogen activator, urokinase	4.4
102925	BE440142	Hs.2943	signal recognition particle 19kD	1.9
102935	BE561850	Hs.80506	small nuclear ribonucleoprotein polypeptide A'	2.4
102968	AU076811	Hs.154672	methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase	2.7
102983	BE387202	Hs.118638	non-metastatic cells 1, protein (NM23A) expressed in	3.1
102985	U95742	Hs.2707	G1 to S phase transition 1	5.2
103023	AW500470	Hs.117950	multifunctional polypeptide similar to SAICAR synthetase and AIR carboxylase	1.6
103038	AA926960	Hs.334883	CDC28 protein kinase 1	2.5
103060	NM_005940	Hs.155324	matrix metalloproteinase 11 (MMP11; stromelysin 3)	4.5
103080	AU077231	Hs.82932	cyclin D1 (PRAD1: parathyroid adenomatosis 1)	3.1
103089	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaphyseal chondrodysplasia)	2.4
103177	BE244377	Hs.46876	farnesyl-diphosphate farnesyltransferase 1	3.5
103178	AA205475	Hs.275865	ribosomal protein S18	9.9
103179	NM_001777	Hs.82585	CD47 antigen (Rh-related antigen, integrin-associated signal transducer)	1.3
103181	X69636	Hs.334731	Homo sapiens, clone IMAGE:3448306, mRNA, partial cds	2.0
103185	NM_006825	Hs.74368	transmembrane protein (83kD), endoplasmic reticulum/Golgi intermediate compartment	1.8
103191	AA401039	Hs.2903	protein phosphatase 4 (formerly X), catalytic subunit	2.5
103193	NM_004768	Hs.75724	coatomer protein complex, subunit beta 2 (beta prime)	2.2
103194	NM_004939	Hs.78580	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1	6.3
103206	X72755	Hs.77367	monokine induced by gamma interferon	6.8
103223	BE275607	Hs.1708	chaperonin containing TCP1, subunit 3 (gamma)	3.0
103232	X75962	Hs.129780	tumor necrosis factor receptor superfamily, member 4	1.8
103238	AI369285	Hs.75189	death-associated protein	5.6
103297	NM_001545	Hs.9078	immature colon carcinoma transcript 1	1.9
103330	AI803447	Hs.77496	small nuclear ribonucleoprotein polypeptide G	2.5
103349	X89059		gb:H.sapiens mRNA for unknown protein expressed in macrophage	1.6
103376	AL036166	Hs.323378	coated vesicle membrane protein	1.8
103391	X94453	Hs.114366	pyrroline-5-carboxylate synthetase (glutamate gamma-semialdehyde synthetase)	2.3
103392	X94563		gb:H.sapiens dbl/acbp gene exon 1 & 2.	4.0
103430	BE564090	Hs.20716	translocase of inner mitochondrial membrane 17 (yeast) homolog A	1.3
103491	AF264750	Hs.288971	myeloid/lymphoid or mixed-lineage leukemia 3	5.6
103505	AL031224	Hs.33102	transcription factor AP-2 beta (activating enhancer-binding protein 2 beta)	5.1
103547	AI376722	Hs.180062	proteasome (prosome, macropain) subunit, beta type, 8 (large multifunctional protease 7)	9.7
103568	NM_006218	Hs.85701	phosphoinositide-3-kinase, catalytic, alpha polypeptide	2.0
103613	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (campomelic dysplasia, autosomal sex-reversal)	1.3
103621	BE379766	Hs.150675	polymerase (RNA) II (DNA directed) polypeptide K (7.0kD)	2.0
103622	AA609685	Hs.278672	membrane component, chromosome 11, surface marker 1	2.3
103727	AI878883	Hs.296381	growth factor receptor-bound protein 2	1.3
103749	AL135301	Hs.8768	hypothetical protein FLJ10849	1.8
103754	AI015709	Hs.172089	Homo sapiens mRNA; cDNA DKFZp586I2022 (from clone DKFZp586I2022)	1.3
103780	AA094752	Hs.169992	hypothetical 43.2 Kd protein	7.5
103795	H26531	Hs.7367	Homo sapiens BTB domain protein (BOPL) mRNA, partial cds	1.2
103797	AA080912		gb:zn04d03.r1 Stratagene hNT neuron (937233) Homo sapiens cDNA clone 5' similar	1.5
103813	AI042582	Hs.181271	CGI-120 protein	1.5
103855	W02363	Hs.302267	hypothetical protein FLJ10330	1.5
103886	AK001278	Hs.105737	hypothetical protein FLJ10416 similar to constitutive photomorphogenic protein 1	6.5
104052	NM_002407	Hs.97644	mammaglobin 2	2.9
104079	AA251242	Hs.103238	ESTs	1.4
104174	AA478984	Hs.6451	PRO0659 protein	5.6
104227	AB002343	Hs.98938	protocadherin alpha 9	1.6
104275	AI751970	Hs.101067	GCN5 (general control of amino-acid synthesis, yeast, homolog)-like 2	5.4
104325	BE379766	Hs.150675	polymerase (RNA) II (DNA directed) polypeptide K (7.0kD)	6.3
104370	AA324597	Hs.21851	Homo sapiens cDNA FLJ12900 fis, clone NT2RP2004321	1.6
104423	R83113	Hs.1432	protein kinase C substrate 80K-H	5.2
104482	AB037762	Hs.44268	myelin gene expression factor 2	1.2
104532	AI498763	Hs.203013	hypothetical protein FLJ12748	2.1
104563	AL117403	Hs.306189	DKFZP434F1735 protein	1.2
104667	AI239923	Hs.30098	ESTs	1.3
104757	AI694413	Hs.332649	olfactory receptor, family 2, subfamily I, member 6	2.3
104804	AI858702	Hs.31803	ESTs, Weakly similar to N-WASP [H.sapiens]	1.3
104806	AB023175	Hs.22982	KIAA0958 protein	2.3
104827	AW052006	Hs.8551	PRP4/STK/WD splicing factor	10.9
104848	AI250789	Hs.32478	ESTs	5.6
104854	AA041276	Hs.154729	3-phosphoinositide dependent protein kinase-1	12.3

104867	AA278898	Hs.225979	hypothetical protein similar to small G proteins, especially RAP-2A	2.0
104871	T78044	Hs.28893	Homo sapiens mRNA; cDNA DKFZp564O2364 (from clone DKFZp564O2364)	1.3
104898	AW015318	Hs.23185	ESTs	17.7
104909	AW408164	Hs.249184	transcription factor 19 (SC1)	5.0
104916	AW958157	Hs.155489	NS1-associated protein 1	1.7
104919	AA026880	Hs.25252	prolactin receptor	1.4
104930	AF043467	Hs.32893	neurexophilin 2	2.2
104973	NM_015310	Hs.6763	KIAA0942 protein	5.0
104974	Y12059	Hs.278675	bromodomain-containing 4	1.4
104975	AL136877	Hs.50758	SMC4 (structural maintenance of chromosomes 4, yeast)-like 1	2.4
104975	AL136877	Hs.50758	SMC4 (structural maintenance of chromoso	2.3
104978	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010317E24 gene, clone IMAGE:3502019, mRNA, partial cds	7.2
104979	AA937934	Hs.321062	ESTs	1.3
104994	AI499930	Hs.334885	mitochondrial GTP binding protein	3.5
105009	BE379584	Hs.34789	dolichyl-diphosphooligosaccharide-protein glycosyltransferase	5.5
105012	AF098158	Hs.9329	chromosome 20 open reading frame 1	3.3
105028	AI050715	Hs.2331	E2F transcription factor 5, p130-binding	2.2
105032	AA127818		gb:zt12a02.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:501674 3'	6.8
105039	AA907305	Hs.36475	ESTs	2.5
105041	AB037716	Hs.26204	KIAA1295 protein	2.2
105045	BE242899	Hs.129951	speckle-type POZ protein	3.8
105079	AA151342	Hs.12677	CGI-147 protein	9.5
105087	AA147884	Hs.9812	Homo sapiens cDNA FLJ14388 fis, clone HEMBA1002716	5.6
105088	H58589	Hs.35156	Homo sapiens cDNA FLJ11027 fis, clone PLACE1004114	2.2
105095	Z78407	Hs.27023	vesicle transport-related protein	2.2
105110	BE387350	Hs.33122	KIAA1160 protein	1.6
105126	AW975433	Hs.36288	ESTs	8.3
105127	AA045648	Hs.301957	nudix (nucleoside diphosphate linked moiety X)-type motif 5	2.1
105141	AA164687	Hs.177576	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isoenzyme A	2.7
105158	AW976357	Hs.234545	hypothetical protein NUF2R	1.9
105169	BE245294	Hs.180789	S164 protein	1.7
105186	AA191512	Hs.28005	Homo sapiens cDNA FLJ11309 fis, clone PLACE1010078	4.8
105254	AA071276	Hs.19469	KIAA0859 protein	1.9
105261	AA263143	Hs.24596	RAD51-interacting protein	2.8
105288	N99673	Hs.3585	ESTs, Weakly similar to AF126743 1 DNAJ domain-containing protein MCJ [H.sapiens]	1.9
105302	AA700122	Hs.3355	sentrin-specific protease	8.0
105331	AW270037	Hs.179507	KIAA0779 protein	1.8
105359	NM_016015	Hs.8054	CGI-68 protein	8.2
105368	BE264645	Hs.282093	hypothetical protein FLJ21918	5.0
105373	AW887701	Hs.32356	hypothetical protein FLJ20628	2.5
105374	BE242803	Hs.262823	hypothetical protein FLJ10326	2.2
105387	AW582146	Hs.108636	membrane protein CH1	2.3
105393	AF167570	Hs.256583	interleukin enhancer binding factor 3, 90kD	5.4
105399	BE386877	Hs.334811	Npw38-binding protein NpwBP	1.6
105400	AF198520	Hs.65648	RNA binding motif protein 8A	1.6
105445	AA252395		gb:zs12g10.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:585026 3', mRNA sequence.	5.0
105507	BE268348	Hs.226318	CCR4-NOT transcription complex, subunit 7	1.6
105529	AA113449	Hs.32471	hypothetical protein FLJ20364	1.3
105530	AB023179	Hs.9059	KIAA0982 protein	3.4
105547	AA262640	Hs.27445	unknown	9.3
105564	BE616594	Hs.288042	hypothetical protein FLJ14299	1.4
105596	AA579535	Hs.18490	hypothetical protein FLJ20452	10.9
105597	AF054284	Hs.334826	splicing factor 3b, subunit 1, 155kD	2.9
105608	AI808201	Hs.287863	hypothetical protein FLJ12475	1.7
105610	AA280072	Hs.99872	fetal Alzheimer antigen	1.4
105617	AK000892	Hs.4069	glucocorticoid modulatory element binding protein 1	1.7
105620	AW302245	Hs.181390	casein kinase 1, gamma 2	5.5
105658	AA985190	Hs.246875	hypothetical protein FLJ20059	9.4
105697	AW499988	Hs.27801	zinc finger protein 278	2.0
105708	R26944	Hs.180777	Homo sapiens mRNA; cDNA DKFZp564M0264 (from clone DKFZp564M0264)	1.7
105743	BE246502	Hs.9598	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short	2.6
105746	AW151952	Hs.46679	hypothetical protein FLJ20739	1.5
105759	AI123118	Hs.15159	chemokine-like factor, alternatively spliced	1.3
105771	AI267720	Hs.153221	synovial sarcoma, translocated to X chromosome	1.6
105820	AA741336	Hs.152108	transcriptional unit N143	2.2
105826	AA478756	Hs.194477	E3 ubiquitin ligase SMURF2	1.3
105856	AI262106	Hs.12653	ESTs	2.4

105858	AF151056	Hs.281426	hypothetical protein	2.9
105875	AK001708	Hs.32271	hypothetical protein FLJ10846	1.4
105930	AF016371	Hs.9880	peptidyl prolyl isomerase H (cyclophilin H)	5.2
106000	AW194426	Hs.20726	ESTs	1.7
106011	AW081202	Hs.12284	Homo sapiens, clone IMAGE:2989556, mRNA, partial cds	2.8
106017	AA477958	Hs.26268	ESTs	1.4
106073	AL157441	Hs.17834	downstream neighbor of SON	1.4
106078	AA130158	Hs.19977	ESTs, Moderately similar to ALU8_HUMAN ALU SUBFAMILY SX SEQUENCE CONTAMINATION	1.6
106094	AA533491	Hs.23317	hypothetical protein FLJ14681	6.8
106140	AB006624	Hs.14912	KIAA0286 protein	1.6
106271	AA251393	Hs.289052	Homo sapiens, Similar to RIKEN cDNA 5430429M05 gene, clone MGC:13155, mRNA, complete cds	10.8
106288	AB037742	Hs.24336	KIAA1321 protein	1.3
106300	Y10043	Hs.19114	high-mobility group (nonhistone chromosomal) protein 4	3.6
106333	AL043114	Hs.22410	ESTs, Weakly similar to A54849 collagen alpha 1(VII) chain precursor [H.sapiens]	5.4
106350	AK001404	Hs.194698	cyclin B2	5.7
106359	AW390282	Hs.31130	transmembrane 7 superfamily member 2	6.3
106381	AB040916	Hs.24106	KIAA1483 protein	6.5
106389	AW748420	Hs.6236	Homo sapiens cDNA: FLJ21487 fis, clone COL05419	2.2
106457	AF119256	Hs.27801	zinc finger protein 278	2.7
106470	D63078	Hs.186180	Homo sapiens cDNA: FLJ23038 fis, clone LNG02039	2.3
106531	AA454036	Hs.8832	ESTs	1.6
106586	AA243837	Hs.57787	ESTs	1.6
106589	AK000933	Hs.28661	Homo sapiens cDNA FLJ10071 fis, clone HEMBA1001702	2.4
106610	AA458882	Hs.79732	fibulin 1	7.9
106624	NM_003595	Hs.26350	tyrosylprotein sulfotransferase 2	7.7
106650	ALD49951	Hs.22370	Homo sapiens mRNA; cDNA DKFZp564O0122 (from clone DKFZp564O0122)	1.6
106669	AV657117	Hs.184164	ESTs, Moderately similar to S65657 alpha-1C-adrenergic receptor splice form 2 [H.sapiens]	1.3
106713	BE614802	Hs.184352	hypothetical protein FLJ12549	4.5
106717	AA600357	Hs.239489	TIA1 cytotoxic granule-associated RNA-binding protein	1.3
106723	BE388094	Hs.21857	ESTs	1.6
106795	AF174487	Hs.293753	Bcl-2-related ovarian killer protein-like	5.7
106829	AW959893	Hs.27099	hypothetical protein FLJ23293 similar to ARL-6 interacting protein-2	16.2
106831	BE564871	Hs.29463	centrin, EF-hand protein, 3 (CDC31 yeast homolog)	1.5
106846	AB037744	Hs.34892	KIAA1323 protein	2.2
106852	AF151031	Hs.300631	hypothetical protein	1.3
106873	N49809	Hs.11197	Homo sapiens, clone IMAGE:3343149, mRNA, partial cds	16.8
106888	W79171	Hs.9567	GL002 protein	1.5
106906	AA861271	Hs.222024	transcription factor BMAL2	2.2
106920	AK001838	Hs.296323	serum/glucocorticoid regulated kinase	3.3
106945	AK000511	Hs.6294	hypothetical protein DKFZp434L1435 similar to valyl tRNA synthetase	6.8
106973	BE156256	Hs.11923	hypothetical protein	6.6
106977	AL043152	Hs.50421	KIAA0203 gene product	4.8
106978	AW631480	Hs.8588	ESTs	6.0
107004	AA146872	Hs.300700	hypothetical protein FLJ20727	1.3
107029	AF264750	Hs.288971	myeloid/lymphoid or mixed-lineage leukemia 3	1.8
107071	AW385224	Hs.35198	ectonucleotide pyrophosphatase/phosphodiesterase 5 (putative function)	1.7
107113	AK000733	Hs.23900	GTPase activating protein	2.5
107125	AK000512	Hs.69388	hypothetical protein FLJ20505	1.7
107136	AV661958	Hs.8207	GK001 protein	4.6
107138	AV661958	Hs.8207	GK001 protein	3.3
107146	AK001455	Hs.5198	Down syndrome critical region gene 2	2.0
107151	AW378085	Hs.8687	ESTs	6.3
107155	AW391927	Hs.7948	KIAA1288 protein	33.5
107174	BE122762	Hs.25338	ESTs	5.2
107197	W15477	Hs.64639	glioma pathogenesis-related protein	6.1
107221	AW888411	Hs.81915	leukemia-associated phosphoprotein p18 (stathmin)	17.4
107243	BE219716	Hs.34727	ESTs, Moderately similar to I38759 zinc finger/leucine zipper protein [H.sapiens]	7.4
107248	AW263124	Hs.315111	nuclear receptor co-repressor/HDAC3 complex subunit	1.8
107263	D60341	Hs.21198	translocase of outer mitochondrial membrane 70 (yeast) homolog A	6.6
107265	BE379594	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION	2.5
107298	N95657	Hs.6820	ESTs, Moderately similar to YOJ1_CAEEL HYPOTHETICAL 63.5 KD PROTEIN ZK353.1 IN	2.5
107298	N95657	Hs.6820	ESTs, Moderately similar to YOJ1_CAEEL H	1.7
107299	BE277457	Hs.30661	hypothetical protein MGC4606	3.2
107316	T63174	Hs.193700	Homo sapiens mRNA; cDNA DKFZp586I0324 (from clone DKFZp586I0324)	2.0
107354	NM_005299	Hs.86448	zinc finger protein 193	5.0
107392	AW299900	Hs.287632	TATA element modulatory factor 1	1.2
107481	AA307703	Hs.279768	kinesin family member 4A	1.6

107529	BE515065	Hs.296585	nucleolar protein (KKE/D repeat)	3.0
107554	AA001388	Hs.59844	ESTs	1.3
107681	BE379594	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION	2.2
107772	AA018587	Hs.303055	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION	2.1
107859	AW732573	Hs.47584	potassium voltage-gated channel, delayed-rectifier, subfamily S, member 3	8.4
107901	L42612	Hs.335952	keratin 6B	2.5
107901	L42612	Hs.335952	keratin 6B	1.6
107922	BE153855	Hs.61460	Ig superfamily receptor LNIR	2.2
107974	AW956103	Hs.61712	pyruvate dehydrogenase kinase, isoenzyme 1	6.7
108040	AL121031	Hs.159971	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily b, member 1	1.5
108230	AA054224	Hs.59847	ESTs	1.3
108274	AF129535	Hs.272027	F-box only protein 5	7.1
108296	N31256	Hs.161823	ESTs	2.5
108496	AA083069	Hs.339659	ESTs	3.5
108507	BE300380	Hs.69476	Homo sapiens cDNA FLJ12758 fis, clone NT2RP2001328	3.4
108621	AA101809	Hs.182685	ESTs	1.6
108634	AW022410	Hs.69507	ESTs	1.7
108547	BE546947	Hs.44276	homeo box C10	9.8
108695	AB029000	Hs.70823	KIAA1077 protein	7.2
108717	AA122393	Hs.70811	hypothetical protein FLJ20516	1.3
108740	AI089575	Hs.9071	progesterone membrane binding protein	2.7
108828	AK001693	Hs.273344	DKFZP564O0463 protein	1.8
108859	AL121500	Hs.178904	ESTs	1.5
108872	H06720	Hs.111680	endosulfine alpha	2.1
108891	AI801235	Hs.48480	ESTs	5.3
108894	AK001431	Hs.5105	hypothetical protein FLJ10569	4.0
108955	AA149754	Hs.195155	Homo sapiens amino acid transport system N2 (SN2) mRNA, complete cds	5.8
108982	AA151708	Hs.171980	homeo box (expressed in ES cells) 1	1.6
108987	AA152178	Hs.23467	hypothetical protein FLJ10633	6.2
109002	AB028987	Hs.72134	KIAA1064 protein	1.7
109011	AA156542	Hs.72127	ESTs	1.4
109026	AA157811		gb:zo35d07.s1 Stratagene colon (937204) Homo sapiens cDNA clone 3' similar to contains Alu repetitive	6.3
109068	AA164293	Hs.72545	ESTs	2.9
109101	AW608930	Hs.52184	hypothetical protein FLJ20618	1.6
109112	AW419198	Hs.257924	hypothetical protein FLJ13782	3.2
109124	AK000684	Hs.183887	hypothetical protein FLJ22104	1.7
109139	AJ132592	Hs.59757	zinc finger protein 281	2.6
109166	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkinesin 6)	2.9
109198	BE568742	Hs.58169	highly expressed in cancer, rich in leucine heptad repeats	2.0
109213	NM_016603	Hs.82035	potential nuclear protein C5ORF5; GAP-like protein	5.3
109220	AW958181	Hs.189998	ESTs	5.7
109233	AU077281	Hs.170285	nucleoporin 214kD (CAIN)	5.3
109270	N99673	Hs.3585	ESTs, Weakly similar to AF126743 1 DNAJ domain-containing protein MCJ [H.sapiens]	1.4
109273	AA375752	Hs.82719	Homo sapiens mRNA; cDNA DKFZp586F1822 (from clone DKFZp586F1822)	2.9
109313	AF153201	Hs.86276	C2H2 (Kruppel-type) zinc finger protein	1.3
109341	AA213506	Hs.115099	EST	2.9
109391	AL096858	Hs.184245	KIAA0929 protein Msx2 interacting nuclear target (MINT) homolog	1.5
109420	H83603	Hs.40408	homeo box C9	2.2
109426	N30531	Hs.42215	protein phosphatase 1, regulatory subunit 6	3.0
109429	AI180029	Hs.61438	ESTs	1.9
109445	AA232103	Hs.189915	ESTs	1.8
109450	AB032969	Hs.173042	KIAA1143 protein	3.7
109468	NM_015310	Hs.6763	KIAA0942 protein	3.2
109478	AW074143	Hs.87134	ESTs	2.0
109570	L40027	Hs.118890	glycogen synthase kinase 3 alpha	2.1
109682	F02814	Hs.27319	ESTs	1.4
109825	R71264	Hs.16788	ESTs	1.3
110039	H11938	Hs.21907	histone acetyltransferase	2.0
110058	AA503041	Hs.279009	matrix Gla protein	2.5
110085	AA603840	Hs.29956	KIAA0460 protein	1.7
110110	T07353	Hs.7948	ESTs	2.9
110129	R51853	Hs.226429	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION	1.7
110154	NM_014521	Hs.17687	SH3-domain binding protein 4	4.2
110240	AI668594	Hs.176588	ESTs, Weakly similar to CP4Y_HUMAN CYTOCHROME P450 4A11 PRECURSOR [H.sapiens]	4.2
110242	N41744	Hs.19978	CGI-30 protein	1.3
110259	H28428	Hs.32408	ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]	2.2
110312	BE256986	Hs.11896	hypothetical protein FLJ12089	2.1

110330	AI288666	Hs.16621	DKFZP434I118 protein	6.2
110501	H55748		gb:yq94e01.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:203400 3'	6.1
110504	H55915	Hs.210859	hypothetical protein FLJ11016	6.1
110525	H57330	Hs.37430	EST	6.3
110568	AK001160	Hs.5999	hypothetical protein FLJ10298	1.3
110699	T97586	Hs.18090	ESTs	1.8
110705	AB007902	Hs.32166	KIAA0442 protein	1.6
110742	AW190338	Hs.28029	hypothetical protein MGC11256	7.6
110761	AL138077	Hs.16157	hypothetical protein FLJ12707	2.5
110782	BE044245	Hs.30011	hypothetical protein MGC2963	9.3
110765	AK000322	Hs.18457	hypothetical protein FLJ20315	5.5
110769	BE000831	Hs.23837	Homo sapiens cDNA FLJ11812 fis, clone HEMBA1006364	2.1
110799	AI089660	Hs.323401	dpy-30-like protein	1.5
110805	T25829	Hs.24048	FK506 binding protein precursor	6.6
110813	AA767373	Hs.35669	ESTs, Moderately similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION	5.7
110820	R33261	Hs.6614	ESTs, Weakly similar to A43932 mucin 2 precursor, intestinal [H.sapiens]	3.4
110840	N31598	Hs.12727	hypothetical protein FLJ21610	1.7
110844	AI740792	Hs.167531	methylcrotonoyl-Coenzyme A carboxylase 2 (beta)	1.7
110854	BE612992	Hs.27931	hypothetical protein FLJ10607 similar to glucosamine-phosphate N-acetyltransferase	4.7
110856	AA992380		gb:ot37g06.s1 Soares_testis_NHT Homo sapiens cDNA clone 3' similar to contains element	2.3
110885	BE384447	Hs.16034	hypothetical protein MGC13186	3.5
110897	AL117430	Hs.6880.	DKFZP434D156 protein	2.2
110915	BE092285	Hs.29724	hypothetical protein FLJ13187	2.6
110918	H04360	Hs.24283	ESTs, Moderately similar to reduced expression in cancer [H.sapiens]	1.9
110958	NM_005864	Hs.24587	signal transduction protein (SH3 containing)	6.7
110963	AK002180	Hs.11449	DKFZP564O123 protein	2.0
110981	AK001980	Hs.24284	ADP-ribosyltransferase (NAD+; poly(ADP-ribose) polymerase)-like 2	1.3
110984	AW813287	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1 (GalNAc-T1)	1.8
111125	N63823	Hs.269115	ESTs, Moderately similar to Z195_HUMAN ZINC FINGER PROTEIN 195 [H.sapiens]	3.6
111132	AB037807	Hs.83293	hypothetical protein	2.1
111164	N46180	Hs.122489	Homo sapiens cDNA FLJ13289 fis, clone OVARC1001170	2.3
111172	R67419	Hs.21851	Homo sapiens cDNA FLJ12900 fis, clone NT2RP2004321	3.7
111174	AL050166	Hs.26295	Homo sapiens mRNA; cDNA DKFZp586D1122 (from clone DKFZp586D1122)	7.5
111179	AK000138	Hs.10760	asporin (LRR class 1)	7.1
111184	AI815486	Hs.243901	Homo sapiens cDNA FLJ20738 fis, clone HEP08257	6.7
111184	AI815486	Hs.243901	Homo sapiens cDNA FLJ20738 fis, clone HE	3.3
111189	N67603	Hs.272130	ESTs, Weakly similar to S65824 reverse transcriptase homolog [H.sapiens]	3.6
111216	AW139408	Hs.152940	ESTs	1.5
111221	AB037782	Hs.15119	KIAA1361 protein	2.6
111223	AA852773	Hs.334838	KIAA1868 protein	4.6
111239	N90956	Hs.17230	hypothetical protein FLJ22087	7.9
111285	AA778711	Hs.4310	eukaryotic translation initiation factor 1A	6.9
111299	AB033091	Hs.74313	KIAA1265 protein	5.0
111312	AI523913	Hs.34504.	ESTs	3.8
111318	T99755	Hs.334728	ESTs	1.2
111337	AA837396	Hs.263925	LIS1-interacting protein NUDE1, rat homolog	5.1
111352	H58589	Hs.35156	Homo sapiens cDNA FLJ11027 fis, clone PLACE1004114	2.2
111370	AI478658	Hs.94631	brefeldin A-inhibited guanine nucleotide-exchange protein 1	2.8
111384	N94606	Hs.288969	HSCARG protein	2.2
111389	AK000987	Hs.169111	oxidation resistance 1	2.1
111391	NM_003896	Hs.225939	sialyltransferase 9 (CMP-NeuAc:lactosylceramide alpha-2,3-sialyltransferase; GM3 synthase)	5.1
111392	W46342	Hs.325081	Homo sapiens, clone IMAGE:3659680, mRNA, partial cds	8.4
111452	R02354	Hs.15999	ESTs	2.7
111486	AI051194	Hs.227978	EST	6.5
111549	W90838	Hs.20321	ESTs, Moderately similar to ZRF1_HUMAN ZUOTIN RELATED FACTOR-1 (M-PHASE	1.4
111585	R10720	Hs.20670	EST	1.6
111627	R52656	Hs.21691	ESTs	1.6
111870	AB037834	Hs.18685	Homo sapiens mRNA for KIAA1413 protein, partial cds	2.4
111937	BE298665	Hs.14846	Homo sapiens mRNA; cDNA DKFZp564D016 (from clone DKFZp564D016)	10.6
111944	AW083791	Hs.21263	suppressor of potassium transport defect 3	6.6
111987	NM_015310	Hs.6763	KIAA0942 protein	5.1
112134	R41823	Hs.7413	ESTs; calsyntenin-2	2.8
112244	AB029000	Hs.70823	KIAA1077 protein	14.6
112388	R45071	Hs.301693	Homo sapiens, clone IMAGE:3638994, mRNA, partial cds	9.0
112456	NM_016248	Hs.232076	A kinase (PRKA) anchor protein 11	1.4
112464	AW007287	Hs.28538	Homo sapiens cDNA: FLJ21086 fis, clone CAS03272	1.4
112506	AI742756	Hs.26079	ESTs	3.2

112513	R58425	Hs.13809	hypothetical protein FLJ10648	2.0
112752	AK001635	Hs.14838	hypothetical protein FLJ10773	1.8
112884	AK000004	Hs.5013	Homo sapiens mRNA for FLJ00004 protein, partial cds	6.6
112923	T10258	Hs.5037	EST	1.5
112936	AW970826	Hs.6185	KIAA1557 protein	3.2
112958	R61388	Hs.6724	ESTs	6.0
112966	Z44718	Hs.102548	glucocorticoid receptor DNA binding factor 1	6.4
112978	AK000272	Hs.7099	hypothetical protein FLJ20265	1.2
112995	AA737033	Hs.7155	ESTs, Moderately similar to 2115357A TYKI protein [M.musculus]	5.6
112996	BE276112	Hs.7165	zinc finger protein 259	2.0
113047	AI571940	Hs.7549	ESTs	1.9
113049	AW965190	Hs.7560	Homo sapiens mRNA for KIAA1729 protein, partial cds	2.4
113089	T40707	Hs.270862	ESTs	1.3
113196	T57317		gb:yb51a03.s1 Stratagene fetal spleen (937205) Homo sapiens cDNA clone IMAGE:74668 3',	1.7
113248	T63857		gb:yc16e01.s1 Stratagene lung (937210) Homo sapiens cDNA clone 3', mRNA sequence	2.8
113254	AK002180	Hs.11449	DKFZP564O123 protein	1.3
113277	AW971049	Hs.11774	protein (peptidyl-prolyl cis/trans isomerase) NIMA-interacting, 4 (parvulin)	3.2
113429	AA888021	Hs.179808	ESTs	1.2
113499	AI467908	Hs.8882	ESTs	5.9
113547	H59588	Hs.15233	ESTs	2.0
113554	AW503990	Hs.142442	HP1-BP74	3.6
113647	AA813687	Hs.188173	Homo sapiens cDNA FLJ12187 fis, clone MAMMA1000831	1.3
113702	T97307		gb:ye53h05.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121497 3',	4.4
113722	AV653556	Hs.184411	albumin	1.3
113759	AW489865	Hs.9458	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5	1.2
113777	BE266947	Hs.10590	zinc finger protein 313	13.4
113783	AL359588	Hs.7041	hypothetical protein DKFZp762B226	1.7
113791	AI269086	Hs.135578	chitobiase, di-N-acetyl-	1.3
113808	W44735	Hs.9286	Homo sapiens cDNA: FLJ21278 fis, clone COL01832	3.3
113811	BE207480	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone HEP09141	3.1
113817	H13325	Hs.332795	hypothetical protein DKFZp761O17121	3.2
113826	AW378212	Hs.24809	hypothetical protein FLJ10826	2.3
113834	T26483	Hs.6059	EGF-containing fibulin-like extracellular matrix protein 2	11.3
113868	W57902	Hs.90744	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11	2.7
113870	AL079314	Hs.16537	hypothetical protein, similar to (U06944) PRAJA1	6.1
113885	AW959486	Hs.21732	ESTs	6.6
113923	AW953484	Hs.3849	hypothetical protein FLJ22041 similar to FK506 binding proteins	1.9
113989	W87544	Hs.268828	ESTs	1.2
114022	AI539519	Hs.120969	Homo sapiens cDNA FLJ11562 fis, clone HEMBA1003197	5.4
114030	AI825386	Hs.184478	hypothetical protein FLJ21939 similar to 5-azacytidine induced gene 2	9.4
114060	AB029551	Hs.7910	RING1 and YY1 binding protein	1.8
114196	AF017445	Hs.150926	fucose-1-phosphate guanylyltransferase	1.5
114226	AB028968	Hs.7989	KIAA1045 protein	1.8
114253	BE149866	Hs.14831	Homo sapiens, Similar to zinc finger protein 136 (clone pHZ-20), clone MGC:10647, mRNA, complete cds	2.3
114262	AL117518	Hs.3686	KIAA0978 protein	1.4
114275	AW515443	Hs.306117	KIAA0308 protein	15.8
114292	AI815395	Hs.184641	fatty acid desaturase 2	1.9
114309	AA332453	Hs.20824	CGI-85 protein	2.4
114392	AA249590	Hs.100748	ESTs, Weakly similar to A28996 proline-rich protein M14 precursor - mouse [M.musculus]	1.8
114407	BE539976	Hs.103305	Homo sapiens mRNA; cDNA DKFZp434B0425 (from clone DKFZp434B0425)	1.2
114455	H37908	Hs.271616	ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAMILY SX SEQUENCE	5.5
114483	AL120247	Hs.40109	KIAA0872 protein	5.2
114484	AI091713	Hs.106597	Homo sapiens, Similar to RIKEN cDNA 1110012M11 gene, clone IMAGE:3688605, mRNA, partial cds	1.2
114471	AA028074	Hs.104613	RP42 homolog	1.8
114480	BE068778	Hs.151678	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 6 (GalNAc-T6)	13.4
114571	AA766268	Hs.268273	hypothetical protein FLJ13346	1.9
114698	AA476966	Hs.110857	polymerase (RNA) III (DNA directed) polypeptide K (12.3 kDa)	3.5
114730	AI373544	Hs.331328	intermediate filament protein syncoilin	3.8
114767	AI859865	Hs.154443	mitotic chromosome maintenance deficient (S. cerevisiae) 4	1.6
114774	AV656017	Hs.184325	CGI-78 protein	3.1
114798	AA159181	Hs.54900	serologically defined colon cancer antigen 1	3.5
114860	AL157545	Hs.42179	bromodomain and PHD finger containing, 3	4.3
114895	AA236177	Hs.76591	KIAA0887 protein	7.1
114896	BE539101	Hs.5324	hypothetical protein	1.3
114911	AA238872		gb:zt29f02.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:723771 3', mRNA sequence.	1.5
114930	AA237022	Hs.188717	ESTs	2.0
114938	AA242834	Hs.58384	ESTs	2.9

114965	AI733881	Hs.72472	BMP-R1B	2.3
115023	AF102546	Hs.63931	dachshund (Drosophila) homolog	1.3
115038	AA252360	Hs.87968	toll-like receptor 9	1.6
115061	AI751438	Hs.41271	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 1913076	11.8
115062	AA253314	Hs.154103	LIM protein (similar to rat protein kha	1.5
115117	AI670847	Hs.5324	hypothetical protein	1.5
115121	AI834549	Hs.88155	ESTs	2.8
115206	AW183695	Hs.186572	ESTs	2.5
115221	AW365434	Hs.79741	hypothetical protein FLJ10116	1.5
115239	BE251328	Hs.73291	hypothetical protein FLJ10881	1.3
115242	AI358236	Hs.283732	ESTs, Moderately similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE	1.4
115278	AK002163	Hs.301724	hypothetical protein FLJ11301	1.5
115285	AW972872	Hs.293738	ESTs	2.4
115291	BE545072	Hs.122579	hypothetical protein FLJ10461	6.2
115400	AI215069	Hs.89113	ESTs	6.6
115468	AA314349	Hs.48499	tumor antigen SLP-8p	7.4
115471	AK001376	Hs.59348	hypothetical protein FLJ10514	1.4
115479	AW301608	Hs.278188	ESTs, Moderately similar to I54374 gene NF2 protein [H.sapiens]	4.0
115486	AW247593	Hs.71619	eukaryotic translation initiation factor 4E binding protein 1	16.3
115500	Y14443	Hs.88219	zinc finger protein 200	5.0
115553	AJ275986	Hs.71414	transcription factor (SMIF gene)	2.5
115581	AI540842	Hs.61082	ESTs	6.1
115587	BE081342	Hs.283037	HSPC039 protein	2.9
115590	AA399477	Hs.87896	7-60 protein	5.3
115646	N36110	Hs.305971	solute carrier family 2 (facilitated glucose transporter), member 10	4.7
115652	BE093589	Hs.38178	hypothetical protein FLJ23468	10.6
115655	AL048269	Hs.288544	Homo sapiens, clone MGC:16063, mRNA, complete cds	12.7
115663	AI138785	Hs.40507	ESTs	2.0
115676	AA953006	Hs.88143	ESTs	3.0
115690	AA625132	Hs.44159	hypothetical protein FLJ21615	1.7
115693	AF231023	Hs.55173	cadherin, EGF LAG seven-pass G-type receptor 3, flamingo (Drosophila) homolog	6.8
115715	BE395161	Hs.1390	proteasome (prosome, macropain) subunit, beta type, 2	1.7
115734	AI950339	Hs.40782	ESTs	2.6
115811	NM_015434	Hs.48504	DKFZP434B168 protein	2.1
115823	AI732742	Hs.87440	ESTs	2.1
115837	AI575217	Hs.42761	ESTs	1.3
115844	AI373062	Hs.332938	hypothetical protein MGC5370	4.4
115868	AW062629	Hs.52081	KIAA0867 protein	7.2
115875	N55669	Hs.333823	mitochondrial ribosomal protein L13	1.2
115941	AI867451	Hs.46679	hypothetical protein FLJ20739	5.5
115968	AB037753	Hs.62767	KIAA1332 protein	9.8
116003	BE275469	Hs.66493	Down syndrome critical region gene 5	1.4
116011	AL359053	Hs.57664	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 2005735	2.4
116108	AA770688	Hs.28777	H2A histone family, member L	1.8
116134	BE243834	Hs.50441	CGI-04 protein	1.4
116189	N35719	Hs.44749	ESTs, Moderately similar to T00358 hypothetical protein KIAA0684 [H.sapiens]	1.2
116195	AW821113	Hs.72402	ESTs	2.1
116238	AV660717	Hs.47144	DKFZP586N0819 protein	1.7
116246	AF265555	Hs.250646	baculoviral IAP repeat-containing 6	1.7
116262	AI936442	Hs.59838	hypothetical protein FLJ10808	1.7
116296	AI955411	Hs.94109	Homo sapiens cDNA FLJ13634 fis, clone PLACE1011133	1.9
116318	AF097845	Hs.58570	deleted in cancer 1; RNA helicase HDB/DICE1	4.9
116325	AI472106	Hs.49303	Homo sapiens cDNA FLJ11663 fis, clone HEMBA1004631	1.4
116336	AL133033	Hs.4084	KIAA1025 protein	1.9
116339	AK000290	Hs.44033	dipeptidyl peptidase 8	1.5
116350	AA497129	Hs.184771	nuclear factor I/C (CCAAT-binding transcription factor)	1.9
116358	AI149586	Hs.38125	interferon-induced protein 75, 52kD	1.9
116365	N50174	Hs.46765	ESTs	6.1
116368	N90466	Hs.71109	KIAA1229 protein	1.6
116417	AW499664	Hs.12484	Human clone 23626 mRNA sequence	7.4
116436	AA161411	Hs.58668	chromosome 21 open reading frame 57	2.1
116482	AF218313	Hs.235828	putative helicase RUVBL	1.5
116470	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	2.1
116470	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	1.2
116575	AA312572	Hs.6241	phosphoinositide-3-kinase, regulatory subunit, polypeptide 1 (p85 alpha)	1.5
116637	AK001043	Hs.92033	integrin-linked kinase-associated serine/threonine phosphatase 2C	2.7
116640	X89984	Hs.211583	B-cell CLL/lymphoma 7A	2.3

116700	AI800202	Hs.317589	hypothetical protein MGC10765	1.4
116705	AW074819	Hs.12313	hypothetical protein FLJ14566	3.4
116732	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]	2.9
116921	AW068115	Hs.821	biglycan	6.3
116926	H73608	Hs.290830	ESTs	1.7
117034	U72209	Hs.180324	YY1-associated factor 2	3.4
117132	AI393666	Hs.42315	p10-binding protein	5.2
117247	N21032		gb:yx46f06.s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:264803 3', mRNA sequence.	5.5
117276	N71183	Hs.121806	Homo sapiens cDNA FLJ11971 fis, clone HEMBB1001208	1.5
117284	AK001701	Hs.183779	Homo sapiens cDNA FLJ10590 fis, clone NT2RP2004392, weakly similar to MNN4 PROTEIN	2.0
117367	AI041793	Hs.42502	ESTs	2.0
117368	AI878942	Hs.90336	ATPase, H+ transporting, lysosomal (vacuolar proton pump), member J	2.1
117382	AF150275	Hs.40173	ESTs	2.7
117412	N32536	Hs.42845	solute carrier family 16 (monocarboxylic acid transporters), member 6	1.4
117557	AF123050	Hs.44532	dubiquitin	3.4
117588	N34895	Hs.44848	ESTs	3.4
117745	BE294925	Hs.46680	CGI-12 protein	3.0
117754	AA121673	Hs.59757	zinc finger protein 281	1.9
117879	N54706	Hs.303025	chromosome 11 open reading frame 24	1.8
117881	AF161470	Hs.260622	butyrate-induced transcript 1	5.7
117904	BE540675	Hs.332938	hypothetical protein MGC5370	5.9
117911	AL137379	Hs.47125	hypothetical protein FLJ13912	1.7
117933	Y10518	Hs.116470	hypothetical protein FLJ20048	1.7
117983	AL110246	Hs.47367	KIAA1785 protein	5.4
118078	N54321	Hs.47790	EST	5.2
118301	AA453902	Hs.293284	ESTs	2.6
118429	AA243332	Hs.74649	cytochrome c oxidase subunit VIc	2.5
118472	AL157545	Hs.42179	bromodomain and PHD finger containing, 3	4.1
118488	AJ277275	Hs.50102	rape-2 (rape gene)	1.2
118509	N22617	Hs.43228	Homo sapiens cDNA FLJ11835 fis, clone HEMBA1006595	1.5
118528	AI949952	Hs.49397	ESTs	7.4
118656	AI458020	Hs.293287	ESTs	2.5
118670	AA332845	Hs.152618	ESTs, Moderately similar to ZN91_HUMAN ZINC FINGER PROTEIN 91 [H.sapiens]	1.2
118698	AB033113	Hs.50187	KIAA1287 protein	2.1
118737	AA199688		gb:zq75g09.r1 Stratagene hNT neuron (937233) Homo sapiens cDNA clone IMAGE:647488 5'	5.2
118925	N92293	Hs.206832	ESTs, Moderately similar to ALU8_HUMAN ALU SUBFAMILY SX SEQUENCE CONTAMINATION	1.4
118984	AI668709	Hs.240722	ESTs, Moderately similar to ALU8_HUMAN ALU SUBFAMILY SX SEQUENCE CONTAMINATION	3.8
118986	AF148713	Hs.125830	bladder cancer overexpressed protein	4.8
119206	W24781	Hs.293798	KIAA1710 protein	1.7
119235	AW453069	Hs.3657	activity-dependent neuroprotective protein	2.2
119235	AW453069	Hs.3657	activity-dependent neuroprotective prote	1.6
119265	BE539706	Hs.285383	ESTs	1.4
119279	N57568	Hs.48028	EST	25.1
119298	NM_001241	Hs.155478	cyclin T2	1.6
119338	AI417240	Hs.320836	ESTs, Weakly similar to A47582 B-cell growth factor precursor [H.sapiens]	1.3
119349	T65004	Hs.163561	ESTs	8.4
119403	AL117554	Hs.119908	nucleolar protein NOP5/NOP58	6.7
119478	AI624342	Hs.170042	ESTs	2.4
119486	AI796730	Hs.55513	ESTs	2.1
119513	W37933		Empirically selected from AFFX single probeset	1.9
119601	AK000155	Hs.91684	Homo sapiens mRNA; cDNA DKFZp6671103 (from clone DKFZp6671103)	3.7
119602	AW675298	Hs.233694	hypothetical protein FLJ11350	3.0
119676	AA243837	Hs.57787	ESTs	1.4
119682	W61019	Hs.57811	ESTs	1.2
119774	AB032977	Hs.6298	KIAA1151 protein	1.8
119780	NM_016625	Hs.191381	hypothetical protein	3.1
119789	BE393948	Hs.50915	kallikrein 5 (KLK5; KLK-L2; stratum corneum tryptic enzyme)	9.2
119805	AJ223810	Hs.43213	ESTs, Weakly similar to IEFS_HUMAN TRANSFORMATION-SENSITIVE PROTEIN IEF SSP	3.6
119818	AA130970	Hs.58382	hypothetical protein FLJ11101	2.5
119853	AA081218	Hs.58606	Homo sapiens cDNA FLJ14206 fis, clone NT2RP3003157	2.7
119905	AW449064	Hs.119571	collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant)	2.6
119966	AA703129	Hs.58963	ESTs	2.7
120132	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	1.2
120206	H26735	Hs.91668	Homo sapiens clone PP1498 unknown mRNA	45.7
120248	AI924294	Hs.173259	uncharacterized bone marrow protein BM033	1.2
120253	AA131376	Hs.326401	fibroblast growth factor 12B	38.9
120269	AW131940	Hs.104030	ESTs	9.6

120274	AA177051		gb:nc02a02.s1 NCI_CGAP_Pr3 Homo sapiens cDNA clone IMAGE:194 similar to contains Alu	4.6
120280	AA190577		gb:zp52g02.s1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone 3', mRNA sequence	2.0
120296	AW995911	Hs.299883	hypothetical protein FLJ23399	1.8
120297	AA191384	Hs.104072	ESTs, Weakly similar to Z195_HUMAN ZINC FINGER PROTEIN 195 [H.sapiens]	15.2
120324	AA195517	Hs.191643	ESTs	5.5
120325	AA195551	Hs.104106	ESTs	6.4
120327	AK000292	Hs.278732	hypothetical protein FLJ20285	16.1
120336	N85785	Hs.181165	eukaryotic translation elongation factor 1 alpha 1	2.9
120342	AW450669	Hs.45068	hypothetical protein DKFZp434I143	5.7
120345	AA210722	Hs.104158	ESTs	4.5
120349	AW969481	Hs.55189	hypothetical protein	16.8
120352	R06859	Hs.193172	ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]	5.0
120356	AF000545	Hs.296433	putative purinergic receptor	28.1
120371	AA219305	Hs.104188	EST	12.4
120382	AA228026	Hs.38774	ESTs	4.0
120383	AL109963	Hs.123122	FSH primary response (LRPR1, rat) homolog 1	9.7
120386	AW969665	Hs.154848	hypothetical protein DKFZp434D0127	32.6
120388	AA232874	Hs.104245	ESTs	3.1
120389	AW967985	Hs.325572	ESTs, Moderately similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION	21.7
120396	AA134006	Hs.79306	eukaryotic translation initiation factor 4E	12.5
120404	AB023230	Hs.96427	KIAA1013 protein	7.2
120418	AW966893	Hs.26813	Homo sapiens mRNA; cDNA DKFZp586F1323 (from clone DKFZp586F1323)	11.4
120423	AA236453	Hs.18978	Homo sapiens cDNA: FLJ22822 fis, clone KAIA3968	1.9
120472	AI950087		gb:wq05c02.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone 3', mRNA sequence	19.4
120473	AA251973	Hs.269988	ESTs	5.4
120484	AA253170	Hs.96473	EST	10.4
120504	AA256837		gb:zr84d10.s1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:682387 3', mRNA sequence.	3.9
120509	BE047718	Hs.96545	ESTs	9.4
120520	AA258501	Hs.161731	EST	2.4
120535	BE350244	Hs.96547	ESTs	2.5
120551	AA279160	Hs.111407	Homo sapiens, clone IMAGE:3613029, mRNA, partial cds	5.2
120570	AA280679	Hs.271445	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION	14.4
120582	BE244830	Hs.284228	ZNF135-like protein	10.2
120590	AW372799	Hs.125790	leucine-rich repeat-containing 2	2.1
120596	AA282074	Hs.237323	N-acetylglucosamine-phosphate mutase	7.5
120619	AW965339	Hs.111471	ESTs	2.5
120624	AW407987	Hs.173518	M-phase phosphoprotein homolog	52.0
120639	AA286942		gb:zs56f05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701505 3' similar to contains Alu	2.4
120648	AA287095	Hs.140309	Homo sapiens, clone IMAGE:3677194, mRNA, partial cds	5.0
120653	AW063659	Hs.191649	ESTs	2.2
120658	AW969638	Hs.112318	6.2 kd protein	2.2
120669	BE536739	Hs.109909	ESTs	1.9
120695	AA976503		gb:oq30a04.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone 3' similar to contains PTR7.t1 PTR7	46.8
120696	AI821539	Hs.97249	ESTs	2.5
120713	AW449855	Hs.96557	Homo sapiens cDNA FLJ12727 fis, clone NT2RP2000027	5.9
120718	AA292747	Hs.97296	ESTs	2.9
120750	AI191410	Hs.96693	ESTs, Moderately similar to 2109260A B cell growth factor [H.sapiens]	7.0
120774	AI608909	Hs.193985	ESTs	7.8
120807	AA346385	Hs.30002	SH3-containing protein SH3GLB2; KIAA1848 protein	6.8
120809	AA346495		gb:EST52657 Fetal heart II Homo sapiens cDNA 3' end similar to EST containing O family repeat	4.4
120938	AA380260	Hs.104832	EST	4.4
120977	AA398155	Hs.97600	ESTs	4.4
120984	BE262951	Hs.99052	ESTs	5.6
120985	AI219899	Hs.97592	ESTs	1.2
121011	AA398360	Hs.97608	EST	3.1
121026	AI439713	Hs.165295	ESTs	3.5
121081	AA398721	Hs.166749	ESTs, Highly similar to I37550 mismatch repair protein MSH2 [H.sapiens]	5.4
121133	AA363307	Hs.97032	ESTs	3.7
121176	AL121523	Hs.97774	ESTs	1.7
121223	AI002110	Hs.97169	ESTs, Weakly similar to dJ667H12.2.1 [H.sapiens]	2.9
121320	AA403008	Hs.301927	c6.1A	1.9
121340	AW956981	Hs.97910	Homo sapiens cDNA FLJ13383 fis, clone PLACE1001024	3.5
121408	AA406137	Hs.98019	EST	6.0
121439	AA410190	Hs.98076	ESTs, Weakly similar to A47582 B-cell growth factor precursor [H.sapiens]	7.4
121450	AA406430	Hs.105362	Homo sapiens, clone MGC:18257, mRNA, complete cds	6.9
121452	AW971063	Hs.292882	ESTs	1.8
121455	H58308	Hs.15165	retinoic acid induced 14	10.5

121457	W07404	Hs.144502	hypothetical protein FLJ22055	3.4
121486	AA442224	Hs.97900	ESTs	14.4
121505	AA494172	Hs.194417	ESTs	13.1
121508	AA402515	Hs.97887	ESTs	26.0
121513	AA416653	Hs.181510	ESTs	6.2
121514	AA412112		gb:zt69b02.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727563 3', mRNA sequence.	2.6
121549	AA412477	Hs.98142	EST	7.4
121558	AA412497		gb:zt95g12.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:730150 3' similar to contains	2.8
121577	AA411970	Hs.98096	EST	3.5
121581	AA416568		gb:zu05c10.s1 Soares_testis_NHT Homo sapiens cDNA clone 3', mRNA sequence	6.1
121589	AD001528	Hs.89718	spermine synthase	3.9
121594	AA626010	Hs.98247	ESTs	2.2
121622	AA416931	Hs.126065	ESTs	4.2
121655	AA421537	Hs.178072	Homo sapiens mRNA; cDNA DKFZp434B1023 (from clone DKFZp434B1023)	7.8
121682	AA418160	Hs.88043	Homo sapiens cDNA FLJ13558 fis, clone PLACE1007743	2.0
121690	AV660305	Hs.110266	ESTs	4.7
121706	U55184	Hs.154145	hypothetical protein FLJ11585	12.7
121714	AA419225	Hs.98269	Homo sapiens cDNA FLJ11953 fis, clone HEMBB1000883	8.1
121729	AI949597	Hs.98325	ESTs	1.8
121731	AA421041	Hs.180744	ESTs	4.0
121744	AA398784	Hs.97514	ESTs	7.1
121748	BE536911	Hs.234545	hypothetical protein NUF2R	19.5
121773	AB033022	Hs.158654	KIAA1196 protein	7.9
121775	AA421773	Hs.161008	ESTs	1.7
121776	AA292579	Hs.125133	hypothetical protein FLJ22501	6.8
121786	AI810774	Hs.98376	ESTs	10.5
121832	AW340797	Hs.98434	ESTs	5.8
121836	AA328348	Hs.218289	ESTs	3.8
121839	AA425691	Hs.191606	ESTs, Highly similar to KIAA1048 protein [H.sapiens]	5.0
121842	AF027406	Hs.104865	serine/threonine kinase 23	2.7
121847	AA446528	Hs.2799	cartilage linking protein 1	2.3
121871	AW972668	Hs.293044	ESTs	2.9
121882	AA426376	Hs.98459	ESTs	5.0
121911	AA427950		gb:zw50f02.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773499 3'	7.2
121915	AA428179	Hs.223405	ESTs, Moderately similar to A46010 X-linked retinopathy protein [H.sapiens]	2.5
121935	AA428647	Hs.98611	EST	2.3
121983	AA298760	Hs.180191	hypothetical protein FLJ14904	3.4
121985	AI862570	Hs.299214	Homo sapiens, clone IMAGE:2822295, mRNA, partial cds	11.4
121995	AA210863	Hs.3532	nemo-like kinase	3.8
121999	AA430211	Hs.98668	EST	6.4
122009	AW292763	Hs.160822	Homo sapiens cDNA: FLJ20863 fis, clone ADKA01804	2.2
122013	AA431085	Hs.98706	ESTs	6.5
122038	W92142	Hs.271963	ESTs, Weakly similar to ALU5_HUMAN ALU SUBFAMILY SC SEQUENCE CONTAMINATION	13.1
122050	AI453076	Hs.166109	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2	9.1
122060	AA431738	Hs.98750	EST	13.1
122114	AW161023	Hs.104921	ESTs	1.5
122188	AA398838		gb:zt80d01.r1 Soares_testis_NHT Homo sapiens cDNA clone 5', mRNA sequence	3.3
122204	AA435936	Hs.98842	EST	5.6
122246	AA329550	Hs.29417	HCF-binding transcription factor Zhangfei	5.1
122257	AA436819	Hs.98899	ESTs	5.6
122302	AA441801	Hs.104947	ESTs	5.8
122341	AW601969	Hs.99010	hypothetical protein FLJ22263 similar to nuclear receptor-binding SET-domain protein 1	2.0
122356	AA443794	Hs.98390	ESTs	7.3
122369	AA443985	Hs.303222	ESTs	12.2
122371	AA868555	Hs.178222	ESTs	5.0
122372	AA446008	Hs.336677	EST	7.6
122378	AB032948	Hs.21356	hypothetical protein DKFZp762K2015	2.6
122405	AA446572	Hs.303223	EST	2.6
122412	AA446869	Hs.119316	ESTs	7.3
122415	AA446918	Hs.99088	EST	1.9
122418	AA446966	Hs.99090	ESTs, Moderately similar to similar to KIAA0766 [H.sapiens]	6.8
122440	AW505139	Hs.9460	Homo sapiens mRNA; cDNA DKFZp547C244 (from clone DKFZp547C244)	2.6
122448	AA447603	Hs.99123	EST	1.8
122448	AA447626	Hs.99127	EST	3.5
122458	AI266139	Hs.104980	ESTs	1.5
122460	AW418788	Hs.99148	ESTs, Weakly similar to S43569 R01H10.6 protein - Caenorhabditis elegans [C.elegans]	9.7
122464	AA448158	Hs.99152	EST	4.8

122490	AA448349	Hs.238151	EST	6.1
122492	AA448417	Hs.104990	ESTs	5.4
122502	AA204969	Hs.234863	Homo sapiens cDNA FLJ12082 fis, clone HEMBB1002492	1.3
122510	AA449232	Hs.99195	ESTs	11.2
122530	AW959741	Hs.40368	adaptor-related protein complex 1, sigma 2 subunit	10.1
122547	AA779725	Hs.164589	ESTs	2.5
122555	AA194055	Hs.293858	ESTs	1.9
122570	AA452578	Hs.262907	ESTs	9.5
122572	AA452601	Hs.99287	EST	11.0
122586	AK001910	Hs.99303	Homo sapiens cDNA FLJ11048 fis, clone PLACE1004516	3.4
122587	AB040893	Hs.6968	KIAA1460 protein	2.0
122598	AI028173	Hs.99329	ESTs	1.7
122599	AL355841	Hs.99330	hypothetical protein FLJ23588	4.4
122602	AA411925	Hs.301960	ESTs	4.8
122607	AA453518	Hs.98023	ESTs	61.5
122614	AA453630	Hs.99339	EST	10.7
122616	AA453638	Hs.161873	ESTs	107.3
122617	AI681535	Hs.148135	serine/threonine kinase 33	121.4
122618	AA453641		gb:zx48e06.s1 Soares_testis_NHT Homo sapiens cDNA clone 3', mRNA sequence	31.1
122622	AA453987	Hs.144802	ESTs	5.6
122717	AA456859	Hs.178358	ESTs	8.5
122762	AI378875	Hs.105119	ESTs	10.4
122829	AW204530	Hs.99500	ESTs	81.8
122834	AA461492	Hs.99545	Homo sapiens cDNA FLJ10658 fis, clone NT2RP2006052	3.6
122836	AA460581	Hs.290996	ESTs	4.5
122837	AA461509	Hs.293565	ESTs, Weakly similar to putative p150 [H.sapiens]	2.7
122838	AA460584	Hs.334386	ESTs	75.3
122854	AA600235	Hs.9625	NIMA (never in mitosis gene a)-related kinase 6	7.7
122856	AI929374	Hs.75367	Src-like-adapter	5.8
122861	AA335721	Hs.119394	ESTs	1.3
122866	BE539656	Hs.283705	ESTs	4.1
122868	AF005216	Hs.115541	Janus kinase 2 (a protein tyrosine kinase)	5.3
122870	AW576312	Hs.318722	Homo sapiens cDNA: FLJ21766 fis, clone COLF7179	9.9
122872	AW081394	Hs.97103	ESTs	5.3
122879	AA769410	Hs.128654	ESTs	13.9
122907	AA470074	Hs.169896	ESTs	11.5
122916	AA470140	Hs.229170	EST	1.7
122981	AA478951	Hs.105629	ESTs	5.0
123013	AW968324	Hs.17384	ESTs	15.4
123018	AW338067	Hs.323231	Homo sapiens cDNA FLJ11946 fis, clone HEMBB1000709	2.8
123034	AL359571	Hs.44054	ninein (GSK3B interacting protein)	8.7
123072	AI382600	Hs.104308	ESTs, Weakly similar to KIAA1395 protein [H.sapiens]	8.8
123082	AA485360	Hs.105661	ESTs	3.9
123088	AI343652	Hs.105667	ESTs	3.8
123110	AA486256	Hs.193510	EST	7.4
123114	BE304942	Hs.265848	myomegalin	2.8
123131	T52027	Hs.271795	ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]	2.4
123132	AI061582	Hs.324179	Homo sapiens cDNA FLJ12371 fis, clone MAMMA1002434	15.6
123136	AW451999	Hs.194024	ESTs	5.1
123149	AI734179	Hs.105676	ESTs	23.8
123152	AW601773	Hs.270259	ESTs	5.2
123258	AA490929	Hs.105274	ESTs, Weakly similar to RMS1_HUMAN REGULATOR OF MITOTIC SPINDLE ASSEMBLY 1 [H.sapiens]	9.3
123315	AA496369		gb:zv37d10.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:755827 3' similar to	4.1
123369	AA504757	Hs.105738	ESTs	6.9
123394	AA731404	Hs.105510	ESTs	3.6
123433	AW450922	Hs.112478	ESTs	3.7
123466	AA599042	Hs.112503	EST	7.4
123470	AW303265	Hs.303632	Human DNA sequence from clone RP11-110H4 on chromosome 5 Contains a pseudogene similar to	3.5
123471	AB021644	Hs.197219	zinc finger protein 14 (KOX 6)	5.2
123475	BE439553	Hs.250528	Homo sapiens, clone IMAGE:4098694, mRNA, partial cds	1.7
123482	N95059	Hs.55098	ESTs	1.6
123488	BE019072	Hs.334602	Homo sapiens cDNA FLJ14680 fis, clone NT2RP2004242, weakly similar to	2.4
123508	AW380368	Hs.155546	KIAA1080 protein; Golgi-associated, gamma-adaptin ear containing, ARF-binding protein 2	2.2
123615	AA609170		gb:af12a12.s1 Soares_testis_NHT Homo sapiens cDNA clone 3', mRNA sequence	7.8
123619	AA602964		gb:mo97c02.s1 NCI_CGAP_Pr2 Homo sapiens cDNA clone, mRNA sequence	2.8
123658	AA609364		gb:zu71d09.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743441 3' similar to contains Alu	1.7
123674	AI269609	Hs.105187	kinesin protein 9 gene	5.7

123735	NM_013241	Hs.85231	FH1/FH2 domain-containing protein	10.0
123738	AA609891	Hs.112777	EST	5.2
123753	AA609955	Hs.234961	Huntingtin interacting protein E	30.6
123804	AA620464	Hs.261915	EST, Weakly similar to S65657 alpha-1C-adrenergic receptor splice form 2 [H.sapiens]	2.1
123811	AA620586		gb:ae60g05.s1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:951320 3'	2.7
123951	AB012922	Hs.173043	metastasis-associated 1-like 1	6.2
123983	AJ272267	Hs.146178	choline dehydrogenase	4.4
124001	L42542	Hs.75447	rsIA binding protein 1	7.0
124006	AI147155	Hs.270016	ESTs	8.1
124070	AI950314	Hs.154762	HIV-1 rev binding protein 2	3.7
124074	H05635	Hs.294030	topoisomerase-related function protein 4-2	1.2
124178	BE463721	Hs.97101	putative G protein-coupled receptor	3.1
124203	AA372796	Hs.269339	ESTs, Weakly similar to AF161356 1 HSPC093 [H.sapiens]	5.7
124352	AA640891	Hs.102408	ESTs	3.1
124375	D87454	Hs.182966	KIAA0265 protein	3.5
124385	AI267847		gb:oq49a10.x1 Stanley Frontal NB pool 2 Homo sapiens cDNA clone similar to contains	57.1
124390	AA317338	Hs.7535	COBW-like protein	2.8
124391	AF155099	Hs.279780	NY-REN-18 antigen	7.1
124417	N34059		gb:yv28h09.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone 3' similar to contains Alu	3.3
124428	H13540	Hs.82202	ribosomal protein L17	2.9
124440	AA532519	Hs.129043	Human DNA sequence from clone 989H11 on chromosome 22q13.1-13.2. Contains part of a	7.8
124466	R10084	Hs.113319	kinesin heavy chain member 2	2.6
124482	N53935		gb:yv59d09.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone 3', mRNA sequence	7.9
124498	H79433	Hs.268997	ESTs	7.8
124515	AA669097	Hs.109370	ESTs	3.3
124608	N71076	Hs.102800	ESTs, Weakly similar to neuronal thread protein AD7c-NTP [H.sapiens]	4.5
124631	NM_014053	Hs.270594	FLVCR protein	3.2
124634	AI765123	Hs.143671	Homo sapiens cDNA FLJ13533 fis, clone PLACE1005371	5.8
124637	AA160474	Hs.75798	hypothetical protein	9.3
124642	AW968856	Hs.278569	sorting nexin 17	3.5
124649	N92593	Hs.313054	ESTs	6.1
124656	AW297702	Hs.102915	ESTs	8.3
124661	R48170	Hs.78438	EphB1	5.6
124683	AA381661	Hs.119878	ESTs, Weakly similar to M3K9_HUMAN MITOGEN-ACTIVATED PROTEIN KINASE KINASE	7.9
124712	R09166	Hs.191148	ESTs	5.7
124735	R22952	Hs.268685	ESTs	11.3
124761	AA374756	Hs.93560	Homo sapiens mRNA for KIAA1771 protein, partial cds	9.0
124768	AW368528	Hs.100855	ESTs	6.1
124775	R41772	Hs.100878	ESTs	4.9
124777	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE	2.8
124788	R43543	Hs.100912	Homo sapiens cDNA: FLJ22726 fis, clone HSI15006	5.1
124809	AL355722	Hs.106875	Homo sapiens EST from clone 35214, full insert	4.2
124811	R46068	Hs.288912	hypothetical protein FLJ22604	14.2
124812	R47948	Hs.188732	ESTs	7.9
124822	AA418160	Hs.86043	Homo sapiens cDNA FLJ13558 fis, clone PLACE1007743	6.6
124825	AA501669	Hs.336693	ESTs	2.3
124833	AW975868	Hs.294100	ESTs	2.7
124857	R63652	Hs.137190	ESTs	2.3
124860	R65763	Hs.101477	EST	23.9
124863	AI382555	Hs.127950	bromodomain-containing 1	2.0
124878	AF135422	Hs.27059	GDP-mannose pyrophosphorylase A	4.4
124878	BE397530	Hs.288057	hypothetical protein FLJ22242	2.7
124902	H37941	Hs.101883	ESTs	5.7
124903	AW296713	Hs.221441	ESTs	32.4
124930	AI076343	Hs.173939	ESTs, Weakly similar to ALUB_HUMAN !!!! ALU CLASS B WARNING ENTRY !!! [H.sapiens]	22.8
124942	R99978	Hs.268892	ESTs, Moderately similar to B34087 hypothetical protein [H.sapiens]	6.1
124958	AI078645	Hs.431	murine leukemia viral (bmi-1) oncogene homolog	1.9
124980	T40841	Hs.98681	ESTs	4.5
125002	T59338	Hs.269463	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION	4.9
125047	T79815	Hs.279793	ESTs	5.0
125051	T79956	Hs.100588	EST	135.3
125056	T81310	Hs.100592	ESTs	5.4
125101	AI472068	Hs.286236	KIAA1856 protein	5.6
125113	T96595	Hs.302270	ESTs, Weakly similar to ALUF_HUMAN !!!! ALU CLASS F WARNING ENTRY !!! [H.sapiens]	1.8
125115	T97341		gb:ye57e05.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121856 3' similar to	9.6
125125	AI222382	Hs.240767	Human DNA sequence from clone RP1-12G14 on chromosome 6q24.1-25.2. Contains the 5' end of the gene	1.5
125147	W38150		Empirically selected from AFFX single probeset	1.7

125161	W44657	Hs.144232	EST	10.7
125249	AA630883	Hs.131375	ESTs, Moderately similar to ALUB_HUMAN !!!! ALU CLASS B WARNING ENTRY !!! [H.sapiens]	1.3
125255	AF098162	Hs.118831	timeless (Drosophila) homolog	9.4
125279	AW401809	Hs.4779	KIAA1150 protein	1.5
125280	AI123705	Hs.106932	ESTs	8.0
125298	AW972542	Hs.289008	Homo sapiens cDNA: FLJ21814 fis, clone HEP01068	1.5
125660	AW292171	Hs.23978	scaffold attachment factor B	5.9
125827	NM_003403	Hs.97496	YY1 transcription factor	1.2
125891	U29589	Hs.7138	cholinergic receptor, muscarinic 3	6.4
126005	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (survivin)	14.3
126202	AA157632	Hs.272630	vacuolar proton pump delta polypeptide	2.4
126695	AA643322	Hs.172028	a disintegrin and metalloproteinase domain 10	9.1
127050	AW411066	Hs.274351	CGI-89 protein	17.0
127274	AW986158	Hs.58582	Homo sapiens cDNA FLJ12789 fis, clone NT2RP2001947	12.8
128355	AW293012	Hs.181623	ESTs	7.3
128493	D87466	Hs.240112	KIAA0278 protein	3.1
128493	D87466	Hs.240112	KIAA0278 protein	1.3
128522	BE173977	Hs.10098	putative nucleolar RNA helicase	9.4
128527	AA504583	Hs.101047	transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)	1.5
128528	R39234	Hs.251699	ESTs, Weakly similar to IDN4-GGTR14 [H.sapiens]	2.8
128595	U31875	Hs.272499	short-chain alcohol dehydrogenase family member	12.1
128599	NM_015366	Hs.102336	Rho GTPase activating protein 8	2.3
128604	AI879099	Hs.102397	GIOT-3 for gonadotropin inducible transcription repressor-3	1.3
128608	BE267994	Hs.102419	zinc finger protein	7.1
128625	AB037841	Hs.102652	hypothetical protein ASH1	1.3
128629	AL096748	Hs.102708	DKFZP434A043 protein	3.2
128639	AW582962	Hs.102897	CGI-47 protein	2.0
128656	AA458542	Hs.10326	coatomer protein complex, subunit epsilon	1.4
128656	AA458542	Hs.10326	coatomer protein complex, subunit epsilo	1.3
128658	BE397354	Hs.324830	diptheria toxin resistance protein required for diphthamide biosynthesis (Saccharomyces)-like 2	2.4
128670	AA975486	Hs.103441	Homo sapiens, Similar to RIKEN cDNA 1700010L19 gene, clone MGC:16214, mRNA, complete cds	7.1
128691	W27939	Hs.103834	hypothetical protein MGC5576	7.7
128698	BE081143	Hs.225977	nuclear receptor coactivator 3	3.8
128700	Y15221	Hs.103982	small inducible cytokine subfamily B (Cys-X-Cys), member 11	1.6
128714	T85231	Hs.179681	tubulin, beta 5	7.6
128717	AK001564	Hs.104222	hypothetical protein FLJ10702	5.5
128733	BE147740	Hs.104558	ESTs, Moderately similar to I38022 hypothetical protein [H.sapiens]	2.7
128737	AF292100	Hs.104613	RP42 homolog	2.8
128742	AA307211	Hs.251531	proteasome (prosome, macropain) subunit, alpha type, 4	4.4
128746	AI470163	Hs.323342	actin related protein 2/3 complex, subunit 4 (20 kD)	2.2
128747	AB027249	Hs.104741	POZ-binding kinase; T-cell originated protein kinase	2.8
128772	BE302796	Hs.105097	thymidine kinase 1, soluble	5.3
128781	N71826	Hs.105465	small nuclear ribonucleoprotein polypeptide F	53.9
128797	NM_002975	Hs.105927	stem cell growth factor; lymphocyte secreted C-type lectin	13.3
128806	AW830942	Hs.106061	RD RNA-binding protein	2.6
128814	AW248431	Hs.256526	nuclear prelamin A recognition factor	2.2
128830	BE281170	Hs.106357	valosin-containing protein	5.9
128835	AK001731	Hs.106390	Homo sapiens mRNA; cDNA DKFZp586H0924 (from clone DKFZp586H0924)	1.6
128854	BE159181	Hs.168232	hypothetical protein FLJ13855	2.2
128854	BE159181	Hs.168232	hypothetical protein FLJ13855	1.9
128868	AA419008	Hs.106730	chromosome 22 open reading frame 3	3.0
128868	AA419008	Hs.106730	chromosome 22 open reading frame 3	2.2
128871	AF189723	Hs.106778	ATPase, Ca++ transporting, type 2C, member 1	1.5
128891	F34856	Hs.292457	Homo sapiens, clone MGC:18362, mRNA, complete cds	13.3
128906	R57988	Hs.10706	epithelial protein lost in neoplasm beta	4.7
128920	AA622037	Hs.166468	programmed cell death 5	1.4
128925	R67419	Hs.21851	Homo sapiens cDNA FLJ12900 fis, clone NT2RP2004321	1.9
128946	Y13153	Hs.107318	kynurenine 3-monooxygenase (kynurenine 3-hydroxylase)	7.2
128949	AA009647	Hs.8850	a disintegrin and metalloproteinase domain 12 (meltrin alpha) (ADAM-12)	2.4
128958	AW139032	Hs.107376	hypothetical protein DKFZp434N035	1.3
128959	AI580127	Hs.107381	hypothetical protein FLJ11200	10.9
128965	AW150697	Hs.107418	ESTs	1.4
128970	AI375672	Hs.165028	ESTs	1.3
128975	BE560779	Hs.284233	NICE-5 protein	14.0
128979	AW271217	Hs.281434	Homo sapiens cDNA FLJ14028 fis, clone HEMBA1003838	1.6
128995	AI816224	Hs.107747	DKFZP566C243 protein	1.9
129019	AI950087		gb:wq05c02.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone 3', mRNA sequence	2.9

129021	AL044675	Hs.173081	KIAA0530 protein	3.8
129021	AL044675	Hs.173081	KIAA0530 protein	2.5
129032	R80088	Hs.108104	ubiquitin-conjugating enzyme E2L 3	3.4
129076	AW296806	Hs.326234	ESTs, Highly similar to T46422 hypothetical protein DKFZp434M2023.1 [H.sapiens]	5.0
129078	AI351010	Hs.102267	lysosomal	2.1
129088	AA744610	Hs.194431	palladin	17.1
129095	L12350	Hs.108823	thrombospondin 2	2.7
129096	AA463189	Hs.288908	WW Domain-Containing Gene	20.9
129097	BE243933	Hs.108842	zinc finger protein 22 (KOX 15)	3.0
129099	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR/MRP), member 5	5.8
129139	W93048	Hs.250723	hypothetical protein MGC2747	5.9
129149	AA356620	Hs.108947	KIAA0050 gene product	6.3
129172	AW162916	Hs.241676	hypothetical protein PRO2577	1.8
129192	AA286914	Hs.183299	ESTs	2.1
129194	AA150797	Hs.109276	latexin protein	3.2
129198	N57532	Hs.109315	KIAA1415 protein	5.8
129207	AI934365	Hs.109439	osteoglycin (osteoinductive factor, mimecan)	8.0
129228	U40714	Hs.239307	tyrosyl-tRNA synthetase	2.9
129229	AF013758	Hs.109843	polyadenylate binding protein-interacting protein 1	3.2
129254	AA252468	Hs.1098	DKFZp434J1813 protein	2.6
129255	AI961727	Hs.109804	H1 histone family, member X	7.3
129288	W26392	Hs.110080	ESTs, Weakly similar to G13495 pregnancy zone protein [H.sapiens]	9.6
129296	AI051967	Hs.110122	ESTs	1.2
129323	AA287239	Hs.5518	Homo sapiens cDNA FLJ11311 fis, clone PLACE1010102	5.1
129340	H75334	Hs.11050	F-box only protein 9	4.8
129347	BE614192	Hs.279869	melanoma-associated antigen recognised by cytotoxic T lymphocytes	7.6
129362	U30246	Hs.110736	solute carrier family 12 (sodium/potassium/chloride transporters), member 2	6.7
129368	BE220806	Hs.184697	Homo sapiens clone 23785 mRNA sequence	8.6
129370	AI686379	Hs.110796	SAR1 protein	1.4
129372	NM_016039	Hs.110803	CGI-99 protein	2.0
129403	AF149785	Hs.111126	pituitary tumor-transforming 1 interacting protein	7.4
129404	AI267700	Hs.317584	ESTs	5.0
129404	AI267700	Hs.317584	ESTs	2.5
129423	AA204686	Hs.234149	hypothetical protein FLJ20647	10.2
129449	AI096988	Hs.111554	ADP-ribosylation factor-like 7	8.0
129453	AW974265	Hs.111632	Lsm3 protein	3.2
129482	AA188185	Hs.289043	spindlin	6.7
129482	AA188185	Hs.289043	spindlin	3.6
129513	AW843633	Hs.306163	hypothetical protein AL110115	7.1
129515	AF255303	Hs.112227	membrane-associated nucleic acid binding protein	2.5
129527	AA769221	Hs.270847	delta-tubulin	3.2
129559	W01296	Hs.11360	hypothetical protein FLJ14784	7.5
129560	AA317841	Hs.7845	hypothetical protein MGC2752	6.8
129570	AI923097	Hs.11441	chromosome 1 open reading frame 8	2.0
129575	F08282	Hs.278428	progestin induced protein	1.6
129587	H14718	Hs.11506	Human clone 23589 mRNA sequence	6.6
129588	BE408300	Hs.301862	postmeiotic segregation increased 2-like 9	1.4
129591	N57423	Hs.179898	HSPC055 protein	7.3
129594	AW403724	Hs.36989	coagulation factor VII (serum prothrombin conversion accelerator)	9.0
129596	AF035537	Hs.115521	REV3 (yeast homolog)-like, catalytic subunit of DNA polymerase zeta	1.8
129628	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4)	2.2
129628	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (mo	1.4
129629	AK000398	Hs.11747	hypothetical protein FLJ20391	3.8
129649	AD000092	Hs.16488	calreticulin	3.3
129675	NM_015556	Hs.172180	KIAA0440 protein	13.4
129680	U03749		gb:Human chromogranin A (CHGA) gene, promoter an	14.1
129689	AW748482	Hs.77873	B7 homolog 3	2.6
129702	AI304968	Hs.12035	ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]	7.4
129720	AA156214	Hs.12152	APMCF1 protein	2.0
129721	NM_001415	Hs.211539	eukaryotic translation initiation factor 2, subunit 3 (gamma, 52kD)	1.7
129726	H15474	Hs.132898	fatty acid desaturase 1	8.3
129778	AK001676	Hs.12457	hypothetical protein FLJ10814	1.8
129779	AA394090	Hs.12460	Homo sapiens clone 23870 mRNA sequence	5.4
129800	AF052112	Hs.12540	lysosomal	1.7
129806	AB023148	Hs.173373	KIAA0931 protein	1.2
129815	BE585817	Hs.26498	hypothetical protein FLJ21657	3.1
129840	NM_006590	Hs.12820	SnRNP assembly defective 1 homolog	1.8

129861	AL049999	Hs.85963	DKFZP564M182 protein	2.2
129864	AI393237	Hs.129914	runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene)	1.7
129869	AI222069	Hs.13015	hypothetical protein similar to mouse Dnaj1	2.7
129922	AF042379	Hs.13388	gamma-tubulin complex protein 2	4.5
129945	BE514378	Hs.165998	PAI-1 mRNA-binding protein	1.8
129953	AA412195	Hs.13740	ESTs	2.5
129972	AW753185	Hs.180628	dynamin 1-like	1.8
129983	U09848	Hs.132390	zinc finger protein 36 (KOX 18)	1.3
129989	AB015856	Hs.247433	activating transcription factor 6	4.0
130010	AA301116	Hs.142838	nucleolar phosphoprotein Nopp34	1.6
130081	AA287325	Hs.14713	ESTs	4.0
130082	S73265	Hs.1473	gastrin-releasing peptide	1.8
130097	AL048962	Hs.14845	forkhead box O3A	2.8
130100	AL135561	Hs.14891	hypothetical protein FLJ21047	2.3
130111	X53002	Hs.149846	integrin, beta 5	2.3
130112	AA916785	Hs.180610	splicing factor proline/glutamine rich (polypyrimidine tract-binding protein-associated)	3.0
130112	AA916785	Hs.180610	splicing factor proline/glutamine rich (	2.1
130128	L76937	Hs.150477	Werner syndrome	1.8
130135	AA311426	Hs.21635	tubulin, gamma 1	6.1
130211	NM_003358	Hs.23703	ESTs, Moderately similar to CEGT_HUMAN CERAMIDE GLUCOSYLTRANSFERASE [H.sapiens]	1.6
130212	D80001	Hs.152629	KIAA0179 protein	1.3
130236	R85367	Hs.51957	splicing factor, arginine/serine-rich 2, interacting protein	2.0
130241	AL035588	Hs.153203	MyoD family inhibitor	3.2
130242	X79201	Hs.153221	synovial sarcoma, translocated to X chromosome	5.4
130249	D81983	Hs.322852	GAS2-related on chromosome 22	4.8
130263	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related kinase 2	1.4
130287	AA479005	Hs.154036	tumor suppressing subtransferable candidate 3	2.6
130310	AB011121	Hs.154248	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 3	6.3
130353	Z19084	Hs.172210	MUF1 protein	6.2
130356	AF127577	Hs.155017	nuclear receptor interacting protein 1	2.4
130357	AJ224442	Hs.155020	putative methyltransferase	3.4
130359	NM_013449	Hs.277401	bromodomain adjacent to zinc finger domain, 2A	8.5
130367	AL135301	Hs.8768	hypothetical protein FLJ10849	1.4
130372	AI077484	Hs.5011	RNA binding motif protein 9	3.3
130393	N89487	Hs.155291	KIAA0005 gene product	1.8
130399	AW374106	Hs.155356	hypothetical protein MGC2840 similar to a putative glucosyltransferase	3.4
130407	BE385099	Hs.334727	hypothetical protein MGC3017	2.3
130409	NM_001197	Hs.155419	BCL2-interacting killer (apoptosis-inducing)	2.7
130419	AF037448	Hs.155489	NS1-associated protein 1	1.6
130441	U63630	Hs.155637	protein kinase, DNA-activated, catalytic polypeptide	2.3
130448	BE513202	Hs.15589	PPAR binding protein	3.9
130455	D90041	Hs.155956	N-acetyltransferase 1 (arylamine N-acetyltransferase)	33.6
130455	D90041	Hs.155956	N-acetyltransferase 1 (arylamine N-acety	4.6
130471	AL121438	Hs.163706	adducin 1 (alpha)	2.7
130485	BE245851	Hs.180779	H2B histone family, member B	5.0
130487	U49844	Hs.77613	ataxia telangiectasia and Rad3 related	4.3
130498	L38951	Hs.180446	karyopherin (importin) beta 1	1.6
130503	BE208491	Hs.295112	KIAA0618 gene product	16.1
130511	L32137	Hs.1584	cartilage oligomeric matrix protein (pseudoachondroplasia, epiphyseal dysplasia 1, multiple)	6.1
130511	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	5.3
130526	AW876523	Hs.15829	hypothetical protein FLJ12910	2.1
130542	U64875	Hs.179825	RAN binding protein 2-like 1	7.8
130544	AA321238	Hs.4310	eukaryotic translation initiation factor 1A	1.5
130553	AF062649	Hs.252587	pituitary tumor-transforming 1	14.4
130556	AI907018	Hs.15977	Empirically selected from AFFX single probeset	4.7
130567	AA383092	Hs.1608	replication protein A3 (14kD)	7.9
130568	AA232119	Hs.16085	putative G-protein coupled receptor	3.3
130574	AF083206	Hs.16178	apoptosis antagonizing transcription factor	1.2
130586	AB007891	Hs.16349	KIAA0431 protein	5.6
130598	AL042210	Hs.16493	hypothetical protein DKFZp762N2316; KIAA1803 protein	1.4
130601	AA609738	Hs.16525	ESTs	1.5
130614	AI354355	Hs.16697	down-regulator of transcription 1, TBP-binding (negative cofactor 2)	1.3
130617	M90516	Hs.1674	glutamine-fructose-6-phosphate transaminase 1	12.1
130617	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	2.4
130618	AA383439	Hs.16758	Spir-1 protein	15.9
130667	BE246961	Hs.17639	Homo sapiens ubiquitin protein ligase (UBE3B) mRNA, partial cds	13.9
130674	AL048842	Hs.194019	ataxin	1.5

130675	AA442233	Hs.17731	hypothetical protein FLJ12892	5.4
130692	AA652501	Hs.13561	hypothetical protein MGC4692	5.0
130693	R68537	Hs.17962	ESTs	2.0
130712	AJ271881	Hs.279762	bromodomain-containing 7	1.8
130714	AI348274	Hs.18212	DNA segment on chromosome X (unique) 9879 expressed sequence	2.0
130730	AB007920	Hs.18586	KIAA0451 gene product	3.7
130744	H59696	Hs.18747	POP7 (processing of precursor, S. cerevisiae) homolog	3.1
130751	AF052105	Hs.18879	chromosome 12 open reading frame	1.4
130757	AL036067	Hs.18925	protein x 0001	5.7
130768	AF258627	Hs.211562	ATP-binding cassette, sub-family A (ABC1), member 1	5.1
130789	AK000355	Hs.6899	sirtuin (silent mating type information regulation 2, S.cerevisiae, homolog) 5	5.2
130815	AB018298	Hs.19822	SEC24 (S. cerevisiae) related gene family, member D	1.5
130836	J05068	Hs.2012	transcobalamin I (vitamin B12 binding protein, R binder family)	15.7
130841	AL157468	Hs.325825	Homo sapiens cDNA FLJ20848 fis, clone ADKA01732	2.8
130843	AA447492	Hs.20183	ESTs, Weakly similar to AF184763 1 protein x 013 [H.sapiens]	1.5
130844	U76248	Hs.20191	seven in absentia (Drosophila) homolog 2	3.4
130855	AJ243706	Hs.143323	putative DNA/chromatin binding motif	1.7
130861	NM_016578	Hs.20509	HBV pX associated protein-8	1.9
130879	NM_003416	Hs.2078	zinc finger protein 7 (KOX 4, clone HF.16)	1.4
130880	BE514434	Hs.20830	kinesin-like 2	2.1
130892	AL120837	Hs.20993	high-glucose-regulated protein 8	2.4
130898	AB033078	Hs.186613	sphingosine-1-phosphate lyase 1	1.7
130911	BE409769	Hs.21189	DnaJ (Hsp40) homolog, subfamily A, member 2	1.8
130919	N79110	Hs.21276	collagen, type IV, alpha 3 (Goodpasture antigen) binding protein	2.3
130944	BE382657	Hs.21486	signal transducer and activator of transcription 1, 91kD	5.4
130971	N39842	Hs.301444	KIAA1673	2.2
130992	BE398091	Hs.74316	desmoplakin (DPI, DPII)	1.8
130993	T97401	Hs.21929	ESTs	1.6
131005	AV658308	Hs.2210	thyroid hormone receptor interactor 3	1.8
131028	AI879165	Hs.2227	CCAAT/enhancer binding protein (C/EBP), gamma	1.2
131042	AI826288	Hs.171637	hypothetical protein MGC2826	1.6
131046	AA321649	Hs.2248	small inducible cytokine subfamily B (Cys-X-Cys), member 10	7.4
131046	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	3.0
131047	H23230	Hs.22481	ESTs, Moderately similar to A46010 X-linked retinopathy protein [H.sapiens]	1.7
131050	AA194422	Hs.22564	myosin VI	5.1
131060	AA194422	Hs.22564	myosin VI	2.5
131070	N53344	Hs.22507	ESTs	7.1
131076	AA749230	Hs.26433	dolichyl-phosphate (UDP-N-acetylglucosamine) N-acetylglucosaminephosphotransferase 1 (	2.0
131076	AA749230	Hs.26433	dolichyl-phosphate (UDP-N-acetylglucosam	1.9
131099	AL133353	Hs.226581	COX15 (yeast) homolog, cytochrome c oxidase assembly protein	7.0
131174	NM_006540	Hs.29131	nuclear receptor coactivator 2	1.9
131185	BE280074	Hs.23960	cyclin B1	5.8
131206	AW138839	Hs.24210	ESTs	2.0
131213	AA885699	Hs.24332	CGI-26 protein	7.0
131225	H62087	Hs.31659	thyroid hormone receptor-associated protein, 95-kD subunit	7.5
131231	N47468	Hs.59757	zinc finger protein 281	2.9
131233	D89053	Hs.266012	fatty-acid-Coenzyme A ligase, long-chain 3	3.5
131243	AW383256	Hs.24752	spectrin SH3 domain binding protein 1	2.8
131245	AL080080	Hs.24766	thioredoxin domain-containing	2.8
131247	AL043100	Hs.326190	fatty acid amide hydrolase	5.6
131281	AA251716	Hs.25227	ESTs	5.7
131283	X80038	Hs.339713	Homo sapiens clone F19374 APO E-C2 gene cluster	1.3
131305	AV656017	Hs.184325	CGI-76 protein	5.0
131320	AA505691	Hs.145696	splicing factor (CC1.3)	1.8
131339	AF058696	Hs.25812	Nijmegen breakage syndrome 1 (nibrin)	2.8
131339	AF058696	Hs.25812	Nijmegen breakage syndrome 1 (nibrin)	2.6
131375	AW293165	Hs.143134	ESTs	5.4
131390	BE269388	Hs.182698	mitochondrial ribosomal protein L20	5.3
131410	BE259110	Hs.279838	HSPC168 protein	2.2
131412	NM_012247	Hs.124027	SELENOPHOSPHATE SYNTHETASE ; Human selenium donor protein	2.0
131429	AL046302	Hs.26750	hypothetical protein FLJ21908	1.4
131458	BE297567	Hs.27047	hypothetical protein FLJ20392	1.7
131475	AA992841	Hs.27263	KIAA1458 protein	2.0
131501	AV661958	Hs.8207	GK001 protein	2.6
131501	AV661958	Hs.8207	GK001 protein	1.8
131511	AA732153	Hs.27865	Homo sapiens cDNA: FLJ21333 fis, clone COL02535	2.0
131528	AU076408	Hs.28309	UDP-glucose dehydrogenase	1.6

131532	BE268278	Hs.28393	hypothetical protein MGC2592	7.4
131543	AW966881	Hs.41639	programmed cell death 2	2.2
131544	AL355715	Hs.28555	programmed cell death 9 (PDCD9)	2.1
131562	NM_003512	Hs.28777	H2A histone family, member L	1.7
131564	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PLACE1004405	5.1
131564	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	1.8
131569	AL389951	Hs.271823	nucleoporin 50kD	5.0
131618	BE393822	Hs.28645	Homo sapiens mRNA; cDNA DKFZp761C029 (from clone DKFZp761C029); partial cds	1.8
131622	R78195	Hs.29692	Homo sapiens cDNA FLJ11436 fis, clone HEMBA1001213	1.3
131623	AB037791	Hs.29716	hypothetical protein FLJ10980	2.2
131623	AB037791	Hs.29716	hypothetical protein FLJ10980	1.9
131643	AW410601	Hs.30026	HSPC182 protein	2.9
131653	AW960597	Hs.30164	ESTs	1.3
131658	AI218918	Hs.30209	KIAA0854 protein	2.8
131669	X52486	Hs.3041	uracil-DNA glycosylase 2	2.8
131692	BE559681	Hs.30736	KIAA0124 protein	5.6
131714	AA642831	Hs.31016	putative DNA binding protein	2.9
131722	D13757	Hs.311	phosphoribosyl pyrophosphate amidotransferase	3.4
131737	AK001641	Hs.31323	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase complex-associated protein	3.8
131760	X76732	Hs.3184	nucleobindin 2	2.9
131760	X76732	Hs.3184	nucleobindin 2	2.8
131763	AI878932	Hs.317	topoisomerase (DNA) I	3.4
131772	AA382590	Hs.170980	KIAA0948 protein	25.5
131774	BE267158	Hs.169474	DKFZP586J0119 protein	5.5
131787	D87077	Hs.196275	KIAA0240 protein	2.4
131793	AW966127	Hs.32246	Homo sapiens cDNA FLJ14656 fis, clone NT2RP2002439	7.9
131795	BE501849	Hs.32317	high-mobility group 20B	1.4
131798	X86098	Hs.301449	adenovirus 5 E1A binding protein	4.1
131817	U20536	Hs.3280	caspase 6, apoptosis-related cysteine protease	4.2
131824	U28838	Hs.32935	TATA box binding protein (TBP)-associated factor, RNA polymerase III, GTF3B subunit 2	3.5
131850	AI251317	Hs.33184	ESTs	5.1
131878	AA083764	Hs.6101	hypothetical protein MGC3178	5.8
131885	BE502341	Hs.3402	ESTs	13.7
131885	BE502341	Hs.3402	ESTs	2.4
131887	W17064	Hs.332848	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1	3.2
131900	AA099014	Hs.231029	Homo sapiens, clone MGC:15961, mRNA, complete cds	8.7
131900	AA099014	Hs.231029	Homo sapiens, clone MGC:15961, mRNA, com	2.0
131904	AF078866	Hs.284296	Homo sapiens cDNA: FLJ22993 fis, clone KAT11914	5.5
131905	AA179298	Hs.3439	stomatin-like 2	11.3
131913	AW207440	Hs.185973	degenerative spermatocyte (homolog Drosophila; lipid desaturase)	1.7
131916	AA025976	Hs.34569	ESTs	5.2
131925	AF151048	Hs.183180	anaphase promoting complex subunit 11 (yeast APC11 homolog)	2.7
131929	BE541211	Hs.34804	Homo sapiens cDNA FLJ11472 fis, clone HEMBA1001711	5.3
131941	BE252983	Hs.35088	ubiquitin specific protease 1	2.3
131950	AA355113	Hs.35380	x 001 protein	1.5
131962	AK000046	Hs.267448	hypothetical protein FLJ20039	2.3
131965	W79283	Hs.35962	ESTs	1.4
131971	BE567100	Hs.154938	hypothetical protein MDS025	3.5
131977	U90441	Hs.3622	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide II	6.5
131985	AA503020	Hs.36563	hypothetical protein FLJ22418	2.4
131991	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1 (yeast homolog), beta	2.1
132019	H56995	Hs.37372	Homo sapiens DNA binding peptide mRNA, partial cds	3.2
132031	AF183844	Hs.3758	COP9 complex subunit 7a	5.8
132062	BE268155	Hs.3832	clathrin-associated protein AP47	1.5
132084	NM_002267	Hs.3866	karyopherin alpha 3 (importin alpha 4)	3.7
132103	BE171921	Hs.3991	ESTs	1.4
132105	AV646076	Hs.39959	ESTs	5.8
132116	AW960474	Hs.40289	ESTs	1.7
132176	AA857025	Hs.8878	kinesin-like 1	3.3
132180	NM_004460	Hs.418	fibroblast activation protein, alpha	14.7
132192	AA206153	Hs.4209	mitochondrial ribosomal protein L37	5.5
132194	R42432	Hs.4212	ESTs	4.4
132203	NM_004782	Hs.194714	synaptosomal-associated protein, 29kD	2.2
132207	BE206939	Hs.42287	E2F transcription factor 6	2.2
132235	AV658411	Hs.42656	KIAA1681 protein	7.8
132240	AB018324	Hs.42678	KIAA0781 protein	1.5
132252	AI566004	Hs.141269	Homo sapiens cDNA: FLJ21550 fis, clone COL06258	1.3

132266	AA301228	Hs.43299	hypothetical protein FLJ12890	5.7
132273	AA227710	Hs.43858	DKFZP586L151 protein	4.2
132276	AA653507	Hs.285711	hypothetical protein FLJ13089	2.1
132288	N36110	Hs.305971	solute carrier family 2 (facilitated glucose transporter), member 10	1.5
132294	AB023191	Hs.44131	KIAA0974 protein	10.0
132298	NM_015986	Hs.7120	cytokine receptor-like molecule 9	1.9
132299	AW405882	Hs.44205	cortistatin	9.2
132325	N37065	Hs.44856	hypothetical protein FLJ12116	2.0
132348	AW067708	Hs.170311	heterogeneous nuclear ribonucleoprotein D-like	6.5
132370	AW572805	Hs.46645	ESTs	3.8
132374	AF155582	Hs.46744	core1 UDP-galactose3N-acetylgalactosamine-alpha-R beta 1,3-galactosyltransferase	1.5
132376	AI279892	Hs.46801	sorting nexin 14	12.5
132384	AA312135	Hs.46967	HSPC034 protein	28.3
132393	AL135094	Hs.47334	hypothetical protein FLJ14495	1.9
132450	AA100012	Hs.48827	hypothetical protein FLJ12085	1.9
132452	AW973521	Hs.247324	mitochondrial ribosomal protein S14	6.1
132458	AB011084	Hs.48924	KIAA0512 gene product; ALEX2	1.7
132465	AW169847	Hs.49169	KIAA1634 protein	8.6
132470	AI224456	Hs.4934	H.sapiens polyA site DNA	5.2
132484	X16660	Hs.119007	RAB4, member RAS oncogene family	1.4
132518	AW885606	Hs.5084	ESTs	6.1
132528	T78736	Hs.50758	SMC4 (structural maintenance of chromosomes 4, yeast)-like 1	3.3
132530	AA306105	Hs.50785	SEC22, vesicle trafficking protein (S. cerevisiae)-like 1	2.0
132532	AA454132	Hs.5080	mitochondrial ribosomal protein L16	2.9
132534	BE388873	Hs.5086	hypothetical protein MGC10433	2.2
132543	BE568452	Hs.5101	protein regulator of cytokinesis 1	7.3
132571	AW674699	Hs.5169	suppressor of G2 allele of SKP1, S. cerevisiae, homolog of	1.7
132574	AW631437	Hs.5184	TH1 drosophila homolog	7.1
132596	AK001484	Hs.5298	CGI-45 protein	2.2
132611	AA345547	Hs.53263	hypothetical protein FLJ13287	2.2
132612	H12751	Hs.5327	PRO1914 protein	6.8
132616	BE262877	Hs.283558	hypothetical protein PRO1855	14.0
132638	AI796870	Hs.54277	DNA segment on chromosome X (unique) 9928 expressed sequence	11.4
132648	U51127	Hs.54434	hypothetical protein MGC1715	1.9
132688	AB018319	Hs.5460	KIAA0776 protein	2.6
132692	AW191962	Hs.249239	collagen, type VIII, alpha 2	2.0
132715	F11675	Hs.5534	Homo sapiens cDNA FLJ12961 fis, clone NT2RP2005845	1.5
132718	NM_004600	Hs.554	Sjogren syndrome antigen A2 (60kD, ribonucleoprotein autoantigen SS-A/Ro)	3.0
132724	AI142265	Hs.55498	geranylgeranyl diphosphate synthase 1	2.4
132731	AI189075	Hs.301872	hypothetical protein MGC4840	12.4
132744	AA010233	Hs.55921	glutamyl-prolyl-tRNA synthetase	14.8
132760	AA125985	Hs.56145	thymosin, beta, identified in neuroblastoma cells	2.7
132771	Y10275	Hs.56407	phosphoserine phosphatase	3.0
132773	AA459713	Hs.295901	KIAA0493 protein	2.3
132784	AI142133	Hs.56845	GDP dissociation inhibitor 2	1.8
132798	AI026701	Hs.5716	KIAA0310 gene product	3.7
132807	U07418	Hs.57301	mutL (E. coli) homolog 1 (colon cancer, nonpolyposis type 2)	1.8
132810	AB007944	Hs.5737	KIAA0475 gene product	5.9
132813	BE313625	Hs.57435	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2	8.7
132815	AI815189	Hs.57475	sex comb on midleg homolog 1	6.4
132817	N27852	Hs.57553	tousled-like kinase 2	3.6
132821	AJ251595	Hs.169610	CD44 antigen (homing function and Indian blood group system)	2.8
132833	U78525	Hs.57783	eukaryotic translation initiation factor 3, subunit 8 (eta, 116kD)	14.6
132842	NM_016154	Hs.279771	Homo sapiens clone PP1598 unknown mRNA	1.6
132844	F12200	Hs.5811	chromosome 21 open reading frame 59	2.5
132851	U09718	Hs.287912	lectin, mannose-binding, 1	1.4
132863	BE268048	Hs.236494	RAB10, member RAS oncogene family	4.2
132869	AW963217	Hs.203961	ESTs, Moderately similar to AF116721 69 PRO2168 [H.sapiens]	2.8
132873	AW007683	Hs.58598	KIAA1266 protein	2.0
132875	NM_004850	Hs.58617	Rho-associated, coiled-coil containing protein kinase 2	1.8
132891	BE267143	Hs.59271	U2(RNU2) small nuclear RNA auxiliary factor 1 (non-standard symbol)	1.4
132897	AW503667	Hs.59545	ring finger protein 15	5.4
132902	AI936442	Hs.59838	hypothetical protein FLJ10808	6.1
132912	AW732760	Hs.167578	Homo sapiens cDNA FLJ11095 fis, clone PLACE1005374	7.1
132913	W78714	Hs.60257	Homo sapiens cDNA FLJ13598 fis, clone PLACE1009921	2.8
132940	T79136	Hs.127243	Homo sapiens mRNA for KIAA1724 protein, partial cds	6.1
132941	AI817165	Hs.6120	hypothetical protein FLJ13222	10.3

132942	AA554458	Hs.197751	KIAA0668 protein	1.8
132952	AI658580	Hs.61426	Homo sapiens mesenchymal stem cell protein DSC96 mRNA, partial cds	2.2
132962	AA576635	Hs.6153	CGI-48 protein	4.9
132972	AA034365	Hs.288924	Homo sapiens cDNA FLJ11392 fis, clone HEMBA1000575	2.7
132973	AA035446	Hs.323277	ESTs	5.3
132977	AA093322	Hs.301404	RNA binding motif protein 3	3.2
132980	AA040696	Hs.62016	ESTs	1.3
132994	AA112748	Hs.279905	clone HO0310 PRO0310p1	3.0
133012	AA847843	Hs.62711	Homo sapiens, clone IMAGE:3351295, mRNA	10.3
133015	AJ002744	Hs.246315	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GalNAc-T7)	2.1
133016	AI439688	Hs.6289	hypothetical protein FLJ20886	1.3
133053	AI065016	Hs.6390	Homo sapiens clone FLB3344 PRO0845 mRNA, complete cds	6.0
133062	AW500374	Hs.84056	PRO0149 protein	5.3
133069	BE247441	Hs.6430	protein with polyglutamine repeat; calcium (ca2+) homeostasis endoplasmic reticulum protein	4.9
133091	AK001828	Hs.64691	KIAA0483 protein	3.5
133110	AA808177	Hs.65228	ESTs	13.1
133134	AF198520	Hs.65648	RNA binding motif protein 8A	1.3
133145	H94227	Hs.6592	Homo sapiens, clone IMAGE:2961368, mRNA, partial cds	2.2
133152	Z11695	Hs.324473	mitogen-activated protein kinase 1	1.3
133174	AA431620	Hs.324178	hypothetical protein MGC2745	17.1
133175	AW955532	Hs.66666	ESTs, Weakly similar to S19560 proline-rich protein MP4 - mouse [M.musculus]	1.8
133177	X97795	Hs.66718	RAD54 (S.cerevisiae)-like	4.9
133197	AI275243	Hs.180201	hypothetical protein FLJ20671	3.1
133208	AI801777	Hs.6774	ESTs	4.4
133226	AW954569	Hs.296287	Homo sapiens, Similar to bromodomain-containing 4, clone IMAGE:3542455, mRNA, partial cds	1.7
133228	AI492924	Hs.6831	golgi phosphoprotein 1	6.0
133240	AK001489	Hs.242894	ADP-ribosylation factor-like 1	1.5
133254	AI567421	Hs.273330	Homo sapiens, clone IMAGE:3544662, mRNA, partial cds	1.4
133266	AI160873	Hs.69233	zinc finger protein	5.6
133268	AW956781	Hs.293937	ESTs, Weakly similar to FXD2_HUMAN FORKHEAD BOX PROTEIN D2 [H.sapiens]	1.9
133285	M76477	Hs.289082	GM2 ganglioside activator protein	4.7
133291	BE297855	Hs.69855	NRAS-related gene	5.0
133314	AA102670	Hs.70725	gamma-aminobutyric acid (GABA) A receptor, pi	2.7
133321	T79526	Hs.178516	integral type I protein	9.3
133327	AL390127	Hs.7104	Kruppel-like factor 13	4.4
133347	BE257758	Hs.71475	acid cluster protein 33	1.8
133360	AI016521	Hs.71816	v-akt murine thymoma viral oncogene homolog 1	5.5
133366	AA292811	Hs.72050	non-metastatic cells 5, protein expressed in (nucleoside-diphosphate kinase)	2.7
133367	AF231919	Hs.16759	KIAA0539 gene product	1.7
133370	AF245505	Hs.72157	DKFZP564I1922 protein	1.8
133383	BE313555	Hs.7252	KIAA1224 protein	1.7
133390	AI950382	Hs.72660	phosphatidylserine receptor	1.3
133391	AW103364	Hs.727	inhibin, beta A (activin A, activin AB alpha polypeptide)	18.1
133394	AA305127	Hs.237225	hypothetical protein HT023	12.2
133437	AL031591	Hs.7370	phosphotidylinositol transfer protein, beta	10.4
133452	NM_002759	Hs.274382	protein kinase, interferon-inducible double stranded RNA dependent	1.2
133453	AI659306	Hs.73826	protein tyrosine phosphatase, non-receptor type 4 (megakaryocyte)	1.7
133500	AW964804	Hs.74260	hypothetical protein FLJ22237	11.1
133529	W45523	Hs.74571	ADP-ribosylation factor 1	2.8
133540	AL037159	Hs.74619	proteasome (prosome, macropain) 26S subunit, non-ATPase, 2	2.9
133543	AU077073	Hs.108327	damage-specific DNA binding protein 1 (127kD)	2.5
133578	AU077050	Hs.75068	transfin	1.5
133579	X75346	Hs.75074	mitogen-activated protein kinase-activated protein kinase 2	2.1
133582	BE391579	Hs.75087	Fas-activated serine/threonine kinase	1.3
133594	AW160781	Hs.172589	nuclear phosphoprotein similar to S. cerevisiae PWP1	2.2
133595	AA393273	Hs.75133	transcription factor 6-like 1 (mitochondrial transcription factor 1-like)	1.5
133599	NM_002885	Hs.75151	RAP1, GTPase activating protein 1	5.7
133621	NM_004893	Hs.75258	H2A histone family, member Y	25.5
133627	NM_002047	Hs.75280	glycyl-tRNA synthetase	15.8
133631	NM_000401	Hs.75334	exostoses (multiple) 2	3.3
133649	U25849	Hs.75393	acid phosphatase 1, soluble	1.6
133690	AV661185	Hs.75574	mitochondrial ribosomal protein L19	4.1
133720	L27841	Hs.75737	pericentriolar material 1	1.5
133722	AW969976	Hs.279009	matrix Gla protein	6.3
133751	AW402048	Hs.334787	Homo sapiens, Similar to likely ortholog of yeast ARV1, clone IMAGE:3506392, mRNA	3.9
133757	T52948	Hs.196209	RAE1 (RNA export 1, S.pombe) homolog	1.7
133760	BE271768	Hs.181357	laminin receptor 1 (67kD, ribosomal protein SA)	1.8

133765	M62194	Hs.75929	cadherin 11, type 2, OB-cadherin (osteoblast)	1.5
133780	AA557660	Hs.78152	decorin	3.5
133784	BE622743	Hs.301084	arfaptin 1	6.8
133791	M34338	Hs.76244	spermidine synthase	2.8
133797	AL133921	Hs.76272	retinoblastoma-binding protein 2	1.4
133822	D50525	Hs.699	peptidylprolyl isomerase B (cyclophilin B)	8.0
133842	AW797468	Hs.285013	putative human HLA class II associated protein I	13.5
133845	AA147026	Hs.76704	ESTs	2.2
133850	W29092	Hs.7678	cellular retinoic acid-binding protein 1	1.8
133859	U86782	Hs.178761	26S proteasome-associated pad1 homolog	2.0
133865	AB011155	Hs.170290	discs, large (Drosophila) homolog 5	2.8
133867	AW340125	Hs.76989	KIAA0097 gene product	6.7
133868	AB012193	Hs.183874	cullin 4A	2.5
133881	U30872	Hs.77204	centromere protein F (350/400kD, mitosin)	3.0
133922	U30825	Hs.77608	splicing factor, arginine/serine-rich 9	1.4
133924	D86326	Hs.325948	vesicle docking protein p115	5.4
133929	NM_006306	Hs.211602	SMC1 (structural maintenance of chromosomes 1, yeast)-like 1	4.9
133936	L17128	Hs.77719	gamma-glutamyl carboxylase	3.7
133941	BE244332	Hs.77770	adaptor-related protein complex 3, mu 2 subunit	12.1
133959	X81789	Hs.77897	splicing factor 3a, subunit 3, 60kD	9.7
133976	AI908165	Hs.169946	GATA-binding protein 3 (T-cell receptor gene activator)	3.1
133989	AL040328	Hs.78202	SWI/SNF related, matrix associated, actin dependent regulator of chromatin	1.3
133997	AI624113	Hs.78281	regulator of G-protein signalling 12	9.7
134010	AB016092	Hs.197114	RNA binding protein; AT-rich element binding factor	2.4
134015	D31764	Hs.278569	sorting nexin 17	2.5
134070	NM_003590	Hs.78946	cullin 3	1.3
134110	U41060	Hs.79136	LIV-1 protein, estrogen regulated	4.2
134129	NM_014742	Hs.79305	KIAA0255 gene product	2.2
134134	H86504	Hs.173328	protein phosphatase 2, regulatory subunit B (B56), epsilon isoform	5.0
134200	BE559598	Hs.197803	KIAA0160 protein	3.2
134206	AF107463	Hs.79968	splicing factor 30, survival of motor neuron-related	2.5
134208	NM_000288	Hs.79993	peroxisomal biogenesis factor 7	2.1
134219	NM_000402	Hs.80206	glucose-6-phosphate dehydrogenase	9.1
134234	BE300078	Hs.80449	Homo sapiens, clone IMAGE:3535294, mRNA, partial cds	2.8
134275	AI878910	Hs.3688	cisplatin resistance-associated overexpressed protein	1.8
134292	AI906291	Hs.81234	immunoglobulin superfamily, member 3	2.0
134301	AW502505	Hs.81360	Homo sapiens cDNA: FLJ21927 fis, clone HEP04178, highly similar to HSU90909	2.5
134305	U61397	Hs.81424	ubiquitin-like 1 (sentrin)	2.8
134324	AB029023	Hs.179946	KIAA1100 protein	10.4
134328	AW903838	Hs.81800	chondroitin sulfate proteoglycan 2 (versican)	1.9
134329	N92036	Hs.81848	RAD21 (S. pombe) homolog	2.6
134337	NM_004922	Hs.81964	SEC24 (S. cerevisiae) related gene family, member C	2.3
134348	AW291946	Hs.82065	interleukin 6 signal transducer (gp130, oncostatin M receptor)	13.0
134367	AA339449	Hs.82265	phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase,	8.8
134376	X06560	Hs.82396	2',5'-oligoadenylate synthetase 1 (40-46 kD)	1.5
134379	AW362124	Hs.323193	hypothetical protein MGC3222	8.1
134384	AI589941	Hs.8254	Homo sapiens, Similar to tumor differentially expressed 1, clone IMAGE:3639252, mRNA, partial cds	2.6
134391	AA417383	Hs.82582	integrin, beta-like 1 (with EGF-like repeat domains)	4.1
134395	AA456539	Hs.8262	lysosomal	1.7
134403	AA334551	Hs.82767	sperm specific antigen 2	2.8
134405	AW067903	Hs.82772	collagen, type XI, alpha 1	1.3
134411	BE272095	Hs.167791	reticulocalbin 1, EF-hand calcium binding domain	3.2
134415	AI750762	Hs.82911	protein tyrosine phosphatase type IVA, member 2	1.9
134421	AU077196	Hs.82985	collagen, type V, alpha 2	10.3
134424	Z44190	Hs.83023	peroxisomal biogenesis factor 11B	2.4
134446	AA112036	Hs.83419	KIAA0252 protein	1.2
134447	M58603	Hs.83426	nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105)	1.6
134470	X54942	Hs.83758	CDC28 protein kinase 2	2.1
134480	NM_005000	Hs.83916	Empirically selected from AFFX single probeset	5.3
134485	X82153	Hs.83942	cathepsin K (pycnodysostosis)	2.5
134498	AW246273	Hs.84131	threonyl-tRNA synthetase	2.1
134513	AA425473	Hs.84429	KIAA0971 protein	3.8
134516	AK001571	Hs.273357	hypothetical protein FLJ10709	2.4
134520	BE091005	Hs.74861	activated RNA polymerase II transcription cofactor 4	6.7
134529	AW411479	Hs.848	FK506-binding protein 4 (59kD)	2.3
134577	BE244323	Hs.85951	exportin, tRNA (nuclear export receptor for tRNAs)	5.5
134582	AA927177	Hs.86041	CGG triplet repeat binding protein 1	5.8

134612	AW068223	Hs.171581	ubiquitin C-terminal hydrolase UCH37	2.2
134624	AF035119	Hs.8700	deleted in liver cancer 1	2.0
134632	X78520	Hs.174139	chloride channel 3	2.3
134654	AK001741	Hs.8739	hypothetical protein FLJ10879	1.4
134664	AA256106	Hs.87507	ESTs	72.9
134668	BE391929	Hs.8752	transmembrane protein 4	8.5
134687	U62317	Hs.88251	arylsulfatase A	8.0
134692	NM_003474	Hs.8850	a disintegrin and metalloproteinase domain 12 (meltrin alpha)	4.3
134705	BE161887	Hs.88799	anaphase-promoting complex subunit 10	2.3
134714	Y14768	Hs.890	lysosomal	6.7
134719	AA852985	Hs.89232	chromobox homolog 5 (Drosophila HP1 alpha)	2.3
134722	AF129536	Hs.284226	F-box only protein 6	2.9
134724	AF045239	Hs.321576	ring finger protein 22	6.6
134748	X07871	Hs.89476	CD2 antigen (p50), sheep red blood cell receptor	2.3
134751	AW830803	Hs.89497	lamin B1	6.2
134790	BE002798	Hs.287850	integral membrane protein 1	1.9
134806	AD001528	Hs.89718	spermine synthase	1.8
134834	AW451370	Hs.8991	adaptor-related protein complex 1, gamma 2 subunit	1.4
134850	AI701162	Hs.90207	hypothetical protein MGC11138	1.4
134853	BE268328	Hs.90280	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase	5.6
134859	D26488	Hs.90315	KIAA0007 protein	2.8
134880	AI879185	Hs.90606	15 kDa selenoprotein	1.7
134910	AA532983	Hs.9100	Homo sapiens cDNA FLJ13100 fis, clone NT2RP3002255	1.7
134925	AW885909	Hs.6975	PRO1073 protein	2.1
134955	AW401361	Hs.91773	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform	1.3
134971	AI097346	Hs.286049	phosphoserine aminotransferase	2.1
134975	R50333	Hs.92186	Leman coiled-coil protein	2.3
135011	AB037835	Hs.92991	KIAA1414 protein	1.6
135022	NM_000408	Hs.93201	glycerol-3-phosphate dehydrogenase 2 (mitochondrial)	3.9
135032	AW301984	Hs.173685	hypothetical protein FLJ12619	6.2
135077	AW503733	Hs.9414	KIAA1488 protein	2.0
135083	AB036063	Hs.94262	p53-inducible ribonucleotide reductase small subunit 2 homolog	1.3
135095	AF027219	Hs.9443	zinc finger protein 202	7.1
135096	AA081258	Hs.132390	zinc finger protein 36 (KOX 18)	3.2
135153	AI093155	Hs.95420	JM27 protein	2.5
135181	BE250865	Hs.279529	px19-like protein	1.4
135199	AA477514	Hs.96247	translin-associated factor X	5.0
135207	N26427	Hs.9634	ESTs, Highly similar to C10_HUMAN PUTATIVE C10 PROTEIN [H.sapiens]	6.1
135214	T78802	Hs.96560	hypothetical protein FLJ11656	4.6
135243	BE463721	Hs.97101	putative G protein-coupled receptor	5.6
135245	AI028767	Hs.262603	ESTs	3.5
135257	AW291023	Hs.97255	ESTs, Weakly similar to A46010 X-linked retinopathy protein [H.sapiens]	1.2
135263	AI088775	Hs.55498	geranylgeranyl diphosphate synthase 1	2.6
135274	AA448460	Hs.112017	GE36 gene	5.3
135294	AA150320	Hs.9800	protein kinase Njmu-R1	9.1
135295	AI090838	Hs.96006	ESTs	2.4
135307	AI743770	Hs.98368	ESTs, Weakly similar to KIAA0822 protein [H.sapiens]	13.3
135321	AI652069	Hs.98614	ribosome binding protein 1 (dog 180kD homolog)	2.6
135354	AA456454	Hs.183418	cell division cycle 2-like 1 (PITSLRE proteins)	8.3
135361	AA373452	Hs.167700	Homo sapiens cDNA FLJ10174 fis, clone HEMBA1003959	1.5
135389	U05237	Hs.99872	fetal Alzheimer antigen	4.9
135400	X78592	Hs.99915	androgen receptor (dihydrotestosterone receptor; testicular feminization; spinal and bulbar	2.0
134975	R50333	Hs.92186	Leman coiled-coil protein	2.6
135011	AB037835	Hs.92991	KIAA1414 protein	1.4
135022	NM_000408	Hs.93201	glycerol-3-phosphate dehydrogenase 2 (mi	1.6
135032	AW301984	Ha.173685	hypothetical protein FLJ12619	1.4
135077	AW503733	Hs.9414	KIAA1488 protein	1.8
135083	AB036063	Hs.94262	p53-inducible ribonucleotide reductase s	2.5
135095	AF027219	Ha.9443	zinc finger protein 202	1.5
135096	AA081258	Ha.132390	zinc finger protein 36 (KOX 18)	2.1
135153	AI093155	Hs.95420	JM27 protein	4.4
135181	BE250865	Ha.279529	px19-like protein	14.9
135199	AA477514	Hs.96247	translin-associated factor X	1.3
135207	N26427	Hs.9634	ESTs, Highly similar to C10_HUMAN PUTATI	1.7
135214	T78802	Hs.96560	hypothetical protein FLJ11656	6.1
135243	BE463721	Hs.97101	putative G protein-coupled receptor	2.7
135245	AI028767	Hs.262603	ESTs	12.2

135257	AW291023	Hs.97255	ESTs, Weakly similar to A46010 X-linked	7.6
135263	AI088775	Hs.55498	geranylgeranyl diphosphate synthase 1	1.8
135274	AA448460	Hs.112017	GE36 gene	4.1
135294	AA150320	Hs.9800	protein kinase Njmu-R1	1.2
135295	AI090838	Hs.96006	ESTs	4.6
135307	AI743770	Hs.98368	ESTs, Weakly similar to KIAA0822 protein	5.8
135321	AI652069	Hs.98614	ribosome binding protein 1 (dog 180kD ho	12.3
135354	AA456454	Hs.183418	cell division cycle 2-like 1 (PITSLRE pr	5.7
135361	AA373452	Hs.167700	Homo sapiens cDNA FLJ10174 fis, clone HE	7.9
135389	U05237	Hs.99872	fetal Alzheimer antigen	1.9
135400	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	13.9
302256	AA857131	Hs.171595	HIV TAT specific factor 1	5.3
302276	AW057736	Hs.323910	HER2 receptor tyrosine kinase (c-erb-b2,	2.2
303135	AW592789	Hs.279474	HSPC070 protein	1.4
303686	AK000714	Hs.109441	MSTP033 protein	5.2
310085	R43191	Hs.101248	Homo sapiens clone IMAGE:32553, mRNA seq	2.3
315518	AA808229	Hs.167771	ESTs	2.8
317781	NM_007057	Hs.42650	ZW10 interactor	2.0
320836	AI268997	Hs.197289	rab3 GTPase-activating protein, non-cata	5.5
321114	AA902256	Hs.78979	Golgi apparatus protein 1	1.4
322221	N24236	Hs.179662	nucleosome assembly protein 1-like 1	1.3
322474	AF118083	Hs.29494	PRO1912 protein	2.9
322556	BE041451	Hs.177507	hypothetical protein	1.6
323541	AF292100	Hs.104613	RP42 homolog	1.8
407827	BE278431	Hs.40323	BUB3 (budding uninhibited by benzimidazo	1.8
408196	AL034548	Hs.43627	SRY (sex determining region Y)-box 22	6.1
408813	AI580090	Hs.48295	RNA helicase family	5.6
409176	R73727	Hs.101617	ESTs, Weakly similar to T32527 hypotheti	2.6
413670	AB000115	Hs.75470	hypothetical protein, expressed in osteo	2.4
414108	AI267592	Hs.75761	SFRS protein kinase 1	1.5
414848	AW304454	Hs.77495	UBX domain-containing 1	4.2
416980	AA361133	Hs.80684	high-mobility group (nonhistone chromoso	23.6
417378	R57256	Hs.82037	TATA box binding protein (TBP)-associate	5.8
418283	S79895	Hs.83942	cathepsin K (pycnodysostosis)	1.3
418467	NM_006910	Hs.85273	retinoblastoma-binding protein 6	1.8
420269	U72937	Hs.96264	alpha thalassemia/mental retardation syn	2.3
420802	U22376	Hs.1334	v-myb avian myeloblastosis viral oncogen	1.6
421225	AA463798	Hs.102696	MCT-1 protein	3.5
421642	AF172066	Hs.106348	retinoic acid repressible protein	4.9
421828	AW891965	Hs.279789	histone deacetylase 3	3.1
421983	AI252640	Hs.110364	peptidylprolyl isomerase C (cyclophilin	1.9
422052	AA302744	Hs.104518	ESTs	2.4
422055	NM_014320	Hs.111029	putative heme-binding protein	4.1
423750	AF165883	Hs.258229	prefoldin 2	7.0
424001	W67883	Hs.137476	paternally expressed 10 (PEG10; KIAA105	4.9
425182	AF041259	Hs.155040	zinc finger protein 217	3.4
425284	AF155568	Hs.155489	NS1-associated protein 1	2.1
426372	BE304680	Hs.169531	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	7.5
428049	AW183765	Hs.182238	GW128 protein	1.7
428477	AW500533	Hs.11482	splicing factor, arginine/serine-rich 11	2.4
437562	AB001636	Hs.5683	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	3.8
438449	AK001333	Hs.6216	Homo sapiens hepatocellular carcinoma-as	5.6
441560	F13386	Hs.7888	Homo sapiens clone 23736 mRNA sequence	2.0
445580	AF167572	Hs.12912	skb1 (S. pombe) homolog	7.5
446999	AA151520	Hs.334822	hypothetical protein MGC4485	2.2
447111	AI017574	Hs.17409	cysteine-rich protein 1 (intestinal)	2.8
447778	BE620592	Hs.71190	ESTs, Weakly similar to S16506 hypotheti	1.7
448873	NM_003677	Hs.22393	density-regulated protein	5.9
449687	W68520	Hs.331328	intermediate filament protein syncoilin	5.6
450701	H39960	Hs.288467	Homo sapiens cDNA FLJ12280 fis, clone MA	1.4
450703	AA011202	Hs.184771	nuclear factor I/C (CCAAT-binding transc	4.7
452461	N78223	Hs.108106	transcription factor	2.9
452511	BE408178	Hs.285165	Homo sapiens cDNA FLJ20845 fis, clone AD	12.1
453157	AF077036	Hs.31989	DKFZP586G1722 protein	4.7
453658	BE541906	Hs.87819	Homo sapiens, clone MGC:2492, mRNA, comp	1.3
100833	AF135168	Hs.108802	N-ethylmaleimide-sensitive factor	3.2
102481	U50360		gb:Human calcium, calmodulin-dependent p	6.2

	102827	BE244588	Hs.6456	chaperonin containing TCP1, subunit 2 (b	7.9
	103549	BE270465	Hs.78793	protein kinase C, zeta	2.0
	104331	AB040450	Hs.279862	cdk inhibitor p21 binding protein	5.3
	110018	AW579842	Hs.104557	hypothetical protein FLJ10697	2.0
5	115008	AK001827	Hs.87889	helicase-moi	5.7
	119075	M10905	Hs.287820	fibronectin 1	1.3
	119615	AL034423	Hs.75875	ubiquitin-conjugating enzyme E2 variant	2.9
	125006	BE065136	Hs.145698	splicing factor (CC1.3)	1.7
	127609	X80031	Hs.530	collagen, type IV, alpha 3 (Goodpasture	2.4
10	129209	R62676	Hs.17820	Rho-associated, coiled-coil containing p	5.2
	129917	M30773	Hs.278540	protein phosphatase 3 (formerly 2B), reg	4.5
	130182	BE267033	Hs.182853	ubiquitin-conjugating enzyme E2G 2 (homo	11.0
	130365	W56119	Hs.155103	eukaryotic translation initiation factor	3.3
	131135	NM_016569	Hs.267182	TBX3-iso protein	1.3
15	131853	AI681917	Hs.3321	ESTs, Highly similar to IRX1_HUMAN IROQU	3.2
	131881	AW361018	Hs.3383	upstream regulatory element binding prot	14.3
	132726	N52298	Hs.55608	hypothetical protein MGC855	3.0
	135193	X95525	Hs.96103	TATA box binding protein (TBP)-associate	2.7
	409487	H19888		gb:yn57e05.r1 Soares adult brain N2b5H	2.3
20	416040	AW819158	Hs.289044	Homo sapiens cDNA FLJ12048 fis, clone HE	7.4

TABLE 4A

Table 4A shows the accession numbers for those pkeys lacking unigeneID's for Table 4. For each probeset, we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT number	Accessions
123615	30686_-15	AA609170
123619	371681_1	AA602964 AA609200
101445	1650_-5	M21259
124385	656394_1	AI267847 N27351
124417	1642364_1	N34059 N46979
124482	1657509_1	N53935 N53950
102481	31281_-28	U50360
103349	11052_-2	X89059
110856	19346_14	AA992380 N33063 N21418 H79958 R21911 H79957 103797 109699_1 AA080912 AA075318 AA083403 AA076594 AA078992 AA084926 AA081881 AA113913 AA113892 AA083821 AA134801 AA082953 AA070343 AA082835 AA075419 AA063293 AA071252 AA078900 AA082836 AW974305
120280	160212_1	AA190577 AA181657
113248	328626_1	T63857 AW971220 AA493469 T63699
120472	44573_2	AI950087 N70208 R97040 N36809 AI308119 AW967677 N35320 AI251473 H59397 AW971573 R97278 W01059 AW967671 AA908598 AA251875 AI820501 AI820532 W87891 T85904 U71456 T82391 BE328571 T75102 R34725 AA884922 BE328517 AI219788 AA884444 N92578 F13493 AA927794 AI560251 AW874068 AL134043 AW235363 AA663345 AW008282 AA488964 AA283144 AI890387 AI950344 AI741346 AI689062 AA282915 AW102898 AI872193 AI763273 AW173586 AW150329 AI653832 AI762688 AA988777 AA488892 AI356394 AW103813 AI539642 AA642789 AA856975 AW505512 AI961530 AW829970 BE612681 AW276997 AW513601 AW512843 AA044209 AW856538 AA180009 AA337499 AW961101 AA251669 AA251874 AI819225 AW205862 AI683338 AI858509 AW276905 AI833006 AA972584 AA908741 AW072629 AW513996 AA293273 AA969759 N75628 N22388 H84729 H60052 T92487 AI022058 AA780419 AA551005 W80701 AW813456 AI373032 AI564269 F00531 H83488 W37181 W78802 R66056 AI002839 R67840 AA300207 AW959581 T63226 F04005
129019	44573_2	AI950087 N70208 R97040 N36809 AI308119 AW967677 N35320 AI251473 H59397 AW971573 R97278 W01059 AW967671 AA908598 AA251875 AI820501 AI820532 W87891 T85904 U71456 T82391 BE328571 T75102 R34725 AA884922 BE328517 AI219788 AA884444 N92578 F13493 AA927794 AI560251 AW874068 AL134043 AW235363 AA663345 AW008282 AA488964 AA283144 AI890387 AI950344 AI741346 AI689062 AA282915 AW102898 AI872193 AI763273 AW173586 AW150329 AI653832 AI762688 AA988777 AA488892 AI356394 AW103813 AI539642 AA642789 AA856975 AW505512 AI961530 AW829970 BE612681 AW276997 AW513601 AW512843 AA044209 AW856538 AA180009 AA337499 AW961101 AA251669 AA251874 AI819225 AW205862 AI683338 AI858509 AW276905 AI833006 AA972584 AA908741 AW072629 AW513996 AA293273 AA969759 N75628 N22388 H84729 H60052 T92487 AI022058 AA780419 AA551005 W80701 AW813456 AI373032 AI564269 F00531 H83488 W37181 W78802 R66056 AI002839 R67840 AA300207 AW959581 T63226 F04005
120695	9683_3	AA976503 AI917802 AA953664 AA404613 AA428771 BE280542 AW194691 AI927301 AI740458 AI796100 AI935603 AW052210 AA970201 AI833384 AA425910 AI017004 AI241295 AA402816 AA291468
122188	275673_1	AA398838 AA435847
121581	283769_1	AA416568 AA442889 AA417233 AA442223
122818	305217_1	AA453841 AA454061
109026	150431_1	AA157811 AA836869
123658	genbank_AA609384	AA609384
123811	genbank_AA620588	AA620588
125115	genbank_T97341	T97341
125147	NOT_FOUND_entrez_W38150	W38150
118737	382979_1	AA199688 N73861
120274	genbank_AA177051	AA177051
113196	genbank_T57317	T57317
120504	genbank_AA256837	AA256837
120639	genbank_AA286942	AA286942

120809	genbank_AA346495	AA346495	
113702	genbank_T97307	T97307	
129680	23162_1	U03749 NM_001275 J03483 J03915 AI214509 AW245744 AL046455 AA318960 AI741505 AA843875 AI829382 AI560122 AI858999 D55958 AI684005 D53170 AA854091 AI025609 D53119 D54729 D55504 D55377 D55313 AW512244 AA846441 AW043898 AI959102 AA405741 AI091983 AA788784 AA706586 AA854361 AW470949 AA843095 AA772028 AI148432 AI038109 AA782478 AA910064 AI220384 AA781296 AA843881 AA854064 AA843125 AA843419 AA319036 AA319054 AI273831 W32275 AI584185 C05724 AA789023 AI686818 D54392 AI022485 AA431410 AA854232 W39212 W15214 AA894441 AI803081 AI167381 AW245389 AA319430 AA335158 AI042646 AA327030 AA725170 T27943 AA889304 AA976599 AI687001 AI621107 AI865540 AA772107 C06286 AA319661 AA405992	
101045	entrez_J05614	J05614	
117247	genbank	N21032	
110501	genbank	H55748	
103392	entrez_X94563	X94563	
105032	genbank	AA127818	
119513	NOT_FOUND_entrez	W37933	
105445	genbank	AA252395	
121514	genbank	AA412112	
121558	genbank	AA412497	
121911	genbank	AA427950	
123315	714071_1	AA496369 AA496646	
114911	genbank	AA236672	
409487	1134778_1	H19886 AW402806 T10231	

TABLE 5: Figure 5 from BRCA 001 US

Table 5 shows genes upregulated in tumor tissue compared to normal breast tissue.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of tumor to normal breast tissue

Pkey	ExAccn	UnigeneID	UnigeneTitle	R1
100114	X02308	Hs.82962	thymidylate synthetase	2.9
100147	D13666	Hs.136348	osteoblast specific factor 2 (fasciclin	7.5
100154	H60720	Hs.81892	KIAA0101 gene product	9.2
100335	AW247529	Hs.6793	platelet-activating factor acetylhydrola	2.7
100666	L05424	Hs.169610	CD44 antigen (homing function and Indian	5.7
100667	L05424	Hs.169610	CD44 antigen (homing function and Indian	9
100668	L05424	Hs.169610	CD44 antigen (homing function and Indian	7.6
100678	AW502935	Hs.740	PTK2 protein tyrosine kinase 2	53.2
100988	AK000405	Hs.76480	ubiquitin-like 4	11.4
101031	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	8.2
101045	J05614		gb:Human proliferating cell nuclear anti	5
101332	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	3.4
101352	AI494299	Hs.16297	COX17 (yeast) homolog, cytochrome c oxid	6.3
101560	NM_012151	Hs.83363	coagulation factor VIII-associated (Intr	5.7
101592	AF064853	Hs.91299	guanine nucleotide binding protein (	5.6
101767	M81057	Hs.180884	carboxypeptidase B1 (tissue)	14.4
101806	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias	8.9
101810	NM_000318	Hs.180612	peroxisomal membrane protein 3 (35kD, Ze	3.2
101983	AI904232	Hs.75323	prohibitin	8.4
102107	BE258602	Hs.182366	heat shock protein 75	1.4
102165	BE313280	Hs.159627	death associated protein 3	4.6
102198	AW950852	Hs.74598	polymerase (DNA directed), delta 2, regu	4.3
102217	AA829978	Hs.301813	JTV1 gene	6.7
102220	U24389	Hs.65436	lysosomal	4.3
102302	AA306342	Hs.69171	protein kinase C-like 2	2.7
102348	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	2
102374	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	8.2
102455	U48705	Hs.75562	discoidin domain receptor family, member	6.9
102568	W81489	Hs.223025	RAB31, member RAS oncogene family	5.3
102618	AL037672	Hs.81071	extracellular matrix protein 1	5.8
102687	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	4.3
102689	U96132	Hs.171280	hydroxyacyl-Coenzyme A dehydrogenase, ty	6
102704	AU077058	Hs.54089	BRCA1 associated RING domain 1	1.9
102705	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	2.3
102801	BE252241	Hs.38041	pyridoxal (pyridoxine, vitamin B6) kinas	6.4
102827	BE244588	Hs.6456	chaperonin containing TCP1, subunit 2 (b	5.6
103060	NM_005940	Hs.155324	matrix metalloproteinase 11 (MMP11; stro	4.5
103080	AU077231	Hs.82932	cyclin D1 (PRAD1: parathyroid adenomatos	3.1
103178	AA205475	Hs.275865	ribosomal protein S18	9.9
103206	X72755	Hs.77367	monokine induced by gamma interferon	8.8
103238	AI369285	Hs.75189	death-associated protein	5.6
103547	AI376722	Hs.180062	proteasome (prosome, macropain) subunit,	9.7
103549	BE270455	Hs.78793	protein kinase C, zeta	7.9
103886	AK001278	Hs.105737	hypothetical protein FLJ10418 similar to	6.5
104325	BE379768	Hs.150675	polymerase (RNA) II (DNA directed) polyp	6.3
104827	AW052008	Hs.8551	PRP4/STK/WD splicing factor	10.9
104846	AI250789	Hs.32478	ESTs	5.6
104854	AA041276	Hs.154729	3-phosphoinositide dependent protein kin	12.3
104867	AA278898	Hs.225979	hypothetical protein similar to small G	2

104896	AW015318	Hs.23165	ESTs	17.7
104909	AW408164	Hs.249184	transcription factor 19 (SC1)	5
104916	AW958157	Hs.155489	NS1-associated protein 1	1.7
104919	AA026880	Hs.25252	prolactin receptor	1.4
104974	Y12059	Hs.278675	bromodomain-containing 4	1.4
104978	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	7.2
105012	AF098158	Hs.9329	chromosome 20 open reading frame 1	3.3
105039	AA907305	Hs.36475	ESTs	2.5
105079	AA151342	Hs.12677	CGI-147 protein	9.5
105088	H58589	Hs.35156	Homo sapiens cDNA FLJ11027 fis, clone PL	2.2
105393	AF167570	Hs.256583	interleukin enhancer binding factor 3, 9	5.4
105547	AA262640	Hs.27445	unknown	9.3
105564	BE616694	Hs.288042	hypothetical protein FLJ14299	1.4
105658	AA985190	Hs.246875	hypothetical protein FLJ20059	9.4
105746	AW151952	Hs.46879	hypothetical protein FLJ20739	1.5
105858	AF151066	Hs.281428	hypothetical protein	2.9
105930	AF016371	Hs.9880	peptidyl prolyl isomerase H (cyclophilin	5.2
106094	AA533491	Hs.23317	hypothetical protein FLJ14681	6.8
106350	AK001404	Hs.194698	cyclin B2	5.7
106359	AW390282	Hs.31130	transmembrane 7 superfamily member 2	6.3
106610	AA458882	Hs.79732	fibulin 1	7.9
106624	NM_003595	Hs.26350	tyrosylprotein sulfotransferase 2	7.7
106713	BE614802	Hs.184352	hypothetical protein FLJ12549	4.5
106829	AW959893	Hs.27099	hypothetical protein FLJ23293 similar to	16.2
106846	AB037744	Hs.34892	KIAA1323 protein	2.2
106873	N49809	Hs.11197	Homo sapiens, clone IMAGE:3343149, mRNA,	16.8
106973	BE156256	Hs.11923	hypothetical protein	6.6
107029	AF264750	Hs.288971	myeloid/lymphoid or mixed-lineage leukem	1.8
107197	W15477	Hs.64639	glioma pathogenesis-related protein	6.1
107859	AW732573	Hs.47584	potassium voltage-gated channel, delayed	8.4
107901	L42612	Hs.335952	keratin 6B	2.5
107922	BE153855	Hs.61460	Ig superfamily receptor LNIR	2.2
107974	AW956103	Hs.61712	pyruvate dehydrogenase kinase, isoenzyme	6.7
108274	AF129535	Hs.272027	F-box only protein 5	7.1
108647	BE546947	Hs.44276	homeo box C10	9.8
108695	AB029000	Hs.70823	KIAA1077 protein	7.2
108894	AK001431	Hs.5105	hypothetical protein FLJ10569	4
109011	AA156542	Hs.72127	ESTs	1.4
109068	AA164293	Hs.72545	ESTs	2.9
109273	AA375752	Hs.82719	Homo sapiens mRNA; cDNA DKFZp586F1822 (f	2.9
109468	NM_015310	Hs.6783	KIAA0942 protein	3.2
110240	AI668594	Hs.176588	ESTs, Weakly similar to CP4Y_HUMAN CYTOC	4.2
110330	AI288668	Hs.16821	DKFZP434I116 protein	6.2
110501	H55748		gb:yq94a01.s1 Soares fetal liver spleen	6.1
110742	AW190338	Hs.28029	hypothetical protein MGC11256	7.6
110762	BE044245	Hs.30011	hypothetical protein MGC2963	9.3
110856	AA992380		gb:ot37g06.s1 Soares_testis_NHT Homo sap	2.3
110958	NM_005864	Hs.24587	signal transduction protein (SH3 contain	6.7
111125	N83823	Hs.269115	ESTs, Moderately similar to Z195_HUMAN Z	3.6
111179	AK000136	Hs.10760	asporin (LRR class 1)	7.1
111239	N90956	Hs.17230	hypothetical protein FLJ22087	7.9
111285	AA778711	Hs.4310	eukaryotic translation initiation factor	6.9
111392	W46342	Hs.325081	Homo sapiens, clone IMAGE:3659680, mRNA,	8.4
111937	BE298565	Hs.14846	Homo sapiens mRNA; cDNA DKFZp564D016 (fr	10.8
112244	AB029000	Hs.70823	KIAA1077 protein	14.6
112995	AA737033	Hs.7155	ESTs, Moderately similar to 2115357A TYK	5.6
113777	BE266947	Hs.10590	zinc finger protein 313	13.4
113791	AI269096	Hs.135578	chitobiase, di-N-acetyl-	1.3
113811	BE207480	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone H	3.1
113834	T26483	Hs.6059	EGF-containing fibulin-like extracellula	11.3
113868	W57902	Hs.90744	proteasome (prosome, macropain) 26S subu	2.7
113870	AL079314	Hs.16537	hypothetical protein, similar to (U06944	6.1
113923	AW953484	Hs.3849	hypothetical protein FLJ22041 similar to	1.9
114275	AW515443	Hs.306117	KIAA0306 protein	15.8
114695	AA236177	Hs.76591	KIAA0887 protein	7.1
114965	AI733881	Hs.72472	BMP-R1B	2.3
115061	AI751438	Hs.41271	Homo sapiens mRNA full length insert cDN	11.8

115278	AK002163	Hs.301724	hypothetical protein FLJ11301	1.5
115291	BE545072	Hs.122579	hypothetical protein FLJ10461	6.2
115652	BE093589	Hs.36178	hypothetical protein FLJ23468	10.6
115693	AF231023	Hs.55173	cadherin, EGF LAG seven-pass G-type rece	6.8
115941	AI867451	Hs.46879	hypothetical protein FLJ20739	5.5
115968	AB037753	Hs.62767	KIAA1332 protein	9.8
116011	AL359053	Hs.57664	Homo sapiens mRNA full length insert cDN	2.4
116417	AW499664	Hs.12484	Human clone 23826 mRNA sequence	7.4
116470	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	2.1
116637	AK001043	Hs.92033	integrin-linked kinase-associated serine	2.7
117132	AI393866	Hs.42315	p10-binding protein	5.2
117881	AF161470	Hs.250622	butyrate-induced transcript 1	5.7
118528	AI949952	Hs.49397	ESTs	7.4
119075	M10905	Hs.287820	fibronectin 1	5.7
119285	BE539706	Hs.285363	ESTs	1.4
119349	T65004	Hs.183561	ESTs	8.4
119403	AL117554	Hs.119906	nucleolar protein NOP5/NOP58	6.7
119789	BE393948	Hs.50915	kallikrein 5 (KLK5; KLK-L2; stratum corn	9.2
120206	H26735	Hs.91568	Homo sapiens clone PP1498 unknown mRNA	45.7
120253	AA131376	Hs.326401	fibroblast growth factor 12B	38.9
120297	AA191384	Hs.104072	ESTs, Weakly similar to Z195_HUMAN ZINC	15.2
120325	AA195651	Hs.104106	ESTs	6.4
120327	AK000292	Hs.278732	hypothetical protein FLJ20285	16.1
120349	AW969481	Hs.55189	hypothetical protein	16.8
120356	AF000545	Hs.296433	putative purinergic receptor	28.1
120371	AA219305	Hs.104196	EST	12.4
120383	AL109983	Hs.123122	FSH primary response (LRPR1, rat) homolo	9.7
120386	AW969665	Hs.154848	hypothetical protein DKFZp434D0127	32.6
120389	AW987985	Hs.325572	ESTs, Moderately similar to ALU7_HUMAN A	21.7
120396	AA134006	Hs.78306	eukaryotic translation initiation factor	12.5
120418	AW966893	Hs.26613	Homo sapiens mRNA; cDNA DKFZp586F1323 (f	11.4
120472	AI950087		gb:wq05c02.x1 NCI_CGAP_Kid12 Homo sapien	19.4
120484	AA253170	Hs.96473	EST	10.4
120570	AA280679	Hs.271445	ESTs, Weakly similar to ALU1_HUMAN ALU S	14.4
120582	BE244830	Hs.284228	ZNF135-like protein	10.2
120596	AA282074	Hs.237323	N-acetylglucosamine-phosphate mutase	7.5
120624	AW407987	Hs.173518	M-phase phosphoprotein homolog	52
120695	AA976503		gb:oq30a04.s1 NCI_CGAP_GC4 Homo sapiens	46.8
120713	AW449855	Hs.96557	Homo sapiens cDNA FLJ12727 fis, clone NT	5.9
120750	AI191410	Hs.96693	ESTs, Moderately similar to 2109260A B c	7
120774	AI608909	Hs.193985	ESTs	7.8
120807	AA346385	Hs.30002	SH3-containing protein SH3GLB2; KIAA1848	6.8
120809	AA346495		gb:EST52657 Fetal heart II Homo sapiens	4.4
120984	BE262951	Hs.99052	ESTs	5.6
121081	AA398721	Hs.186749	ESTs, Highly similar to I37550 mismatch	5.4
121408	AA408137	Hs.98019	EST	6
121505	AA494172	Hs.194417	ESTs	13.1
121508	AA402515	Hs.97887	ESTs	28
121513	AA416653	Hs.181510	ESTs	6.2
121549	AA412477	Hs.98142	EST	7.4
121558	AA412497		gb:zt95g12.s1 Soares_testis_NHT Homo sap	2.8
121655	AA421537	Hs.178072	Homo sapiens mRNA; cDNA DKFZp434B1023 (f	7.8
121744	AA398784	Hs.97514	ESTs	7.1
121748	BE536911	Hs.234545	hypothetical protein NUF2R	19.5
121773	AB033022	Hs.158654	KIAA1196 protein	7.9
121832	AW340797	Hs.88434	ESTs	5.8
121839	AA425691	Hs.191606	ESTs, Highly similar to KIAA1048 protein	5
121882	AA426376	Hs.98459	ESTs	5
121911	AA427950		gb:zw50f02.s1 Soares_total_fetus_Nb2HF8_	7.2
121999	AA430211	Hs.98668	EST	6.4
122013	AA431085	Hs.98706	ESTs	6.5
122036	W92142	Hs.271963	ESTs, Weakly similar to ALU5_HUMAN ALU S	13.1
122356	AA443794	Hs.98390	ESTs	7.3
122371	AA868555	Hs.178222	ESTs	5
122372	AA446008	Hs.336677	EST	7.6
122460	AW416788	Hs.99148	ESTs, Weakly similar to S43569 R01H10.6	9.7
122490	AA448349	Hs.238151	EST	6.1

122492	AA448417	Hs.104990	ESTs	5.4
122510	AA449232	Hs.99195	ESTs	11.2
122530	AW959741	Hs.40368	adaptor-related protein complex 1, sigma	10.1
122572	AA452601	Hs.99287	EST	11
122607	AA453518	Hs.98023	ESTs	61.5
122614	AA453630	Hs.99339	EST	10.7
122616	AA453638	Hs.161873	ESTs	107.3
122618	AA453641		gb:zx48e06.s1 Soares_testis_NHT Homo sap	31.1
122622	AA453987	Hs.144802	ESTs	5.6
122717	AA456859	Hs.178358	ESTs	8.5
122829	AW204530	Hs.99500	ESTs	81.8
122838	AA460584	Hs.334386	ESTs	75.3
122856	AI929374	Hs.75357	Src-like-adapter	5.8
122868	AF005216	Hs.115541	Janus kinase 2 (a protein tyrosine kinas	5.3
122907	AA470074	Hs.169896	ESTs	11.5
123016	AW338067	Hs.323231	Homo sapiens cDNA FLJ11946 fis, clone HE	2.8
123034	AL359571	Hs.44054	ninein (GSK3B interacting protein)	8.7
123136	AW451999	Hs.194024	ESTs	5.1
123152	AW601773	Hs.270259	ESTs	5.2
123394	AA731404	Hs.105510	ESTs	3.6
123468	AA599042	Hs.112503	EST	7.4
123488	BE019072	Hs.334802	Homo sapiens cDNA FLJ14680 fis, clone NT	2.4
123615	AA609170		gb:af12a12.s1 Soares_testis_NHT Homo sap	7.8
123735	NM_013241	Hs.85231	FH1/FH2 domain-containing protein	10
123753	AA609955	Hs.234961	Huntingtin interacting protein E	30.6
124008	AI147155	Hs.270016	ESTs	8.1
124385	AI267847		gb:aq49a10.x1 Stanley Frontal NB pool 2	57.1
124440	AA532519	Hs.129043	Human DNA sequence from clone 989H11 on	7.8
124656	AW297702	Hs.102915	ESTs	8.3
124683	AA381661	Hs.119878	ESTs, Weakly similar to M3K9_HUMAN MITOG	7.9
124735	R22952	Hs.268685	ESTs	11.3
124761	AA374756	Hs.93560	Homo sapiens mRNA for KIAA1771 protein,	9
124768	AW368528	Hs.100855	ESTs	8.1
124788	R43543	Hs.100912	Homo sapiens cDNA: FLJ22726 fis, clone H	5.1
124811	R46068	Hs.288912	hypothetical protein FLJ22604	14.2
124812	R47948	Hs.188732	ESTs	7.9
124822	AA418160	Hs.86043	Homo sapiens cDNA FLJ13558 fis, clone PL	6.6
124860	R65763	Hs.101477	EST	23.9
124903	AW298713	Hs.221441	ESTs	32.4
124930	AI076343	Hs.173939	ESTs, Weakly similar to ALUB_HUMAN !!!!	22.8
124942	R99978	Hs.268892	ESTs, Moderately similar to B34087 hypot	6.1
125051	T79956	Hs.100588	EST	135.3
125056	T81310	Hs.100592	ESTs	5.4
125101	AI472068	Hs.288238	KIAA1856 protein	5.6
125115	T97341		gb:ye57e05.s1 Soares fetal liver spleen	9.6
125280	AI123705	Hs.106932	ESTs	8
127274	AW966158	Hs.58582	Homo sapiens cDNA FLJ12789 fis, clone NT	12.8
128528	R39234	Hs.251699	ESTs, Weakly similar to IDN4-GGTR14 [H.s	2.8
128670	AA975486	Hs.103441	Homo sapiens, Similar to RIKEN cDNA 1700	7.1
128691	W27939	Hs.103834	hypothetical protein MGC5578	7.7
128772	BE302796	Hs.105097	thymidine kinase 1, soluble	5.3
128781	N71826	Hs.105465	small nuclear ribonucleoprotein polypept	53.9
128797	NM_002975	Hs.105927	stem cell growth factor; lymphocyte secr	13.3
128868	AA419008	Hs.106730	chromosome 22 open reading frame 3	3
128891	F34656	Hs.292457	Homo sapiens, clone MGC:16362, mRNA, com	13.3
128948	Y13153	Hs.107318	kynurenine 3-monooxygenase (kynurenine 3	7.2
128975	BE560779	Hs.284233	NICE-5 protein	14
128995	AI816224	Hs.107747	DKFZP566C243 protein	1.9
129019	AI950087		gb:wq05c02.x1 NCI_CGAP_Kid12 Homo sapien	2.9
129078	AW296806	Hs.326234	ESTs, Highly similar to T46422 hypothetl	5
129088	AA744610	Hs.194431	palladin	17.1
129096	AA463189	Hs.288906	WW Domain-Containing Gene	20.9
129198	N57532	Hs.109315	KIAA1415 protein	5.8
129347	BE614192	Hs.279869	melanoma-associated antigen recognised b	7.6
129362	U30246	Hs.110736	solute carrier family 12 (sodium/potassi	8.7
129372	NM_016039	Hs.110803	CGI-99 protein	2
129404	AI267700	Hs.317584	ESTs	5

129482	AA188185	Hs.289043	spindlin	6.7
129559	W01296	Hs.11360	hypothetical protein FLJ14784	7.5
129587	H14718	Hs.11508	Human clone 23589 mRNA sequence	6.8
129629	AK000398	Hs.11747	hypothetical protein FLJ20391	3.8
129649	AD000092	Hs.16488	catrodicutin	3.3
129680	U03749		gb:Human chromogranin A (CHGA) gene, pro	14.1
129689	AW748482	Hs.77873	B7 homolog 3	2.6
129702	AI304956	Hs.12035	ESTs, Weakly similar to I38022 hypothetl	7.4
129720	AA156214	Hs.12152	APMCF1 protein	2
130010	AA301116	Hs.142838	nucleolar phosphoprotein Nopp34	1.6
130097	AL046962	Hs.14845	forkhead box O3A	2.8
130135	AA311426	Hs.21635	tubulin, gamma 1	6.1
130211	NM_003358	Hs.23703	ESTs, Moderately similar to CEGT_HUMAN C	1.6
130242	X79201	Hs.153221	synovial sarcoma, translocated to X chro	5.4
130359	NM_013449	Hs.277401	bromodomain adjacent to zinc finger doma	8.5
130365	W58119	Hs.155103	eukaryotic translation initiation factor	11
130448	BE513202	Hs.15589	PPAR binding protein	3.9
130455	D90041	Hs.155958	N-acetyltransferase 1 (arylamine N-acety	33.6
130471	AL121438	Hs.183706	adducin 1 (alpha)	2.7
130503	BE208491	Hs.295112	KIAA0618 gene product	16.1
130511	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	6.1
130542	U64675	Hs.179825	RAN binding protein 2-like 1	7.8
130553	AF052849	Hs.252587	pituitary tumor-transforming 1	14.4
130556	AI907018	Hs.15977	Empirically selected from AFFX single pr	4.7
130567	AA383092	Hs.1608	replication protein A3 (14kD)	7.9
130574	AF083208	Hs.18178	apoptosis antagonizing transcription fac	1.2
130617	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	12.1
130667	BE246961	Hs.17639	Homo sapiens ubiquitin protein ligase (U	13.9
130693	R68537	Hs.17962	ESTs	2
130744	H59696	Hs.18747	POP7 (processing of precursor, S. cerevi	3.1
130757	AL036087	Hs.18925	protein x 0001	5.7
130880	BE514434	Hs.20830	kinesin-like 2	2.1
130944	BE382657	Hs.21486	signal transducer and activator of trans	5.4
131046	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	7.4
131060	AA194422	Hs.22564	myosin VI	5.1
131099	AL133353	Hs.226581	COX15 (yeast) homolog, cytochrome c oxid	7
131135	NM_016569	Hs.267182	TBX3-iso protein	3.3
131185	BE280074	Hs.23960	cyclin B1	5.8
131225	H62087	Hs.31659	thyroid hormone receptor-associated prot	7.5
131245	AL080080	Hs.24766	thioredoxin domain-containing	2.8
131283	X80038	Hs.339713	Homo sapiens clone F19374 APO E-C2 gene	1.3
131569	AL389951	Hs.271623	nucleoporin 50kD	5
131643	AW410601	Hs.30026	HSPC182 protein	2.9
131714	AA642831	Hs.31016	putative DNA binding protein	2.9
131722	D13757	Hs.311	phosphoribosyl pyrophosphate amidotransf	3.4
131760	X76732	Hs.3184	nucleobindin 2	2.9
131793	AW966127	Hs.32246	Homo sapiens cDNA FLJ14656 fis, clone N7	7.9
131885	BE502341	Hs.3402	ESTs	13.7
131900	AA099014	Hs.231029	Homo sapiens, clone MGC:15961, mRNA, com	8.7
131905	AA179298	Hs.3439	stomatin-like 2	11.3
131941	BE252983	Hs.35086	ubiquitin specific protease 1	2.3
131971	BE567100	Hs.154938	hypothetical protein MDS025	3.5
132180	NM_004460	Hs.418	fibroblast activation protein, alpha	14.7
132203	NM_004782	Hs.194714	synaptosomal-associated protein, 29kD	7.8
132273	AA227710	Hs.43658	DKFZP586L151 protein	10
132288	N36110	Hs.305971	solute carrier family 2 (facilitated glu	9.2
132294	AB023191	Hs.44131	KIAA0974 protein	2
132348	AW067708	Hs.170311	heterogeneous nuclear ribonucleoprotein	12.5
132370	AW572805	Hs.46645	ESTs	26.3
132384	AA312135	Hs.46967	HSPC034 protein	6.1
132450	AA100012	Hs.48827	hypothetical protein FLJ12085	8.6
132465	AW169847	Hs.49169	KIAA1634 protein	6.1
132532	AA454132	Hs.5080	mitochondrial ribosomal protein L16	7.1
132574	AW631437	Hs.5184	TH1 drosophila homolog	14
132638	AI796870	Hs.54277	DNA segment on chromosome X (unique) 99212.4	
132718	NM_004600	Hs.554	Sjogren syndrome antigen A2 (60kD, ribon	3.7
132726	N52298	Hs.55608	hypothetical protein MGC855	14.3

132731	AI169075	Hs.301872	hypothetical protein MGC4840	5.9
132744	AA010233	Hs.55921	glutamyl-prolyl-tRNA synthetase	6.4
132773	AA459713	Hs.295901	KIAA0493 protein	14.6
132798	AI026701	Hs.5716	KIAA0310 gene product	2.5
132810	AB007944	Hs.5737	KIAA0475 gene product	4.2
132833	U78525	Hs.57783	eukaryotic translation initiation factor	6.1
132842	NM_016154	Hs.279771	Homo sapiens clone PP1596 unknown mRNA	7.1
132851	U09716	Hs.287912	lectin, mannose-binding, 1	6.1
132891	BE267143	Hs.59271	U2(RNU2) small nuclear RNA auxiliary fac	2.7
132941	AI817165	Hs.6120	hypothetical protein FLJ13222	2.1
132972	AA034355	Hs.288924	Homo sapiens cDNA FLJ11392 fis, clone HE	3.5
132980	AA040696	Hs.62016	ESTs	1.3
132994	AA112748	Hs.279905	clone HQ0310 PRO0310p1	17.1
133016	AI439688	Hs.6289	hypothetical protein FLJ20886	4.4
133177	X97795	Hs.66716	RAD54 (S.cerevisiae)-like	4.4
133208	AI801777	Hs.6774	ESTs	5.5
133254	AI567421	Hs.273330	Homo sapiens, clone IMAGE:3544662, mRNA,	1.3
133266	AI160873	Hs.69233	zinc finger protein	16.1
133268	AW956781	Hs.293937	ESTs, Weakly similar to FXD2_HUMAN FORKH	12.2
133285	M76477	Hs.289082	GM2 ganglioside activator protein	10.4
133390	AI950382	Hs.72660	phosphatidylserine receptor	5.7
133391	AW103364	Hs.727	inhibin, beta A (activin A, activin AB a	25.5
133540	AL037159	Hs.74619	proteasome (prosome, macropain) 26S subu	1.7
133594	AW160781	Hs.172589	nuclear phosphoprotein similar to S. cer	2.8
133621	NM_004893	Hs.75258	H2A histone family, member Y	13.5
133720	L27841	Hs.75737	pericentriolar material 1	6.7
133760	BE271758	Hs.181357	laminin receptor 1 (67kD, ribosomal prot	5.4
133784	BE622743	Hs.301064	*artaptin 1*	12.1
133791	M34338	Hs.76244	spermidine synthase	9.7
133797	AL133921	Hs.76272	retinoblastoma-binding protein 2	1.3
133822	D50525	Hs.699	peptidylprolyl isomerase B (cyclophilin	9.7
133850	W29092	Hs.7678	cellular retinoic acid-binding protein 1	4.2
133865	AB011155	Hs.170290	discs, large (Drosophila) homolog 5	5
133881	U30872	Hs.77204	centromere protein F (350/400kD, mitosin	9.1
133924	D86326	Hs.325948	vesicle docking protein p115	1.8
133959	X81789	Hs.77897	splicing factor 3a, subunit 3, 60kD	10.4
133989	AL040328	Hs.78202	SWI/SNF related, matrix associated, acti	2.8
133997	AI824113	Hs.78281	regulator of G-protein signalling 12	13
134234	BE300078	Hs.80449	Homo sapiens, clone IMAGE:3535294, mRNA,	10.3
134348	AW291946	Hs.82065	interleukin 6 signal transducer (gp130,	6.7
134376	X06560	Hs.82398	2',5'-oligoadenylate synthetase 1 (40-46	5.5
134379	AW362124	Hs.323193	hypothetical protein MGC3222	5.8
134405	AW067903	Hs.82772	collagen, type XI, alpha 1	72.9
134421	AU077196	Hs.82985	collagen, type V, alpha 2	6.7
134480	NM_005000	Hs.83916	Empirically selected from AFFX single pr	8.2
134516	AK001571	Hs.273357	hypothetical protein FLJ10709	1.4
134529	AW411479	Hs.848	FK506-binding protein 4 (59kD)	2.8
134751	AW630803	Hs.89497	lamin B1	6.1
134790	BE002798	Hs.287850	integral membrane protein 1	1.2
134806	AD001528	Hs.89718	spermine synthase	2.6
134850	AI701162	Hs.90207	hypothetical protein MGC11138	9.1
134859	D26488	Hs.90315	KIAA0007 protein	13.3
134971	AI097346	Hs.288049	phosphoserine aminotransferase	2
135181	BE250865	Hs.279529	px19-like protein	14.9
135207	N26427	Hs.9634	ESTs, Highly similar to C10_HUMAN PUTATI	1.7
135245	AI028787	Hs.262603	ESTs	12.2
135257	AW291023	Hs.97255	ESTs, Weakly similar to A46010 X-linked	7.6
135307	AI743770	Hs.98368	ESTs, Weakly similar to KIAA0822 protein	5.8
135321	AI652069	Hs.98614	ribosome binding protein 1 (dog 180kD ho	12.3
135354	AA456454	Hs.183416	cell division cycle 2-like 1 (PITSLRE pr	5.7
135400	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	13.9
302276	AW057736	Hs.323910	HER2 receptor tyrosine kinase (c	5.3
317781	NM_007057	Hs.42650	ZW10 interactor	2.8
321114	AA902256	Hs.78979	Golgi apparatus protein 1	5.5
322556	BE041451	Hs.177507	hypothetical protein	2.9
420802	U22376	Hs.1334	v-myb avian myeloblastosis viral oncogen	2.3
424001	W67883	Hs.137476	paternally expressed 10 (PEG10; KIAA105	7

428182	AF041259	Hs.165040	zinc finger protein 217	2.3
446999	AA151520	Hs.334822	hypothetical protein MGC4485	7.5
450701	H39960	Hs.288467	Homo sapiens cDNA FLJ12280 fis, clone MA	5.6
452461	N78223	Hs.108106	transcription factor	4.7
453157	AF077036	Hs.31989	DKFZP566G1722 protein	12.1

TABLE 5A

Table 5A shows the accession numbers for those pkeys lacking unigeneID's for Table 5. For each probeset, we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT number	Accessions
123615	30686_-15	AA609170
124385	656394_1	AI267847 N27351
110858	19346_14	AA992380 N33063 N21418 H79958 R21911 H79957
120472	44573_2	AI950087 N70208 R97040 N36809 AI308119 AW967677 N35320 AI251473 H59397 AW971573 R97278 W01059 AW967671 AA908598 AA251875 AI820501 AI820532 W87891 T85904 U71456 T82391 BE328571 T75102 R34725 AA884922 BE328517 AI219788 AA884444 N92578 F13493 AA927794 AI560251 AW874068 AL134043 AW235363 AA683345 AW008282 AA488964 AA283144 AI890387 AI950344 AI741346 AI689062 AA282915 AW102898 AI872193 AI763273 AW173586 AW150329 AI653832 AI762688 AA988777 AA488892 AI356394 AW103813 AI539642 AA642789 AA856975 AW505512 AI961530 AW629970 BE612881 AW276997 AW513601 AW512843 AA044209 AW856538 AA180009 AA337499 AW961101 AA251669 AA251874 AI819225 AW205862 AI683338 AI858509 AW276905 AI633006 AA972584 AA908741 AW072629 AW513996 AA293273 AA969759 N75628 N22388 H84729 H60052 T92487 AI022058 AA780419 AA551005 W80701 AW613456 AI373032 AI564269 F00531 H83488 W37181 W76802 R66056 AI002839 R67840 AA300207 AW959581 T63226 F04005
129019	44573_2	AI950087 N70208 R97040 N36809 AI308119 AW967677 N35320 AI251473 H59397 AW971573 R97278 W01059 AW967671 AA908598 AA251875 AI820501 AI820532 W87891 T85904 U71456 T82391 BE328571 T75102 R34725 AA884922 BE328517 AI219788 AA884444 N92578 F13493 AA927794 AI560251 AW874068 AL134043 AW235363 AA683345 AW008282 AA488964 AA283144 AI890387 AI950344 AI741346 AI689062 AA282915 AW102898 AI872193 AI763273 AW173586 AW150329 AI653832 AI762688 AA988777 AA488892 AI356394 AW103813 AI539642 AA642789 AA856975 AW505512 AI961530 AW629970 BE612881 AW276997 AW513601 AW512843 AA044209 AW856538 AA180009 AA337499 AW961101 AA251669 AA251874 AI819225 AW205862 AI683338 AI858509 AW276905 AI633006 AA972584 AA908741 AW072629 AW513996 AA293273 AA969759 N75628 N22388 H84729 H60052 T92487 AI022058 AA780419 AA551005 W80701 AW613456 AI373032 AI564269 F00531 H83488 W37181 W76802 R66056 AI002839 R67840 AA300207 AW959581 T63226 F04005
120695	9683_3	AA976503 AI917802 AA953664 AA404613 AA428771 BE280542 AW194691 AI927301 AI740458 AI796100 AI935603 AW052210 AA970201 AI533384 AA425910 AI017004 AI241295 AA402816 AA291468
122618	305217_1	AA453641 AA454081
125115	genbank_T97341	T97341
120809	genbank_AA346495	AA346495
129680	23162_1	U03749 NM_001275 J03483 J03915 AI214509 AW245744 AL046455 AA318960 AI741505 AA843875 AI829382 AI560122 AI858999 D55958 AI684005 D53170 AA854091 AI025609 D53119 D54729 D55504 D55377 D55313 AW512244 AA846441 AW043898 AI969102 AA405741 AI091983 AA788784 AA706586 AA854361 AW470949 AA843095 AA772028 AI148432 AI038109 AA782478 AA910064 AI220384 AA781298 AA843881 AA854084 AA843125 AA843419 AA319036 AA319054 AI273831 W32275 AI584185 C05724 AA789023 AI686818 D54392 AI022485 AA431410 AA854232 W39212 W15214 AA894441 AI803081 AI167381 AW245389 AA319430 AA335156 AI042646 AA327030 AA725170 T27943 AA889304 AA976699 AI687001 AI821107 AI865540 AA772107 C06286 AA319661 AA405992
101045	entrez_J05614	J05614
110501	genbank_H55748	H55748
121558	genbank_AA412497	AA412497
121911	genbank_AA427950	AA427950

TABLE 6: Figure 6 from BRCA 001 US

Table 6 shows genes upregulated in tumor tissue compared to normal breast tissue.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of tumor to normal breast tissue

Pkey	ExAccn	UnigeneID	UnigeneTitle	R1
100147	D13666	Hs.136348	osteoblast specific factor 2 (fasciclin	7.5
100678	AW502935	Hs.740	PTK2 protein tyrosine kinase 2	53.2
101806	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias	8.9
102455	U48705	Hs.75582	discoidin domain receptor family, member	6.9
103208	X72755	Hs.77367	monokine induced by gamma interferon	6.8
105743	BE246502	Hs.9598	sema domain, immunoglobulin domain (Ig),	2.6
105746	AW151952	Hs.46679	hypothetical protein FLJ20739	1.5
106373	AW503807	Hs.21907	histone acetyltransferase	1.8
110240	AI668594	Hs.176588	ESTs, Weakly similar to CP4Y_HUMAN CYTOC	4.2
119260	AK001724	Hs.102950	coat protein gamma-cop	3.2
120206	H26735	Hs.91668	Homo sapiens clone PP1498 unknown mRNA	45.7
120253	AA131376	Hs.326401	fibroblast growth factor 12B	38.9
120297	AA191384	Hs.104072	ESTs, Weakly similar to Z195_HUMAN ZINC	15.2
120624	AW407987	Hs.173518	M-phase phosphoprotein homolog	52
120695	AA976503		gb:oq30a04.s1 NCI_CGAP_GC4 Homo sapiens	46.8
120807	AA346385	Hs.30002	SH3-containing protein SH3GLB2; KIAA1848	6.8
121508	AA402515	Hs.97887	ESTs	28
122607	AA453518	Hs.98023	ESTs	61.5
122616	AA453638	Hs.161873	ESTs	107.3
122618	AA453641		gb:zx48e06.s1 Soares_testis_NHT Homo sap	31.1
122829	AW204530	Hs.99500	ESTs	61.8
122838	AA460584	Hs.334388	ESTs	75.3
123753	AA609955	Hs.234961	Huntingtin interacting protein E	30.6
124385	AI267847		gb:aq49a10.x1 Stanley Frontal NB pool 2	57.1
124860	R65763	Hs.101477	EST	23.9
124930	AI076343	Hs.173939	ESTs, Weakly similar to ALUB_HUMAN !!!!	22.8
125051	T79956	Hs.100588	EST	135.3
128781	N71826	Hs.105465	small nuclear ribonucleoprotein polypept	53.9
129096	AA463189	Hs.288906	WW Domain-Containing Gene	20.9
129347	BE614192	Hs.278869	melanoma-associated antigen recognised b	7.6
129689	AW748482	Hs.77873	B7 homolog 3	2.6
130503	BE208491	Hs.295112	KIAA0618 gene product	16.1
130511	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	6.1
131046	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	7.4
131643	AW410501	Hs.30026	HSPC182 protein	2.9
131925	AF151046	Hs.183180	anaphase promoting complex subunit 11 (y	2.7
132180	NM_004460	Hs.418	fibroblast activation protein, alpha	14.7
132370	AW572805	Hs.46845	ESTs	28.3
132994	AA112748	Hs.279905	clone HQ0310 PRO0310p1	17.1
133016	AI439688	Hs.8289	hypothetical protein FLJ20886	4.4
133266	AI160873	Hs.69233	zinc finger protein	16.1
133391	AW103364	Hs.727	inhibin, beta A (activin A, activin AB a	25.5
134169	AI690916	Hs.178137	transducer of ERBB2, 1	1.2
134219	NM_000402	Hs.80208	glucose-6-phosphate dehydrogenase	1.9
134405	AW067903	Hs.82772	collagen, type XI, alpha 1	72.9
134529	AW411479	Hs.848	FKS06-binding protein 4 (59kD)	2.8
134975	R50333	Hs.92186	Leman coiled-coil protein	2.8
135181	BE250865	Hs.279529	px19-like protein	14.9
322556	BE041451	Hs.177507	hypothetical protein	2.9

TABLE 6A

Table 6A shows the accession numbers for those pkeys lacking unigeneID's for Table 6. For each probeset, we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT number	Accessions
124385	656394_1	AI267847 N27351
120695	9683_3	AA976503 AI917802 AA953684 AA404613 AA428771 BE280542 AW194691 AI927301 AI740458 AI796100 AI935603 AW052210 AA970201 AI633384 AA425910 AI017004 AI241295 AA402816 AA291468
122618	305217_1	AA453841 AA454061

TABLE 7: Figure 7 from BRCA 001-1 US

Table 7 shows genes upregulated in tumor tissue compared to normal breast tissue. Open reading frames in the sequences have been characterized as having a signal sequence (SS), a transmembrane domain (TM) or other.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of tumor to normal breast tissue
ORF struct info: Structural characterization of open reading frame for the sequence of the gene

Pkey	ExAccn	UnigeneID	UnigeneTitle	R1	ORF struct info
100113	NM_001269	Hs.84748	chromosome condensation 1	2.3	TM
100114	X02308	Hs.82962	thymidylate synthetase	2.9	other
100131	D12485	Hs.11951	ectonucleotide pyrophosphatase/phosphodi	1.9	other
100146	BE185499	Hs.2471	KIAA0020 gene product	1.9	TM
100147	D13666	Hs.136348	osteoblast specific factor 2 (fasciclin	7.6	other
100154	H60720	Hs.81892	KIAA0101 gene product	9.2	other
100163	W44671	Hs.124	gene predicted from cDNA with a complete	1.6	other
100220	AW015534	Hs.217493	annexin A2	2	other
100265	D38521	Hs.112396	KIAA0077 protein	1.5	other
100271	BE160081	Hs.256290	S100 calcium-binding protein A11 (calgiz	13.5	other
100275	BE242802	Hs.154797	KIAA0090 protein	5.1	other
100323	D50920	Hs.23106	KIAA0130 gene product	1.9	TM
100335	AW247529	Hs.6793	platelet-activating factor acetylhydrola	2.7	other
100364	NM_004341	Hs.154868	carbamoyl-phosphate synthetase 2, aspart	2	other
100372	NM_014781	Hs.184339	KIAA0175 gene product	2.6	other
100393	D84145	Hs.39913	novel RGD-containing protein	3.2	other
100400	AW954324	Hs.75790	phosphatidylinositol glycan, class C	1.5	other
100418	D86978	Hs.84790	KIAA0225 protein	2	other
100482	M65028	Hs.81361	heterogeneous nuclear ribonucleoprotein	2.9	other
100518	NM_004415	Hs.74316	desmoplakin (DPI, DPII)	1.9	other
100666	L05424	Hs.169610	CD44 antigen (homing function and Indian	5.7	other
100667	L05424	Hs.169610	CD44 antigen (homing function and Indian	9	?
100668	L05424	Hs.169610	CD44 antigen (homing function and Indian	7.7	other
100678	AW502935	Hs.740	PTK2 protein tyrosine kinase 2	53.2	other
100783	AF078847	Hs.191356	general transcription factor IIH, polype	6	other
100892	BE245294	Hs.180789	S164 protein	1.7	?
100945	AF002225	Hs.180688	ubiquitin protein ligase E3A (human papi	1.5	other
100969	AA157634	Hs.79172	solute carrier family 25 (mitochondrial	6.3	other
100988	AK000405	Hs.76480	ubiquitin-like 4	11.4	?
100999	H38765	Hs.80706	diaphorase (NADH/NADPH) (cytochrome b-5	1.8	other
101031	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	8.4	other
101045	J05614		gb:Human proliferating cell nuclear anti	5	?
101077	N99692	Hs.75227	Empirically selected from AFFX single pr	2.6	other
101093	L06419	Hs.75093	procollagen-lysine, 2-oxoglutarate 5-dio	1.4	?
101186	AA020956	Hs.179881	core-binding factor, beta subunit	2	TM
101216	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	1.8	other
101228	AA333387	Hs.82916	chaperonin containing TCP1, subunit 6A (	1.7	TM
101247	AA132666	Hs.78802	glycogen synthase kinase 3 beta	1.9	other
101249	L18964	Hs.1904	protein kinase C, iota	1.5	other
101332	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	5.3	other
101352	AI494299	Hs.16297	COX17 (yeast) homolog, cytochrome c oxid	4.2	other
101396	BE267931	Hs.78996	proliferating cell nuclear antigen	1.9	TM
101445	M21259		gb:Human Alu repeats in the region 5' to	1.8	TM
101470	NM_000546	Hs.1846	tumor protein p53 (Li-Fraumeni syndrome)	2.5	other
101478	NM_002890	Hs.758	RAS p21 protein activator (GTPase activa	5.5	other

101483	M24486	Hs.76768	procollagen-proline, 2-oxoglutarate 4-di	2.1	other
101540	J04977	Hs.84981	X-ray repair complementing defective rep	1.6	other
101573	AW248421	Hs.250758	proteasome (prosome, macropain) 26S subu	5.7	other
101580	NM_012151	Hs.83363	coagulation factor VIII-associated (intr	1.8	other
101592	AF064853	Hs.91299	guanine nucleotide binding protein (G pr	5.6	?
101621	BE391804	Hs.62661	guanylate binding protein 1, interferon-	2.4	other
101702	AW504089	Hs.179574	protein phosphatase 2 (formerly 2A), reg	1.3	other
101734	M74099	Hs.147049	cut (Drosophila)-like 1 (CCAAT displacem	2.1	?
101759	M80244	Hs.184601	solute carrier family 7 (cationic amino	5	TM
101767	M81057	Hs.180884	carboxypeptidase B1 (tissue)	14.4	SS,
101782	AA306495	Hs.1869	phosphoglucomutase 1	5.2	other
101805	AW409747	Hs.75612	stress-induced-phosphoprotein 1 (Hsp70/H	8.6	other
101806	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias	8.9	SS,TM
101810	NM_000318	Hs.180612	peroxisomal membrane protein 3 (35kD, Ze	3.2	TM
101879	AA176374	Hs.243886	nuclear autoantigenic sperm protein (his	1.8	other
101911	AA441787	Hs.119689	glycoprotein hormones, alpha polypeptide	31.3	?
101920	AF162645	Hs.8024	IK cytokine, down-regulator of HLA II	1.8	other
101973	U41514	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp	2.4	other
102009	BE245149	Hs.82643	protein tyrosine kinase 9	1.3	other
102036	BE250127	Hs.82906	CDC20 (cell division cycle 20, S. cerevi	2	?
102083	T35901	Hs.75117	interleukin enhancer binding factor 2, 4	1.6	other
102107	BE258602	Hs.182368	heat shock protein 75	1.4	other
102123	NM_001809	Hs.1594	centromere protein A (17kD)	1.8	other
102165	BE313280	Hs.159627	death associated protein 3	4.6	?
102198	AW950852	Hs.74598	polymerase (DNA directed), delta 2, regu	4.4	?
102217	AA829978	Hs.301613	JTV1 gene	6.7	other
102220	U24389	Hs.65436	lysosomal	4.4	TM
102234	AW163390	Hs.278554	heterochromatin-like protein 1	1.9	TM
102260	AL039104	Hs.159557	karyopherin alpha 2 (RAG cohort 1, impor	4.4	other
102302	AA306342	Hs.69171	protein kinase C-like 2	2.7	?
102330	BE298083	Hs.77254	chromobox homolog 1 (Drosophila HP1 beta	1.5	other
102339	BE378432	Hs.95577	cyclin-dependent kinase 4	2.3	TM
102348	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	2	TM
102349	AU077055	Hs.289107	baculoviral IAP repeat-containing 2	3.2	other
102369	U39840	Hs.299867	hepatocyte nuclear factor 3, alpha	2	other
102374	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	6.2	other
102391	AA296874	Hs.77494	deoxyguanosine kinase	1.5	TM
102455	U48705	Hs.75562	discoidin domain receptor family, member	7	other
102465	NM_001359	Hs.81548	2,4-dienoyl CoA reductase 1, mitochondri	1.8	SS,
102488	U50939	Hs.61828	amyloid beta precursor protein-binding p	1.5	?
102489	AL080116	Hs.74420	origin recognition complex, subunit 3 (y	3.3	other
102494	AI188137	Hs.75193	COP9 homolog	2.1	other
102501	AF217197	Hs.74562	sish binding protein 1; FBP interacting	3.2	other
102522	BE250944	Hs.183556	solute carrier family 1 (neutral amino a	2.8	?
102532	AF040253	Hs.70186	suppressor of Ty (S.cerevisiae) 5 homolo	5.7	?
102564	U59423	Hs.79067	MAD (mothers against decapentaplegic, Dr	2.3	other
102568	W81489	Hs.223025	RAB31, member RAS oncogene family	5.3	other
102580	U60808	Hs.152981	CDP-diacylglycerol synthase (phosphatida	2.1	other
102581	AU077226	Hs.77256	enhancer of zeste (Drosophila) homolog 2	1.6	?
102582	U61232	Hs.32675	tubulin-specific chaperone e	2.1	other
102617	AW161453	Hs.198767	COP9 (constitutive photomorphogenic, Ara	1.8	other
102618	AL037672	Hs.81071	extracellular matrix protein 1	5.8	other
102627	AL021918	Hs.158174	zinc finger protein 184 (Kruppel-like)	1.3	other
102663	NM_002270	Hs.168075	karyopherin (importin) beta 2	1.8	TM
102676	BE262989	Hs.12045	putative protein	2.3	other
102687	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	4.4	?
102689	U96132	Hs.171280	hydroxyacyl-Coenzyme A dehydrogenase, ty	6	?
102696	BE540274	Hs.239	forkhead box M1	4.2	other
102704	AU077058	Hs.54089	BRCA1 associated RING domain 1	1.9	other
102705	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	2.3	SS,TM
102750	AB014460	Hs.66196	nth (E.coli endonuclease III)-like 1	1.2	TM
102801	BE252241	Hs.38041	pyridoxal (pyridoxine, vitamin B6) kinas	6.5	other
102812	U90549	Hs.236774	high-mobility group (nonhistone chromoso	1.8	other
102827	BE244588	Hs.6456	chaperonin containing TCP1, subunit 2 (b	5.6	TM
102844	AV653790	Hs.324275	WW domain-containing protein 1	1.3	TM
102868	X02419	Hs.77274	plasminogen activator, urokinase	4.4	other
102925	BE440142	Hs.2943	signal recognition particle 19kD	1.9	other

102935	BE561850	Hs.80506	small nuclear ribonucleoprotein polypept	2.4	?
102968	AU076611	Hs.154872	methylene tetrahydrofolate dehydrogenase	2.7	other
102983	BE387202	Hs.118638	non-metastatic cells 1, protein (NM23A)	3.1	other
102985	U85742	Hs.2707	G1 to S phase transition 1	5.2	?
103023	AW500470	Hs.117850	multifunctional polypeptide similar to S	1.6	other
103038	AA926960	Hs.334883	CDC28 protein kinase 1	2.5	TM
103060	NM_005940	Hs.155324	matrix metalloproteinase 11 (MMP11; stro	4.5	other
103080	AU077231	Hs.82932	cyclin D1 (PRAD1: parathyroid adenomatos	3.1	other
103089	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	2.4	other
103177	BE244377	Hs.46876	farnesyl-diphosphate farnesyltransferase	3.5	other
103178	AA205475	Hs.275865	ribosomal protein S18	9.9	?
103179	NM_001777	Hs.82685	CD47 antigen (Rh-related antigen, integr	1.3	other
103181	X69636	Hs.334731	Homo sapiens, clone IMAGE:3446306, mRNA,	2	other
103185	NM_006825	Hs.74366	transmembrane protein (63kD), endoplasmi	1.6	other
103191	AA401039	Hs.2903	protein phosphatase 4 (formerly X), cata	2.5	other
103193	NM_004766	Hs.75724	coatomer protein complex, subunit beta 2	2.2	TM
103194	NM_004939	Hs.78580	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	6.3	TM
103206	X72755	Hs.77367	monokine induced by gamma interferon	8.8	TM
103223	BE275607	Hs.1708	chaperonin containing TCP1, subunit 3 (g	3	other
103232	X75962	Hs.129780	tumor necrosis factor receptor superfami	1.8	other
103238	AI369285	Hs.75189	death-associated protein	5.6	TM
103297	NM_001545	Hs.9078	immature colon carcinoma transcript 1	1.9	?
103330	AI803447	Hs.77496	small nuclear ribonucleoprotein polypept	2.5	other
103349	X89059		gb:H.sapiens mRNA for unknown protein ex	1.6	other
103376	AL036166	Hs.323378	coated vesicle membrane protein	1.8	other
103391	X94453	Hs.114366	pyrroline-5-carboxylate synthetase (glut	2.3	other
103392	X94563		gb:H.sapiens dbVacbp gene exon 1 & 2.	4	TM
103430	BE564090	Hs.20716	translocase of inner mitochondrial membr	1.3	other
103491	AF264750	Hs.288971	myeloid/lymphoid or mixed-lineage leukem	5.7	?
103505	AL031224	Hs.33102	transcription factor AP-2 beta (activati	5.1	other
103547	AI376722	Hs.180062	proteasome (prosome, macropain) subunit,	9.7	?
103588	NM_006218	Hs.85701	phosphoinositide-3-kinase, catalytic, al	2	other
103613	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (ca	1.3	?
103621	BE379766	Hs.150675	polymerase (RNA) II (DNA directed) polyp	2	other
103622	AA609685	Hs.278672	membrane component, chromosome 11, surfa	2.3	TM
103727	AI878883	Hs.296381	growth factor receptor-bound protein 2	1.3	other
103754	AI015709	Hs.172089	Homo sapiens mRNA; cDNA DKFZp586I2022 (f	1.3	other
103780	AA094752	Hs.169992	hypothetical 43.2 Kd protein	7.6	?
103795	H26531	Hs.7367	Homo sapiens BTB domain protein (BDPL) m	1.3	SS,TM
103797	AA080912		gb:zn04d03.r1 Stratagene hNT neuron (937	1.6	other
103813	AI042582	Hs.181271	CGI-120 protein	1.6	other
103855	W02383	Hs.302267	hypothetical protein FLJ10330	1.6	other
103886	AK001278	Hs.105737	hypothetical protein FLJ10416 similar to	6.6	TM
104052	NM_002407	Hs.97644	mammaglobin 2	2.9	other
104079	AA251242	Hs.103238	ESTs	1.4	other
104174	AA478984	Hs.6451	PRO0659 protein	5.6	TM
104227	AB002343	Hs.98938	protocadherin alpha 9	1.6	other
104275	AI751970	Hs.101067	GCN5 (general control of amino-acid synt	5.4	other
104325	BE379766	Hs.150675	polymerase (RNA) II (DNA directed) polyp	6.4	other
104370	AA324597	Hs.21851	Homo sapiens cDNA FLJ12900 fis, clone NT	1.6	other
104423	R83113	Hs.1432	protein kinase C substrate 80K-H	5.2	other
104482	AB037762	Hs.44268	myotin gene expression factor 2	1.2	other
104667	AI239923	Hs.30098	ESTs	1.4	other
104757	AI694413	Hs.332649	olfactory receptor, family 2, subfamily	2.4	other
104804	AI858702	Hs.31803	ESTs, Weakly similar to N-WASP [H.sapien	1.4	other
104806	AB023175	Hs.22982	KIAA0958 protein	2.4	other
104827	AW052006	Hs.8551	PRP4/STK/WD splicing factor	10.9	other
104846	AI250789	Hs.32478	ESTs	5.7	other
104854	AA041276	Hs.154729	3-phosphoinositide dependent protein kin	12.3	?
104867	AA278898	Hs.225979	hypothetical protein similar to small G	2.1	other
104871	T78044	Hs.28893	Homo sapiens mRNA; cDNA DKFZp564O2364 (f	1.4	other
104896	AW015318	Hs.23165	ESTs	17.7	other
104909	AW408164	Hs.249184	transcription factor 19 (SC1)	5.1	TM
104916	AW958157	Hs.155489	NS1-associated protein 1	1.8	other
104919	AA026880	Hs.28252	prolactin receptor	1.5	other
104930	AF043467	Hs.32893	neurexophilin 2	2.3	other
104973	NM_015310	Hs.6763	KIAA0942 protein	5.1	other

	104974	Y12059	Hs.278675	bromodomain-containing 4	1.5	other
	104975	AL135877	Hs.50758	SMC4 (structural maintenance of chromoso	2.4	other
	104978	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	7.3	other
	104979	AA937934	Hs.321082	ESTs	1.3	other
5	104994	AI499930	Hs.334885	mitochondrial GTP binding protein	3.6	?
	105009	BE379584	Hs.34789	dolichyl-diphosphooligosaccharide-protei	5.6	other
	105012	AF098158	Hs.9329	chromosome 20 open reading frame 1	3.4	other
	105028	AI050715	Hs.2331	E2F transcription factor 5, p130-binding	2.2	other
	105041	AB037716	Hs.26204	KIAA1295 protein	2.2	other
10	105045	BE242899	Hs.129951	speckle-type POZ protein	3.9	?
	105079	AA151342	Hs.12677	CGI-147 protein	9.5	TM
	105087	AA147884	Hs.9812	Homo sapiens cDNA FLJ14388 fis, clone HE	5.7	other
	105088	H58589	Hs.35156	Homo sapiens cDNA FLJ11027 fis, clone PL	2.2	other
	105095	Z78407	Hs.27023	vesicle transport-related protein	2.2	other
15	105110	BE387350	Hs.33122	KIAA1160 protein	1.6	other
	105126	AW975433	Hs.36288	ESTs	6.4	?
	105127	AA045848	Hs.301957	nudix (nucleoside diphosphate linked mol	2.2	other
	105141	AA164687	Hs.177576	mannosyl (alpha-1,3-)-glycoprotein beta-	2.8	other
	105158	AW976357	Hs.234545	hypothetical protein NUF2R	2	other
20	105169	BE245294	Hs.180789	S164 protein	1.7	other
	105188	AA191512	Hs.28005	Homo sapiens cDNA FLJ11309 fis, clone PL	4.9	SS,TM
	105254	AA071276	Hs.19469	KIAA0859 protein	2	TM
	105281	AA263143	Hs.24596	RAD51-interacting protein	2.9	?
	105288	N99673	Hs.3585	ESTs, Weakly similar to AF126743 1 DNAJ	1.9	TM
25	105302	AA700122	Hs.3355	sentrin-specific protease	8.2	?
	105331	AW270037	Hs.179507	KIAA0779 protein	1.8	SS,
	105359	NM_016015	Hs.8054	CGI-68 protein	8.4	other
	105366	BE264645	Hs.282093	hypothetical protein FLJ21918	5.1	other
	105373	AW887701	Hs.32356	hypothetical protein FLJ20628	2.6	other
30	105374	BE242803	Hs.262823	hypothetical protein FLJ10326	2.2	TM
	105387	AW592146	Hs.108636	membrane protein CH1	2.3	SS,TM
	105393	AF157570	Hs.256583	interleukin enhancer binding factor 3, 9	5.5	SS,
	105399	BE386877	Hs.334811	Npw38-binding protein NpwBP	1.6	other
	105400	AF198620	Hs.65648	RNA binding motif protein 8A	1.6	other
35	105445	AA252395		gb:zs12g10.s1 NCI_CGAP_GCB1 Homo sapiens	5.1	?
	105507	BE268348	Hs.226318	CCR4-NOT transcription complex, subunit	1.6	other
	105529	AA113449	Hs.32471	hypothetical protein FLJ20364	1.3	other
	105530	AB023179	Hs.9059	KIAA0962 protein	3.5	other
	105547	AA262640	Hs.27445	unknown	9.3	other
40	105564	BE616694	Hs.268042	hypothetical protein FLJ14299	1.4	other
	105598	AA579535	Hs.18490	hypothetical protein FLJ20452	10.9	TM
	105597	AF054284	Hs.334826	splicing factor 3b, subunit 1, 155kD	2.9	TM
	105608	AI808201	Hs.287863	hypothetical protein FLJ12475	1.7	?
	105610	AA280072	Hs.99872	fetal Alzheimer antigen	1.4	other
45	105617	AK000892	Hs.4089	glucocorticoid modulatory element bindin	1.7	TM
	105620	AW302245	Hs.181390	casein kinase 1, gamma 2	5.6	other
	105658	AA985190	Hs.246875	hypothetical protein FLJ20059	9.4	other
	105697	AW499988	Hs.27801	zinc finger protein 278	2	TM
	105708	R26944	Hs.180777	Homo sapiens mRNA; cDNA DKFZp564M0264 (f	1.7	other
50	105743	BE246502	Hs.9598	sema domain, immunoglobulin domain (Ig),	2.7	other
	105746	AW151952	Hs.46879	hypothetical protein FLJ20739	1.5	?
	105759	AI123118	Hs.15159	chemokine-like factor, alternatively spl	1.3	other
	105771	AI267720	Hs.153221	synovial sarcoma, translocated to X chro	1.6	other
	105820	AA741336	Hs.152108	transcriptional unit N143	2.2	other
55	105828	AA478756	Hs.194477	E3 ubiquitin ligase SMURF2	1.3	other
	105856	AI262106	Hs.12653	ESTs	2.4	other
	105858	AF151066	Hs.281428	hypothetical protein	2.9	other
	105875	AK001708	Hs.32271	hypothetical protein FLJ10846	1.4	other
	105930	AF016371	Hs.9880	peptidyl prolyl isomerase H (cyclophilin	5.3	other
60	106000	AW194426	Hs.20726	ESTs	1.7	other
	106011	AW081202	Hs.12284	Homo sapiens, clone IMAGE:2989556, mRNA,	2.8	other
	106017	AA477956	Hs.26268	ESTs	1.4	other
	106073	AL157441	Hs.17834	downstream neighbor of SON	1.4	other
	106078	AA130158	Hs.19977	ESTs, Moderately similar to ALU8_HUMAN A	1.6	?
65	106094	AA533491	Hs.23317	hypothetical protein FLJ14681	6.9	other
	106140	AB006624	Hs.14912	KIAA0286 protein	1.6	other
	106271	AA251393	Hs.289052	Homo sapiens, Similar to RIKEN cDNA 5430	10.8	?

	106288	AB037742	Hs.24338	KIAA1321 protein	1.3	other
	106300	Y10043	Hs.19114	high-mobility group (nonhistone chromoso	3.7	other
	106333	AL043114	Hs.22410	ESTs, Weakly similar to A54849 collagen	5.5	SS,
	106350	AK001404	Hs.194698	cyclin B2	5.8	other
5	106359	AW390282	Hs.31130	transmembrane 7 superfamily member 2	6.4	other
	106381	AB040916	Hs.24106	KIAA1483 protein	6.8	other
	106389	AW748420	Hs.6236	Homo sapiens cDNA: FLJ21487 fis, clone C	2.2	TM
	106457	AF119256	Hs.27801	zinc finger protein 278	2.7	other
	106470	D63078	Hs.186180	Homo sapiens cDNA: FLJ23038 fis, clone L	2.3	other
10	106586	AA243837	Hs.57787	ESTs	1.8	other
	106589	AK000933	Hs.28661	Homo sapiens cDNA FLJ10071 fis, clone HE	2.4	?
	106610	AA458882	Hs.79732	fibulin 1	6	SS,
	106624	NM_003595	Hs.26350	tyrosylprotein sulfotransferase 2	7.8	other
	106650	AL049951	Hs.22370	Homo sapiens mRNA; cDNA DKFZp564O0122 (f	1.8	other
15	106669	AV657117	Hs.184184	ESTs, Moderately similar to SG5657 alpha	1.3	TM
	106713	BE614802	Hs.184352	hypothetical protein FLJ12549	4.6	other
	106717	AA600357	Hs.239489	TIA1 cytotoxic granule-associated RNA-bi	1.3	other
	106723	BE388094	Hs.21857	ESTs	1.8	SS,
	106795	AF174487	Hs.293753	Bcl-2-related ovarian killer protein-lik	5.7	other
20	106829	AW959893	Hs.27099	hypothetical protein FLJ23293 similar to	16.2	TM
	106831	BE564871	Hs.29463	centrin, EF-hand protein, 3 (CDC31 yeast	1.5	other
	106848	AB037744	Hs.34892	KIAA1323 protein	2.2	other
	106852	AF151031	Hs.300631	hypothetical protein	1.3	other
	106873	N49809	Hs.11197	Homo sapiens, clone IMAGE:3343149, mRNA,	16.8	other
25	106886	W79171	Hs.9567	GL002 protein	1.5	TM
	106906	AA861271	Hs.222024	transcription factor BMAL2	2.2	other
	106920	AK001838	Hs.296323	serum/glucocorticoid regulated kinase	3.4	other
	106945	AK000511	Hs.6294	hypothetical protein DKFZp434L1435 simil	6.8	?
	106973	BE156256	Hs.11923	hypothetical protein	6.7	other
30	106978	AW631480	Hs.8688	ESTs	6.1	SS,
	107004	AA146872	Hs.300700	hypothetical protein FLJ20727	1.3	other
	107029	AF264750	Hs.268971	myeloid/lymphoid or mixed-lineage leukem	1.8	other
	107071	AW385224	Hs.35198	ectonucleotide pyrophosphatase/phosphodi	1.7	other
	107113	AK000733	Hs.23900	GTPase activating protein	2.5	other
35	107125	AK000512	Hs.69388	hypothetical protein FLJ20505	1.7	other
	107136	AV661958	Hs.8207	GK001 protein	4.7	other
	107146	AK001455	Hs.5198	Down syndrome critical region gene 2	2	other
	107151	AW378065	Hs.8687	ESTs	6.4	TM
	107155	AW391927	Hs.7948	KIAA1268 protein	33.5	other
40	107174	BE122762	Hs.25338	ESTs	5.2	?
	107197	W15477	Hs.84639	glioma pathogenesis-related protein	6.1	other
	107221	AW888411	Hs.81915	leukemia-associated phosphoprotein p18 (	17.4	other
	107243	BE219716	Hs.34727	ESTs, Moderately similar to I38759 zinc	7.4	?
	107248	AW263124	Hs.315111	nuclear receptor co-repressor/HDAC3 comp	1.8	other
45	107263	D60341	Hs.21198	translocase of outer mitochondrial membr	6.7	other
	107265	BE379594	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN A	2.5	other
	107299	BE277457	Hs.30681	hypothetical protein MGC4606	3.2	TM
	107316	T63174	Hs.193700	Homo sapiens mRNA; cDNA DKFZp566I0324 (f	2	TM
	107354	NM_006299	Hs.96448	zinc finger protein 193	5	?
50	107392	AW299900	Hs.267632	TATA element modulatory factor 1	1.2	other
	107481	AA307703	Hs.279766	kinesin family member 4A	1.6	other
	107529	BE515065	Hs.296585	nucleolar protein (KKE/D repeat)	3	TM
	107554	AA001386	Hs.59844	ESTs	1.4	other
	107681	BE379594	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN A	2.3	SS,TM
55	107772	AA018587	Hs.303055	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.2	?
	107859	AW732573	Hs.47584	potassium voltage-gated channel, delayed	8.4	TM
	107901	L42612	Hs.335952	keratin 6B	2.5	other
	107922	BE153855	Hs.61460	Ig superfamily receptor LNIR	2.3	other
	107974	AW956103	Hs.61712	pyruvate dehydrogenase kinase, isoenzyme	6.8	other
60	108040	AL121031	Hs.159971	SWI/SNF related, matrix associated, acti	1.8	other
	108230	AA054224	Hs.59847	ESTs	1.3	other
	108274	AF129535	Hs.272027	F-box only protein 5	7.2	?
	108298	N31256	Hs.161623	ESTs	2.6	other
	108496	AA083069	Hs.339659	ESTs	3.6	other
65	108607	BE300380	Hs.69476	Homo sapiens cDNA FLJ12758 fis, clone NT	3.5	other
	108621	AA101809	Hs.182685	ESTs	1.7	other
	108634	AW022410	Hs.69507	ESTs	1.8	SS,TM

108647	BE546947	Hs.44276	homeo box C10	9.8	other
108695	AB029000	Hs.70823	KIAA1077 protein	7.3	other
108740	AI089575	Hs.9071	progesterone membrane binding protein	2.8	?
108828	AK001693	Hs.273344	DKFZP564O0463 protein	1.9	other
108859	AL121500	Hs.178904	ESTs	1.8	TM
108872	H06720	Hs.111680	endosulfine alpha	2.2	other
108891	AI801235	Hs.48480	ESTs	5.4	other
108894	AK001431	Hs.5105	hypothetical protein FLJ10569	4.1	TM
108955	AA149754	Hs.195155	Homo sapiens amino acid transport system	5.7	?
108982	AA151708	Hs.171980	homeo box (expressed in ES cells) 1	1.7	other
108987	AA152178	Hs.23467	hypothetical protein FLJ10633	6.3	other
109002	AB028987	Hs.72134	KIAA1064 protein	1.7	other
109011	AA156542	Hs.72127	ESTs	1.5	other
109026	AA157811		gb:zo35d07.s1 Stratagene colon (937204)	5.4	other
109068	AA164293	Hs.72545	ESTs	3	other
109101	AW608930	Hs.52184	hypothetical protein FLJ20618	1.8	SS,
109112	AW419186	Hs.257924	hypothetical protein FLJ13782	3.3	TM
109124	AK000684	Hs.183887	hypothetical protein FLJ22104	1.7	other
109139	AJ132592	Hs.59757	zinc finger protein 281	2.7	other
109168	AA219691	Hs.73825	RAB6 interacting, kinesin-like (rabkines	3	TM
109198	BE568742	Hs.58169	highly expressed in cancer, rich in leuc	2.1	other
109213	NM_016603	Hs.82035	potential nuclear protein C5ORF5; GAP-li	5.4	other
109220	AW958181	Hs.189998	ESTs	5.8	other
109233	AU077281	Hs.170285	nucleoporin 214kD (CAIN)	5.3	other
109270	N99673	Hs.3585	ESTs, Weakly similar to AF126743 1 DNAJ	1.4	other
109273	AA375752	Hs.82719	Homo sapiens mRNA; cDNA DKFZp586F1822 (f	3	other
109313	AF153201	Hs.86276	C2H2 (Kruppel-type) zinc finger protein	1.3	other
109341	AA213506	Hs.115099	EST	3	?
109391	AL096858	Hs.184245	KIAA0929 protein Msx2 interacting nucleo	1.5	other
109420	H83603	Hs.40408	homeo box C9	2.2	SS,
109426	N30531	Hs.42215	protein phosphatase 1, regulatory subuni	3.1	TM
109429	AI160029	Hs.61438	ESTs	2	?
109445	AA232103	Hs.189915	ESTs	1.8	other
109450	AB032989	Hs.173042	KIAA1143 protein	3.8	other
109468	NM_015310	Hs.6763	KIAA0942 protein	3.3	other
109478	AW074143	Hs.87134	ESTs	2	TM
109570	L40027	Hs.118890	glycogen synthase kinase 3 alpha	2.1	other
109582	F02614	Hs.27319	ESTs	1.4	other
109825	R71264	Hs.16798	ESTs	1.3	other
110039	H11938	Hs.21907	histone acetyltransferase	2	other
110056	AA503041	Hs.279009	matrix Gla protein	2.5	other
110085	AA603840	Hs.29956	KIAA0460 protein	1.7	other
110110	T07353	Hs.7948	ESTs	2.9	other
110129	R51853	Hs.226429	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.7	SS,
110154	NM_014521	Hs.17687	SH3-domain binding protein 4	4.3	other
110240	AI668594	Hs.176588	ESTs, Weakly similar to CP4Y_HUMAN CYTOC	4.3	?
110242	N41744	Hs.19978	CGI-30 protein	1.3	other
110259	H28428	Hs.32406	ESTs, Weakly similar to I38022 hypothet	2.2	other
110312	BE256986	Hs.11896	hypothetical protein FLJ12089	2.1	other
110501	H55748		gb:yq94a01.s1 Soares fetal liver spleen	6.1	?
110504	H55915	Hs.210859	hypothetical protein FLJ11016	6.1	TM
110525	H57330	Hs.37430	EST	6.4	other
110568	AK001160	Hs.5999	hypothetical protein FLJ10298	1.3	?
110699	T97586	Hs.18090	ESTs	1.8	other
110705	AB007902	Hs.32168	KIAA0442 protein	1.6	TM
110742	AW190338	Hs.28029	hypothetical protein MGC11256	7.8	other
110761	AL138077	Hs.16157	hypothetical protein FLJ12707	2.5	other
110762	BE044245	Hs.30011	hypothetical protein MGC2963	9.3	?
110765	AK000322	Hs.18457	hypothetical protein FLJ20315	5.5	SS,
110769	BE000831	Hs.23837	Homo sapiens cDNA FLJ11812 fis, clone HE	2.1	TM
110799	AI089660	Hs.323401	dpy-30-like protein	1.5	TM
110805	T25829	Hs.24048	FK506 binding protein precursor	6.7	TM
110813	AA767373	Hs.35669	ESTs, Moderately similar to ALU1_HUMAN A	5.7	other
110820	R33261	Hs.6614	ESTs, Weakly similar to A43932 mucin 2 p	3.4	other
110840	N31598	Hs.12727	hypothetical protein FLJ21610	1.7	TM
110844	AI740792	Hs.167531	methylcrotonoyl-Coenzyme A carboxylase 2	1.7	other
110854	BE612992	Hs.27931	hypothetical protein FLJ10607 similar to	4.7	other

110856	AA992380		gb:ol37g06.s1 Soares_testis_NHT Homo sap	2.3	other
110885	BE384447	Hs.16034	hypothetical protein MGC13186	3.6	?
110897	AL117430	Hs.6880	DKFZP434D156 protein	2.2	?
110915	BE092285	Hs.29724	hypothetical protein FLJ13187	2.6	SS,
110918	H04360	Hs.24283	ESTs, Moderately similar to reduced expr	1.9	TM
110958	NM_005864	Hs.24587	signal transduction protein (SH3 contain	6.7	other
110963	AK002180	Hs.11449	DKFZP564O123 protein	2	other
110981	AK001980	Hs.24284	ADP-ribosyltransferase (NAD+, poly(ADP-r	1.3	other
110984	AW613287	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp	1.8	?
111125	N63823	Hs.269115	ESTs, Moderately similar to Z195_HUMAN Z	3.7	other
111132	AB037807	Hs.83293	hypothetical protein	2.1	TM
111164	N46180	Hs.122489	Homo sapiens cDNA FLJ13289 fis, clone OV	2.3	other
111172	R67419	Hs.21851	Homo sapiens cDNA FLJ12900 fis, clone NT	3.7	other
111174	AL050168	Hs.26295	Homo sapiens mRNA; cDNA DKFZp586D1122 (f	7.5	other
111179	AK000136	Hs.10760	asporin (LRR class 1)	7.1	other
111184	AI815488	Hs.243901	Homo sapiens cDNA FLJ20738 fis, clone HE	6.8	other
111189	N67603	Hs.272130	ESTs, Weakly similar to S65824 reverse t	3.8	SS,
111216	AW139408	Hs.152940	ESTs	1.5	other
111221	AB037782	Hs.15119	KIAA1381 protein	2.6	other
111223	AA852773	Hs.334838	KIAA1866 protein	4.7	other
111239	N90956	Hs.17230	hypothetical protein FLJ22087	7.9	?
111285	AA778711	Hs.4310	eukaryotic translation initiation factor	7	other
111299	AB033091	Hs.74313	KIAA1265 protein	5	other
111312	AI523913	Hs.34504	ESTs	3.8	other
111318	T99755	Hs.334726	ESTs	1.2	TM
111337	AA837396	Hs.263925	LIS1-interacting protein NUDE1, rat homo	5.1	other
111352	H58589	Hs.35158	Homo sapiens cDNA FLJ11027 fis, clone PL	2.2	other
111370	AI478658	Hs.94631	brefeldin A-inhibited guanine nucleotide	2.8	?
111384	N94606	Hs.288969	HSCARG protein	2.2	other
111389	AK000987	Hs.169111	oxidation resistance 1	2.1	other
111452	R02354	Hs.15999	ESTs	2.7	TM
111486	AI051194	Hs.227978	EST	6.6	other
111549	W90638	Hs.20321	ESTs, Moderately similar to ZRF1_HUMAN Z	1.4	other
111585	R10720	Hs.20670	EST	1.6	?
111627	R52656	Hs.21691	ESTs	1.6	other
111870	AB037834	Hs.18685	Homo sapiens mRNA for KIAA1413 protein,	2.4	other
111937	BE298665	Hs.14846	Homo sapiens mRNA; cDNA DKFZp564D016 (fr	10.6	other
111944	AW083791	Hs.21263	suppressor of potassium transport defect	6.6	TM
111987	NM_015310	Hs.6763	KIAA0942 protein	5.1	other
112134	R41823	Hs.7413	ESTs; calsyntenin-2	2.8	other
112244	AB029000	Hs.70823	KIAA1077 protein	14.6	other
112388	R46071	Hs.301693	Homo sapiens, clone IMAGE:3638994, mRNA,	9	other
112456	NM_016248	Hs.232076	A kinase (PRKA) anchor protein 11	1.4	other
112464	AW007287	Hs.28538	Homo sapiens cDNA: FLJ21088 fis, clone C	1.4	TM
112506	AI742756	Hs.26079	ESTs	3.2	other
112513	R68425	Hs.13809	hypothetical protein FLJ10848	2	TM
112752	AK001635	Hs.14838	hypothetical protein FLJ10773	1.8	other
112884	AK000004	Hs.5013	Homo sapiens mRNA for FLJ00004 protein,	6.6	other
112923	T10258	Hs.5037	EST	1.5	?
112936	AW970826	Hs.6185	KIAA1557 protein	3.2	other
112958	R61388	Hs.6724	ESTs	6.1	other
112966	Z44718	Hs.102548	glucocorticoid receptor DNA binding fact	6.5	other
112978	AK000272	Hs.7099	hypothetical protein FLJ20265	1.2	other
112995	AA737033	Hs.7155	ESTs, Moderately similar to 2115357A TYK	5.6	other
112996	BE276112	Hs.7165	zinc finger protein 259	2	other
113047	AI571940	Hs.7549	ESTs	1.9	other
113049	AW965190	Hs.7560	Homo sapiens mRNA for KIAA1729 protein,	2.4	TM
113089	T40707	Hs.270882	ESTs	1.3	SS,
113196	T57317		gb:yb51a03.s1 Stratagene fetal spleen (9	1.7	other
113248	T63857		gb:yc16e01.s1 Stratagene lung (937210) H	2.6	other
113254	AK002180	Hs.11449	DKFZP564O123 protein	1.3	other
113277	AW971049	Hs.11774	protein (peptidyl-prolyl cis/trans isome	3.2	other
113429	AA688021	Hs.179808	ESTs	1.2	other
113489	AI467908	Hs.8882	ESTs	8	other
113547	H59588	Hs.15233	ESTs	2	SS,
113647	AA813887	Hs.188173	Homo sapiens cDNA FLJ12187 fis, clone MA	1.3	SS,
113702	T97307		gb:ye53h05.s1 Soares fetal liver spleen	4.4	other

113759	AW499665	Hs.9456	SWI/SNF related, matrix associated, acti	1.2	other	
113777	BE266947	Hs.10590	zinc finger protein 313	13.4	other	
113783	AL359588	Hs.7041	hypothetical protein DKFZp762B226	1.7	other	
113791	AI269098	Hs.135578	chitobiase, di-N-acetyl-	1.3	other	
113808	W44735	Hs.9286	Homo sapiens cDNA: FLJ21278 fis, clone C	3.3	other	
113811	BE207480	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone H	3.1	other	
113817	H13325	Hs.332795	hypothetical protein DKFZp761O17121	3.2	other	
113826	AW378212	Hs.24809	hypothetical protein FLJ10826	2.3	?	
113834	T26483	Hs.6059	EGF-containing fibulin-like extracellula	11.3	TM	
113868	W57902	Hs.90744	proteasome (prosome, macropain) 26S subu	2.7	other	
113870	AL079314	Hs.16537	hypothetical protein, similar to (U06944	6.1	other	
113885	AW959486	Hs.21732	ESTs	6.6	other	
113923	AW953484	Hs.3849	hypothetical protein FLJ22041 similar to	1.9	?	
113989	W87544	Hs.268828	ESTs	1.2	other	
114022	AI539519	Hs.120969	Homo sapiens cDNA FLJ11562 fis, clone HE	5.4	other	
114030	AI825386	Hs.164478	hypothetical protein FLJ21939 similar to	9.4	other	
114060	AB029551	Hs.7910	RING1 and YY1 binding protein	1.8	other	
114196	AF017445	Hs.150926	fucose-1-phosphate guanylyltransferase	1.5	other	
114226	AB028968	Hs.7989	KIAA1045 protein	1.8	other	
114253	BE149866	Hs.14831	Homo sapiens, Similar to zinc finger pro	2.3	other	
114262	AL117518	Hs.3688	KIAA0978 protein	1.4	TM	
114275	AW515443.comp		Hs.306117	KIAA0306 protein	15.8	other
114292	AI815395	Hs.184841	fatty acid desaturase 2	1.9	TM	
114309	AA332453	Hs.20824	CGI-85 protein	2.4	other	
114392	AA249590	Hs.100748	ESTs, Weakly similar to A28996 proline-r	1.9	other	
114407	BE539976	Hs.103305	Homo sapiens mRNA; cDNA DKFZp434B0425 (f	1.3	TM	
114455	H37908	Hs.271616	ESTs, Weakly similar to ALU8_HUMAN ALU S	5.6	other	
114463	AL120247	Hs.40109	KIAA0872 protein	5.3	TM	
114464	AI091713	Hs.106597	Homo sapiens, Similar to RIKEN cDNA 1110	1.3	other	
114471	AA028074	Hs.104613	RP42 homolog	1.9	?	
114480	BE066778	Hs.151678	UDP-N-acetyl-alpha-D-galactosamine:polyp	13.4	other	
114671	AA766268	Hs.266273	hypothetical protein FLJ13346	2	other	
114699	AA476966	Hs.110857	polymerase (RNA) III (DNA directed) poly	3.6	other	
114730	AI373544	Hs.331328	intermediate filament protein syncoilin	3.9	other	
114767	AI859865	Hs.154443	minichromosome maintenance deficient (S.	1.7	other	
114774	AV656017	Hs.184325	CGI-76 protein	3.2	other	
114798	AA159181	Hs.54900	serologically defined colon cancer antig	3.6	other	
114860	AL157545	Hs.42179	bromodomain and PHD finger containing, 3	4.4	other	
114895	AA236177	Hs.76591	KIAA0887 protein	7.2	other	
114896	BE539101	Hs.5324	hypothetical protein	1.3	other	
114911	AA236672		gb:zt29f02.s1 Soares ovary tumor NbHOT H	1.5	other	
114930	AA237022	Hs.188717	ESTs	2	SS,	
114938	AA242634	Hs.58384	ESTs	2.9	other	
114965	AI733881	Hs.72472	BMP-R1B	2.3	?	
115023	AF102546	Hs.63931	dachshund (Drosophila) homolog	1.3	other	
115038	AA252360	Hs.87868	toll-like receptor 9	1.6	other	
115061	AI751438	Hs.41271	Homo sapiens mRNA full length insert cDN	11.8	other	
115117	AI670847	Hs.5324	hypothetical protein	1.5	other	
115206	AW183695	Hs.186572	ESTs	2.5	other	
115221	AW365434	Hs.76741	hypothetical protein FLJ10116	1.5	other	
115239	BE251328	Hs.73291	hypothetical protein FLJ10881	1.3	TM	
115242	AI368236	Hs.283732	ESTs, Moderately similar to ALU1_HUMAN A	1.4	other	
115278	AK002163	Hs.301724	hypothetical protein FLJ11301	1.5	other	
115285	AW972872	Hs.293736	ESTs	2.4	other	
115291	BE545072	Hs.122579	hypothetical protein FLJ10461	6.3	SS,	
115400	AI215069	Hs.89113	ESTs	6.7	?	
115468	AA314349	Hs.46499	tumor antigen SLP-8p	7.5	?	
115471	AK001376	Hs.59346	hypothetical protein FLJ10514	1.4	TM	
115479	AW301608	Hs.278188	ESTs, Moderately similar to I54374 gene	4.1	TM	
115498	AW247593	Hs.71819	eukaryotic translation initiation factor	16.3	other	
115500	Y14443	Hs.88219	zinc finger protein 200	5	other	
115553	AJ275986	Hs.71414	transcription factor (SMIF gene)	2.5	other	
115581	AI540842	Hs.61082	ESTs	6.2	other	
115587	BE081342	Hs.283037	HSPC039 protein	2.9	other	
115590	AA399477	Hs.87896	7-60 protein	5.3	TM	
115646	N36110	Hs.305971	solute carrier family 2 (facilitated glu	4.8	?	
115652	BE093589	Hs.38178	hypothetical protein FLJ23468	10.6	other	

115655	AL048269	Hs.288544	Homo sapiens, clone MGC:16063, mRNA, com	12.7	TM
115663	AI138785	Hs.40507	ESTs	2	other
115676	AA953006	Hs.88143	ESTs	3.1	other
115690	AA825132	Hs.44159	hypothetical protein FLJ21615	1.7	TM
115693	AF231023	Hs.55173	cadherin, EGF LAG seven-pass G-type rece	6.9	other
115715	BE395161	Hs.1390	proteasome (prosome, macropain) subunit,	1.7	other
115734	AI950339	Hs.40782	ESTs	2.7	TM
115811	NM_015434	Hs.48604	DKFZP434B168 protein	2.1	other
115823	AI732742	Hs.87440	ESTs	2.1	other
115837	AI675217	Hs.42761	ESTs	1.3	other
115844	AI373062	Hs.332938	hypothetical protein MGC5370	4.4	other
115866	AW062629	Hs.52061	KIAA0867 protein	7.3	other
115875	N55669	Hs.333823	mitochondrial ribosomal protein L13	1.2	other
115941	AI867451	Hs.46679	hypothetical protein FLJ20739	5.5	other
115968	AB037753	Hs.62767	KIAA1332 protein	9.8	other
116003	BE275469	Hs.66493	Down syndrome critical region gene 5	1.4	other
116011	AL359053	Hs.57664	Homo sapiens mRNA full length insert cDN	2.4	other
116108	AA770688	Hs.28777	H2A histone family, member L	1.8	other
116134	BE243834	Hs.50441	CGI-04 protein	1.4	other
116189	N35719	Hs.44749	ESTs, Moderately similar to T00358 hypot	1.2	other
116196	AW821113	Hs.72402	ESTs	2.1	other
116238	AV660717	Hs.47144	DKFZP586N0819 protein	1.7	other
116246	AF265555	Hs.250646	baculoviral IAP repeat-containing 6	1.7	other
116262	AI936442	Hs.59838	hypothetical protein FLJ10808	1.8	?
116298	AI955411	Hs.94109	Homo sapiens cDNA FLJ13834 fis, clone PL	1.9	other
116318	AF097645	Hs.58570	deleted in cancer 1; RNA helicase HDB/DI	5	SS,
116325	AI472106	Hs.49303	Homo sapiens cDNA FLJ11663 fis, clone HE	1.4	SS,
116336	AL133033	Hs.4084	KIAA1025 protein	1.9	?
116339	AK000290	Hs.44033	dipeptidyl peptidase 8	1.5	other
116350	AA497129	Hs.184771	nuclear factor I/C (CCAAT-binding transc	1.9	?
116358	AI149586	Hs.38125	interferon-induced protein 75, 52kD	1.9	?
116365	N50174	Hs.48765	ESTs	6.1	other
116368	N90466	Hs.71109	KIAA1229 protein	1.8	?
116417	AW499664	Hs.12484	Human clone 23826 mRNA sequence	7.4	other
116436	AA161411	Hs.58668	chromosome 21 open reading frame 57	2.1	other
116462	AF218313	Hs.236828	putative helicase RUVBL	1.5	TM
116470	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	2.1	TM
116575	AA312572	Hs.6241	phosphoinositide-3-kinase, regulatory su	1.5	other
116637	AK001043	Hs.92033	integrin-linked kinase-associated serine	2.7	other
116640	X89984	Hs.211563	B-cell CLL/lymphoma 7A	2.3	other
116700	AI800202	Hs.317589	hypothetical protein MGC10765	1.4	other
116705	AW074819	Hs.12313	hypothetical protein FLJ14566	3.4	other
116732	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypothetl	2.9	other
116926	H73808	Hs.290830	ESTs	1.7	TM
117034	U72209	Hs.180324	YY1-associated factor 2	3.4	TM
117132	AI393666	Hs.42315	p10-binding protein	5.2	?
117247	N21032		gb:yx46f06.s1 Soares melanocyte 2NbHM Ho	5.5	TM
117276	N71183	Hs.121806	Homo sapiens cDNA FLJ11971 fis, clone HE	1.5	TM
117284	AK001701	Hs.183779	Homo sapiens cDNA FLJ10590 fis, clone NT	2	other
117357	AI041793	Hs.42502	ESTs	2	other
117368	AI878942	Hs.90336	ATPase, H+ transporting, lysosomal (vacu	2.1	?
117382	AF150275	Hs.40173	ESTs	2.7	TM
117412	N32536	Hs.42645	solute carrier family 16 (monocarboxylic	1.4	other
117557	AF123050	Hs.44532	diubiquitin	3.4	TM
117588	N34895	Hs.44648	ESTs	3.4	?
117745	BE294925	Hs.46680	CGI-12 protein	3	SS,
117754	AA121673	Hs.59757	zinc finger protein 281	1.9	other
117879	N54706	Hs.303025	chromosome 11 open reading frame 24	1.8	other
117904	BE540675	Hs.332938	hypothetical protein MGC5370	8	?
117911	AL137379	Hs.47125	hypothetical protein FLJ13912	1.7	other
117933	Y10518	Hs.116470	hypothetical protein FLJ20048	1.7	other
117983	AL110246	Hs.47367	KIAA1785 protein	5.4	other
118078	N54321	Hs.47790	EST	5.2	other
118301	AA453902	Hs.293264	ESTs	2.6	other
118429	AA243332	Hs.74849	cytochrome c oxidase subunit VIc	2.5	TM
118472	AL157545	Hs.42179	bromodomain and PHD finger containing, 3	4.1	other
118488	AJ277275	Hs.50102	rapa-2 (rapa gene)	1.2	other

118509	N22617	Hs.43228	Homo sapiens cDNA FLJ11835 fis, clone HE	1.5	other
118528	AI949952	Hs.49397	ESTs	7.4	?
118656	AI458020	Hs.293287	ESTs	2.5	other
118670	AA332845	Hs.152618	ESTs, Moderately similar to ZN91_HUMAN Z	1.2	TM
118698	AB033113	Hs.50187	KIAA1287 protein	2.1	TM
118737	AA199686		gb:zq75g09.r1 Stratagene hNT neuron (937	5.2	other
118925	N92293	Hs.206832	ESTs, Moderately similar to ALU8_HUMAN A	1.4	other
118984	AI668709	Hs.240722	ESTs, Moderately similar to ALU8_HUMAN A	3.6	other
118986	AF148713	Hs.125830	bladder cancer overexpressed protein	4.9	?
119206	W24781	Hs.293798	KIAA1710 protein	1.7	TM
119235	AW453069	Hs.3657	activity-dependent neuroprotective prote	2.2	other
119265	BE339706	Hs.285383	ESTs	1.4	?
119279	N57568	Hs.48028	EST	25.1	other
119298	NM_001241	Hs.155478	cyclin T2	1.6	?
119338	AI417240	Hs.320836	ESTs, Weakly similar to A47582 B-cell gr	1.3	other
119403	AL117554	Hs.119908	nucleolar protein NOP5/NOP58	6.7	TM
119478	AI624342	Hs.170042	ESTs	2.4	other
119488	AI798730	Hs.55513	ESTs	2.1	other
119513	W37933		Empirically selected from AFFX single pr	1.9	other
119601	AK000155	Hs.91684	Homo sapiens mRNA; cDNA DKFZp667I103 (fr	3.7	TM
119602	AW675298	Hs.233694	hypothetical protein FLJ11350	3	other
119676	AA243837	Hs.57787	ESTs	1.4	other
119682	W61019	Hs.57811	ESTs	1.2	?
119774	AB032977	Hs.6298	KIAA1151 protein	1.8	TM
119780	NM_016625	Hs.191381	hypothetical protein	3.1	other
119789	BE393948	Hs.50915	kallikrein 5 (KLK5; KLK-L2; stratum corn	9.2	other
119805	AJ223810	Hs.43213	ESTs, Weakly similar to 1EFS_HUMAN TRANS	3.6	TM
119818	AA130970	Hs.58382	hypothetical protein FLJ11101	2.5	?
119863	AA081218	Hs.58608	Homo sapiens cDNA FLJ14206 fis, clone NT	2.7	TM
119905	AW449064	Hs.119571	collagen, type III, alpha 1 (Ehlers-Danl	2.6	other
119966	AA703129	Hs.58963	ESTs	2.7	other
120132	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	1.2	other
120206	H26735	Hs.91668	Homo sapiens clone PP1498 unknown mRNA	45.7	other
120248	AI924294	Hs.173259	uncharacterized bone marrow protein BM03	1.2	other
120269	AW131940	Hs.104030	ESTs	9.6	other
120274	AA177051		gb:nc02a02.s1 NCI_CGAP_Pr3 Homo sapiens	4.7	other
120280	AA190577		gb:zp52g02.s1 Stratagene HeLa cell s3 93	2.1	other
120296	AW995911	Hs.299883	hypothetical protein FLJ23399	1.9	TM
120297	AA191384	Hs.104072	ESTs, Weakly similar to Z195_HUMAN ZINC	15.2	other
120324	AA195517	Hs.191843	ESTs	5.6	?
120325	AA195651	Hs.104106	ESTs	6.5	other
120327	AK000292	Hs.278732	hypothetical protein FLJ20285	16.1	other
120336	N85785	Hs.181165	eukaryotic translation elongation factor	3	other
120342	AW450869	Hs.45068	hypothetical protein DKFZp434I143	5.8	other
120345	AA210722	Hs.104158	ESTs	4.6	SS,TM
120349	AW969481	Hs.55189	hypothetical protein	18.8	other
120352	R06859	Hs.193172	ESTs, Weakly similar to I38022 hypothet	5.1	other
120356	AF000545	Hs.296433	putative purinergic receptor	28.1	TM
120371	AA219305	Hs.104196	EST	12.4	?
120382	AA226026	Hs.38774	ESTs	4.1	TM
120383	AL109963	Hs.123122	FSH primary response (LRPR1, rat) homolo	9.7	TM
120386	AW969665	Hs.154848	hypothetical protein DKFZp434D0127	32.6	other
120388	AA232874	Hs.104245	ESTs	3.2	other
120389	AW967985	Hs.325572	ESTs, Moderately similar to ALU7_HUMAN A	21.7	other
120396	AA134006	Hs.79306	eukaryotic translation initiation factor	12.5	other
120404	AB023230	Hs.98427	KIAA1013 protein	7.3	other
120418	AW966893	Hs.26813	Homo sapiens mRNA; cDNA DKFZp586F1323 (I	11.4	other
120423	AA236453	Hs.18978	Homo sapiens cDNA: FLJ22822 fis, clone K	1.9	other
120472	AI950087		gb:wq05c02.x1 NCI_CGAP_Kid12 Homo sapien	19.4	other
120473	AA251973	Hs.269988	ESTs	5.5	?
120484	AA253170	Hs.98473	EST	10.4	?
120504	AA256837		gb:zr84d10.s1 Soares_NhHMPu_S1 Homo sapi	4	?
120509	BE047718	Hs.96545	ESTs	9.4	other
120520	AA258501	Hs.161731	EST	2.4	other
120535	BE350244	Hs.98547	ESTs	2.5	?
120551	AA279160	Hs.111407	Homo sapiens, clone IMAGE:3613029, mRNA,	5.3	other
120570	AA280679	Hs.271445	ESTs, Weakly similar to ALU1_HUMAN ALU S	14.4	?

120582	BE244830	Hs.284228	ZNF135-like protein	10.2	?
120590	AW372799	Hs.125790	leucine-rich repeat-containing 2	2.2	?
120596	AA282074	Hs.237323	N-acetylglucosamine-phosphate mutase	7.6	other
120619	AW985339	Hs.111471	ESTs	2.5	other
120624	AW407987	Hs.173518	M-phase phosphoprotein homolog	52	other
120639	AA286942		gb:zs56f05.s1 NCI_CGAP_GCB1 Homo sapiens	2.4	other
120648	AA287095	Hs.140309	Homo sapiens, clone IMAGE:3677194, mRNA,	5	other
120653	AW063659	Hs.191649	ESTs	2.2	other
120668	AW969638	Hs.112316	6.2 kd protein	2.2	TM
120669	BE536739	Hs.109909	ESTs	1.9	TM
120695	AA976503		gb:oq30a04.s1 NCI_CGAP_GC4 Homo sapiens	46.8	TM
120696	AI821539	Hs.97249	ESTs	2.5	other
120713	AW449855	Hs.96557	Homo sapiens cDNA FLJ12727 fis, clone NT	6	other
120718	AA292747	Hs.97296	ESTs	2.9	other
120750	AI191410	Hs.96693	ESTs, Moderately similar to 2109260A B c	7.1	SS,
120774	AI608909	Hs.193985	ESTs	7.9	other
120807	AA346385	Hs.30002	SH3-containing protein SH3GLB2; KIAA1848	7	TM
120809	AA346495		gb:EST52657 Fetal heart II Homo sapiens	4.5	other
120938	AA386260	Hs.104632	EST	4.5	?
120977	AA398155	Hs.97600	ESTs	4.5	other
120984	BE262951	Hs.99052	ESTs	5.8	other
120985	AI219896	Hs.97592	ESTs	1.3	other
121011	AA398360	Hs.97608	EST	3.2	other
121026	AI439713	Hs.165295	ESTs	3.8	other
121081	AA398721	Hs.186749	ESTs, Highly similar to I37550 mismatch	5.5	other
121133	AA363307	Hs.97032	ESTs	3.8	other
121176	AL121523	Hs.97774	ESTs	1.7	TM
121223	AI002110	Hs.97169	ESTs, Weakly similar to dJ687H12.2.1 [H.	2.9	other
121320	AA403008	Hs.301927	c6.1A	1.9	other
121340	AW956981	Hs.97910	Homo sapiens cDNA FLJ13383 fis, clone PL	3.5	other
121408	AA408137	Hs.98019	EST	6.1	?
121439	AA410190	Hs.98076	ESTs, Weakly similar to A47582 B-cell gr	7.5	other
121450	AA408430	Hs.105382	Homo sapiens, clone MGC:18257, mRNA, com	7.1	other
121452	AW971063	Hs.292882	ESTs	1.8	other
121455	H58306	Hs.15165	retinoic acid induced 14	10.5	other
121457	W07404	Hs.144502	hypothetical protein FLJ22055	3.5	TM
121496	AA442224	Hs.97900	ESTs	14.4	other
121505	AA494172	Hs.194417	ESTs	13.1	other
121508	AA402515	Hs.97887	ESTs	28	other
121513	AA416653	Hs.181510	ESTs	6.3	other
121514	AA412112		gb:zt69b02.s1 Soares_testis_NHT Homo sap	2.7	SS,
121549	AA412477	Hs.98142	EST	7.5	?
121558	AA412497		gb:zt95g12.s1 Soares_testis_NHT Homo sap	2.8	other
121577	AA411970	Hs.98098	EST	3.5	?
121581	AA416568		gb:zu05c10.s1 Soares_testis_NHT Homo sap	6.2	TM
121589	AD001528	Hs.89718	spermine synthase	4	other
121594	AA626010	Hs.98247	ESTs	2.2	other
121622	AA416931	Hs.126065	ESTs	4.3	TM
121655	AA421537	Hs.178072	Homo sapiens mRNA; cDNA DKFZp434B1023 (f	7.9	other
121682	AA416160	Hs.86043	Homo sapiens cDNA FLJ13558 fis, clone PL	2	other
121690	AV660305	Hs.110288	ESTs	4.7	?
121706	U55184	Hs.154145	hypothetical protein FLJ11585	12.7	other
121714	AA419225	Hs.98269	Homo sapiens cDNA FLJ11953 fis, clone HE	8.3	?
121729	AI949597	Hs.98325	ESTs	1.8	TM
121731	AA421041	Hs.180744	ESTs	4.1	TM
121744	AA398784	Hs.97514	ESTs	7.1	SS,
121748	BE536911	Hs.234545	hypothetical protein NUF2R	19.5	other
121773	AB033022	Hs.158654	KIAA1196 protein	8	other
121775	AA421773	Hs.161008	ESTs	1.7	other
121776	AA292579	Hs.125133	hypothetical protein FLJ22501	6.7	other
121788	AI810774	Hs.98376	ESTs	10.5	other
121832	AW340797	Hs.98434	ESTs	5.9	other
121836	AA328348	Hs.218289	ESTs	3.9	other
121839	AA425691	Hs.191608	ESTs, Highly similar to KIAA1048 protein	5	other
121842	AF027406	Hs.104865	serine/threonine kinase 23	2.7	?
121847	AA446628	Hs.2799	cartilage linking protein 1	2.3	other
121871	AW972668	Hs.293044	ESTs	2.9	TM

121882	AA426376	Hs.98459	ESTs	5	other
121911	AA427950		gb:zw50f02.s1 Soares_total_fetus_Nb2HF8_	7.3	TM
121915	AA428179	Hs.223405	ESTs, Moderately similar to A46010 X-lin	2.5	other
121935	AA428547	Hs.98611	EST	2.3	other
121983	AA298760	Hs.180191	hypothetical protein FLJ14904	3.4	other
121985	AI882570	Hs.299214	Homo sapiens, clone IMAGE:2822295, mRNA,	11.4	other
121995	AA210883	Hs.3532	nemo-like kinase	3.8	?
121999	AA430211	Hs.98668	EST	6.5	other
122009	AW282763	Hs.160822	Homo sapiens cDNA: FLJ20863 fis, clone A	2.2	other
122013	AA431085	Hs.98706	ESTs	6.6	other
122036	W92142	Hs.271983	ESTs, Weakly similar to ALU5_HUMAN ALU S	13.1	other
122050	AI453076	Hs.166109	ELAV (embryonic lethal, abnormal vision,	9.1	other
122060	AA431738	Hs.98750	EST	13.1	?
122114	AW161023	Hs.104921	ESTs	1.5	other
122188	AA398838		gb:zf80d01.r1 Soares_testis_NHT Homo sap	3.4	other
122204	AA435936	Hs.98842	EST	5.6	other
122246	AA329550	Hs.29417	HCF-binding transcription factor Zhangfe	5.2	other
122257	AA436819	Hs.98899	ESTs	5.6	other
122302	AA441801	Hs.104947	ESTs	5.8	other
122341	AW601969	Hs.99010	hypothetical protein FLJ22263 similar to	2	other
122356	AA443784	Hs.98390	ESTs	7.4	SS,TM
122369	AA443985	Hs.303222	ESTs	12.2	?
122371	AA868555	Hs.178222	ESTs	5	?
122372	AA446008	Hs.336677	EST	7.8	?
122378	AB032948	Hs.21356	hypothetical protein DKFZp762K2015	2.5	?
122405	AA446572	Hs.303223	EST	2.8	TM
122412	AA446859	Hs.119316	ESTs	7.4	other
122415	AA446918	Hs.99088	EST	1.9	other
122418	AA446986	Hs.99090	ESTs, Moderately similar to similar to K	6.9	?
122440	AW505139	Hs.9460	Homo sapiens mRNA; cDNA DKFZp547C244 (fr	2.6	other
122445	AA447603	Hs.99123	EST	1.8	TM
122448	AA447626	Hs.99127	EST	3.5	other
122458	AI266159	Hs.104980	ESTs	1.5	other
122460	AW418788	Hs.99148	ESTs, Weakly similar to S43569 R01H10.6	9.7	other
122464	AA448158	Hs.99152	EST	4.9	other
122490	AA448349	Hs.238151	EST	6.2	?
122492	AA448417	Hs.104990	ESTs	5.5	other
122502	AA204969	Hs.234863	Homo sapiens cDNA FLJ12082 fis, clone HE	1.3	other
122510	AA449232	Hs.99195	ESTs	11.2	?
122530	AW959741	Hs.40368	adaptor-related protein complex 1, sigma	10.1	other
122547	AA779725	Hs.164589	ESTs	2.5	SS,
122555	AA194055	Hs.293858	ESTs	1.9	other
122570	AA452578	Hs.262907	ESTs	9.5	other
122572	AA452601	Hs.99287	EST	11	?
122586	AK001910	Hs.99303	Homo sapiens cDNA FLJ11048 fis, clone PL	3.4	other
122587	AB040893	Hs.6968	KIAA1460 protein	2	other
122598	AI028173	Hs.99329	ESTs	1.7	?
122599	AL355841	Hs.99330	hypothetical protein FLJ23588	4.4	?
122602	AA411925	Hs.301960	ESTs	4.7	other
122607	AA453518	Hs.98023	ESTs	61.5	other
122614	AA453630	Hs.99339	EST	10.7	?
122616	AA453638	Hs.161873	ESTs	107.3	?
122617	AI681535	Hs.148135	serine/threonine kinase 33	121.4	other
122618	AA453641		gb:zx48e06.s1 Soares_testis_NHT Homo sap	31.1	SS,
122622	AA453987	Hs.144802	ESTs	5.6	other
122717	AA456859	Hs.178358	ESTs	8.5	SS,
122762	AI376875	Hs.105119	ESTs	10.4	other
122829	AW204530	Hs.99500	ESTs	81.8	?
122834	AA481492	Hs.99545	Homo sapiens cDNA FLJ10658 fis, clone NT	3.7	?
122836	AA460581	Hs.290996	ESTs	4.6	other
122837	AA461509	Hs.293565	ESTs, Weakly similar to putative p150 [H	2.7	TM
122838	AA460584	Hs.334386	ESTs	75.3	other
122854	AA600235	Hs.9625	NIMA (never in mitosis gene a)-related k	7.8	other
122856	AI929374	Hs.75387	Src-like-adapter	5.8	other
122861	AA335721	Hs.119394	ESTs	1.3	other
122866	BE539656	Hs.283705	ESTs	4.2	other
122868	AF005216	Hs.115541	Janus kinase 2 (a protein tyrosine kinas	5.3	other

122870	AW576312	Hs.318722	Homo sapiens cDNA: FLJ21766 fis, clone C	9.9	?
122872	AW081394	Hs.97103	ESTs	5.3	other
122879	AA769410	Hs.126854	ESTs	13.9	other
122907	AA470074	Hs.169898	ESTs	11.5	other
122916	AA470140	Hs.229170	EST	1.7	TM
122981	AA478951	Hs.105529	ESTs	5	other
123013	AW968324	Hs.17384	ESTs	15.4	other
123016	AW338087	Hs.323231	Homo sapiens cDNA FLJ11948 fis, clone HE	2.8	other
123034	AL359571	Hs.44054	ninein (GSK3B interacting protein)	8.7	other
123072	AI382600	Hs.104308	ESTs, Weakly similar to KIAA1395 protein	8.8	other
123082	AA485360	Hs.105661	ESTs	4	?
123088	AI343652	Hs.105687	ESTs	3.8	other
123110	AA486256	Hs.193510	EST	7.4	other
123114	BE304942	Hs.265848	myomegalin	2.8	?
123131	T52027	Hs.271795	ESTs, Weakly similar to I38022 hypotheti	2.4	other
123132	AI061582	Hs.324179	Homo sapiens cDNA FLJ12371 fis, clone MA	15.6	TM
123136	AW451999	Hs.194024	ESTs	5.2	other
123149	AI734179	Hs.105676	ESTs	23.8	TM
123152	AW601773	Hs.270259	ESTs	5.2	other
123258	AA490929	Hs.105274	ESTs, Weakly similar to RMS1_HUMAN REGUL	9.3	?
123315	AA496369		gb:zv37d10.s1 Soares ovary tumor NbHOT H	4.2	TM
123369	AA504757	Hs.105738	ESTs	7	other
123394	AA731404	Hs.105510	ESTs	3.7	other
123433	AW450922	Hs.112478	ESTs	3.8	other
123466	AA599042	Hs.112503	EST	7.4	other
123470	AW303285	Hs.303632	Human DNA sequence from clone RP11-110H4	3.5	other
123471	AB021844	Hs.197219	zinc finger protein 14 (KOX 6)	5.2	?
123475	BE439553	Hs.250528	Homo sapiens, clone IMAGE:4098694, mRNA,	1.7	other
123482	N95059	Hs.55098	ESTs	1.6	other
123486	BE019072	Hs.334802	Homo sapiens cDNA FLJ14680 fis, clone NT	2.4	other
123508	AW380388	Hs.155546	KIAA1080 protein; Golgi-associated, gamm	2.2	TM
123615	AA609170		gb:af12e12.s1 Soares_testis_NHT Homo sap	7.9	other
123619	AA602964		gb:no97c02.s1 NCI_CGAP_Pr2 Homo sapiens	2.8	other
123658	AA609364		gb:zu71d09.s1 Soares_testis_NHT Homo sap	1.7	?
123674	AI269609	Hs.105187	kinesin protein 9 gene	5.7	?
123735	NM_013241	Hs.95231	FH1/FH2 domain-containing protein	10	other
123738	AA609891	Hs.112777	EST	5.2	other
123753	AA609955	Hs.234961	Huntingtin interacting protein E	30.6	TM
123804	AA620464	Hs.261915	EST, Weakly similar to S65657 alpha-1C-a	2.1	other
123811	AA620586		gb:ae60g05.s1 Stratagene lung carcinoma	2.7	other
123951	AB012922	Hs.173043	metastasis-associated 1-like 1	6.3	?
123983	AJ272267	Hs.146178	choline dehydrogenase	4.4	other
124001	L42542	Hs.75447	ralA binding protein 1	7.1	?
124006	AI147155	Hs.270016	ESTs	8.3	SS,
124070	AI950314	Hs.154762	HIV-1 rev binding protein 2	3.8	other
124074	H05635	Hs.294030	topoisomerase-related function protein 4	1.2	SS,
124178	BE463721	Hs.97101	putative G protein-coupled receptor	3.2	?
124203	AA372796	Hs.269339	ESTs, Weakly similar to AF161356 1 HSPC0	5.7	other
124352	AA640891	Hs.102408	ESTs	3.1	TM
124375	D87454	Hs.192966	KIAA0255 protein	3.5	other
124385	AI267847		gb:aq49a10.x1 Stanley Frontal NB pool 2	57.1	?
124390	AA317338	Hs.7535	COBW-like protein	2.8	other
124391	AF155099	Hs.279780	NY-REN-18 antigen	7.1	other
124417	N34059		gb:yv28h09.s1 Soares fetal liver spleen	3.3	other
124428	H13540	Hs.82202	ribosomal protein L17	2.9	other
124440	AA532519	Hs.129043	Human DNA sequence from clone 989H11 on	7.9	other
124468	R10084	Hs.113319	kinesin heavy chain member 2	2.6	TM
124482	N53935		gb:yv59d09.s1 Soares fetal liver spleen	7.9	TM
124498	H79433	Hs.268997	ESTs	7.8	other
124515	AA669097	Hs.109370	ESTs	3.3	other
124608	N71076	Hs.102800	ESTs, Weakly similar to neuronal thread	4.6	?
124631	NM_014053	Hs.270594	FLVCR protein	3.2	other
124634	AI765123	Hs.143571	Homo sapiens cDNA FLJ13533 fis, clone PL	5.8	other
124637	AA160474	Hs.75798	hypothetical protein	9.3	other
124642	AW968856	Hs.278569	sorting nexin 17	3.5	other
124649	N92593	Hs.313054	ESTs	8.1	TM
124661	R48170	Hs.78436	EphB1	5.6	other

124683	AA381661	Hs.119878	ESTs, Weakly similar to M3K9_HUMAN MITOG	7.9	TM
124712	R09166	Hs.191148	ESTs	5.7	other
124735	R22952	Hs.268685	ESTs	11.3	?
124761	AA374756	Hs.93560	Homo sapiens mRNA for KIAA1771 protein,	9	other
124768	AW368528	Hs.100855	ESTs	8.3	other
124775	R41772	Hs.100878	ESTs	4.9	other
124777	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.8	other
124788	R43543	Hs.100912	Homo sapiens cDNA: FLJ22726 fis, clone H	5.1	other
124809	AL355722	Hs.106875	Homo sapiens EST from clone 35214, full	4.2	other
124811	R46068	Hs.288912	hypothetical protein FLJ22604	14.2	other
124812	R47948	Hs.188732	ESTs	7.9	other
124822	AA418160	Hs.86043	Homo sapiens cDNA FLJ13558 fis, clone PL	6.6	other
124825	AA501669	Hs.336693	ESTs	2.3	SS,TM
124833	AW975868	Hs.294100	ESTs	2.7	SS,TM
124857	R63652	Hs.137190	ESTs	2.3	other
124860	R65763	Hs.101477	EST	23.9	?
124863	AI382555	Hs.127950	bromodomain-containing 1	2	other
124876	AF135422	Hs.27059	GDP-mannose pyrophosphorylase A	4.4	SS,
124878	BE397530	Hs.288057	hypothetical protein FLJ22242	2.7	other
124902	H37941	Hs.101883	ESTs	5.7	other
124903	AW296713	Hs.221441	ESTs	32.4	other
124930	AI076343	Hs.173939	ESTs, Weakly similar to ALUB_HUMAN IIII	22.8	other
124942	R99978	Hs.288892	ESTs, Moderately similar to B34087 hypot	6.1	other
124958	AI078645	Hs.431	murine leukemia viral (bmi-1) oncogene h	1.9	other
124980	T40841	Hs.98681	ESTs	4.5	?
125002	T59338	Hs.269483	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.9	other
125047	T79815	Hs.279793	ESTs	5	?
125051	T79956	Hs.100588	EST	135.3	?
125056	T81310	Hs.100592	ESTs	5.4	other
125101	AI472068	Hs.286236	KIAA1856 protein	5.6	other
125113	T96595	Hs.302270	ESTs, Weakly similar to ALUF_HUMAN IIII	1.8	other
125115	T97341		gb:ye57e05.s1 Soares fetal liver spleen	9.6	?
125125	AI222382	Hs.240767	Human DNA sequence from clone RP1-12G14	1.5	TM
125147	W38150		Empirically selected from AFFX single pr	1.7	?
125161	W44657	Hs.144232	EST	10.7	?
125249	AA630863	Hs.131375	ESTs, Moderately similar to ALUB_HUMAN I	1.3	other
125255	AF098162	Hs.118631	timeless (Drosophila) homolog	9.4	other
125279	AW401809	Hs.4779	KIAA1150 protein	1.5	?
125280	AI123705	Hs.105932	ESTs	8.1	?
125298	AW972542	Hs.289008	Homo sapiens cDNA: FLJ21814 fis, clone H	1.5	other
125660	AW292171	Hs.23978	scaffold attachment factor B	5.9	other
125827	NM_003403	Hs.97496	YY1 transcription factor	1.2	?
125891	U29589	Hs.7138	cholinergic receptor, muscarinic 3	6.5	?
126005	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	14.3	?
126202	AA157632	Hs.272630	vacuolar proton pump delta polypeptide	2.5	SS,
126695	AA643322	Hs.172028	a disintegrin and metalloproteinase doma	9.1	SS,TM
127050	AW411066	Hs.274351	CGI-89 protein	17	other
127274	AW966158	Hs.58582	Homo sapiens cDNA FLJ12789 fis, clone NT	12.8	other
128355	AW293012	Hs.161623	ESTs	7.4	SS,
128493	D87466	Hs.240112	KIAA0276 protein	3.1	TM
128522	BE173977	Hs.10098	putative nucleolar RNA helicase	9.4	other
128527	AA504583	Hs.101047	transcription factor 3 (E2A immunoglobul	1.5	other
128528	R39234	Hs.251699	ESTs, Weakly similar to IDN4-GGTR14 [H.s	2.8	other
128595	U31875	Hs.272499	short-chain alcohol dehydrogenase family	12.1	TM
128599	NM_015368	Hs.102336	Rho GTPase activating protein 8	2.4	?
128604	AI879099	Hs.102397	GIOT-3 for gonadotropin inducible transc	1.3	other
128608	BE267994	Hs.102419	zinc finger protein	7.2	other
128625	AB037841	Hs.102652	hypothetical protein ASH1	1.3	other
128629	AL096748	Hs.102708	DKFZP434A043 protein	3.2	other
128639	AW582962	Hs.102897	CGI-47 protein	2	TM
128658	AA458542	Hs.10326	coatomer protein complex, subunit epsilo	1.4	other
128658	BE397354	Hs.324830	diptheria toxin resistance protein requi	2.5	other
128670	AA975486	Hs.103441	Homo sapiens, Similar to RIKEN cDNA 1700	7.1	?
128691	W27939	Hs.103834	hypothetical protein MGC5576	7.8	?
128696	BE081143	Hs.225977	nuclear receptor coactivator 3	3.8	other
128700	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	1.6	other
128714	T85231	Hs.179661	tubulin, beta 5	7.8	other

128717	AK001564	Hs.104222	hypothetical protein FLJ10702	5.5	other
128733	BE147740	Hs.104558	ESTs, Moderately similar to I38022 hypot	2.7	TM
128737	AF292100	Hs.104613	RP42 homolog	2.8	TM
128742	AA307211	Hs.251531	proteasome (prosome, macropain) subunit,	4.5	?
128746	AI470163	Hs.323342	actin related protein 2/3 complex, subun	2.2	other
128747	AB027249	Hs.104741	PDZ-binding kinase; T-cell originated pr	2.8	other
128772	BE302798	Hs.105097	thymidine kinase 1, soluble	5.4	other
128781	N71826	Hs.105465	small nuclear ribonucleoprotein polypept	53.9	TM
128797	NM_002975	Hs.105927	stem cell growth factor; lymphocyte secr	13.3	other
128806	AW630942	Hs.106061	RD RNA-binding protein	2.6	other
128814	AW248431	Hs.256528	nuclear prelamin A recognition factor	2.2	other
128830	BE281170	Hs.106357	valosin-containing protein	6	other
128835	AK001731	Hs.106390	Homo sapiens mRNA; cDNA DKFZp586H0924 (f	1.6	SS,
128854	BE159181	Hs.168232	hypothetical protein FLJ13855	2.3	other
128871	AF189723	Hs.106778	ATPase, Ca++ transporting, type 2C, memb	1.5	?
128906	R57988	Hs.10706	epithelial protein lost in neoplasm beta	4.8	other
128920	AA622037	Hs.166468	programmed cell death 5	1.4	other
128925	R67419	Hs.21851	Homo sapiens cDNA FLJ12900 fis, clone NT	1.9	other
128946	Y13153	Hs.107318	kynurenine 3-monooxygenase (kynurenine 3	7.3	?
128949	AA009647	Hs.8850	a disintegrin and metalloproteinase doma	2.5	other
128959	AI580127	Hs.107381	hypothetical protein FLJ11200	1.3	other
128985	AW150697	Hs.107418	ESTs	1.4	?
128970	AI375672	Hs.165028	ESTs	1.3	other
128975	BE560779	Hs.284233	NICE-5 protein	14	other
128979	AW271217	Hs.281434	Homo sapiens cDNA FLJ14028 fis, clone HE	1.6	TM
128995	AI818224	Hs.107747	DKFZP566C243 protein	1.9	other
129019	AI950087		gb:wq05c02.x1 NCI_CGAP_Kid12 Homo sapien	2.9	other
129021	AL044675	Hs.173081	KIAA0530 protein	3.8	other
129032	R80088	Hs.108104	ubiquitin-conjugating enzyme E2L 3	3.4	other
129076	AW296806	Hs.326234	ESTs, Highly similar to T46422 hypothet	5	other
129078	AI351010	Hs.102267	lysosomal	2.1	other
129088	AA744610	Hs.194431	palladin	17.1	other
129095	L12350	Hs.108623	thrombospondin 2	2.7	other
129096	AA463189	Hs.288906	WW Domain-Containing Gene	20.9	TM
129097	BE243933	Hs.108642	zinc finger protein 22 (KOX 15)	3	other
129099	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	5.8	TM
129136	W93048	Hs.250723	hypothetical protein MGC2747	6	other
129149	AA356620	Hs.108947	KIAA0050 gene product	6.4	TM
129172	AW162916	Hs.241578	hypothetical protein PRO2577	1.8	TM
129192	AA286914	Hs.183299	ESTs	2.1	?
129194	AA150797	Hs.109278	latexin protein	3.3	SS,TM
129198	N57532	Hs.109315	KIAA1415 protein	5.9	other
129207	AI934365	Hs.109439	osteoglycin (osteoinductive factor, mime	8.1	other
129228	U40714	Hs.239307	tyrosyl-tRNA synthetase	2.9	other
129229	AF013758	Hs.109643	polyadenylate binding protein-interactin	3.3	?
129254	AA252458	Hs.1098	DKFZp434J1813 protein	2.6	SS,TM
129255	AI961727	Hs.109804	H1 histone family, member X	7.4	other
129268	W26392	Hs.110080	ESTs, Weakly similar to S13495 pregnancy	9.6	other
129286	AI051967	Hs.110122	ESTs	1.2	other
129323	AA287239	Hs.5518	Homo sapiens cDNA FLJ11311 fis, clone PL	5.2	other
129340	H75334	Hs.11050	F-box only protein 9	4.7	SS,
129347	BE614192	Hs.279869	melanoma-associated antigen recognised b	7.7	TM
129362	U30246	Hs.110736	solute carrier family 12 (sodium/potassi	6.7	TM
129366	BE220806	Hs.184697	Homo sapiens clone 23785 mRNA sequence	8.6	SS,
129370	AI686379	Hs.110796	SAR1 protein	1.4	TM
129372	NM_016039	Hs.110803	CGI-99 protein	2	other
129403	AF149785	Hs.111126	pituitary tumor-transforming 1 interacti	7.5	other
129404	AI267700	Hs.317584	ESTs	5.1	other
129423	AA204686	Hs.234149	hypothetical protein FLJ20647	10.2	other
129482	AA188185	Hs.289043	spindlin	6.8	other
129513	AW843633	Hs.306163	hypothetical protein AL110115	7.1	SS,
129515	AF255303	Hs.112227	membrane-associated nucleic acid binding	2.6	other
129527	AA769221	Hs.270847	delta-tubulin	3.2	other
129559	W01296	Hs.11360	hypothetical protein FLJ14784	7.5	other
129560	AA317841	Hs.7845	hypothetical protein MGC2752	6.8	other
129570	AI923097	Hs.11441	chromosome 1 open reading frame 8	2.1	other
129575	F08282	Hs.278428	progestin induced protein	1.6	other

129587	H14718	Hs.11506	Human clone 23589 mRNA sequence	6.8	other
129588	BE408300	Hs.301662	postmeiotic segregation increased 2-like	1.4	TM
129591	N57423	Hs.179898	HSPC055 protein	7.4	other
129594	AW403724	Hs.36989	coagulation factor VII (serum prothrombi	9	?
129596	AF035537	Hs.116521	REV3 (yeast homolog)-like, catalytic sub	1.6	other
129628	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	2.2	other
129649	AD000092	Hs.16468	calreticulin	3.3	other
129675	NM_015556	Hs.172180	KIAA0440 protein	13.4	other
129680	U03749		gb:Human chromogranin A (CHGA) gene, pro	14.1	?
129689	AW748482	Hs.77873	67 homolog 3	2.6	other
129702	AI304966	Hs.12035	ESTs, Weakly similar to I38022 hypothetl	7.5	TM
129720	AA156214	Hs.12152	APMCF1 protein	2	other
129721	NM_001415	Hs.211539	eukaryotic translation initiation factor	1.7	TM
129778	AK001676	Hs.12457	hypothetical protein FLJ10814	1.8	other
129779	AA394090	Hs.12460	Homo sapiens clone 23870 mRNA sequence	5.5	TM
129800	AF052112	Hs.12540	lysosomal	1.7	?
129806	AB023148	Hs.173373	KIAA0931 protein	1.2	other
129815	BE565817	Hs.26498	hypothetical protein FLJ21657	3.1	other
129840	NM_006590	Hs.12820	SnRNP assembly defective 1 homolog	1.8	other
129861	AL049999	Hs.85863	DKFZP564M182 protein	2.3	other
129864	AI393237	Hs.129914	runt-related transcription factor 1 (acu	1.7	SS,
129869	AI222069	Hs.13015	hypothetical protein similar to mouse Dn	2.8	TM
129945	BE514376	Hs.165998	PAI-1 mRNA-binding protein	1.8	other
129953	AA412195	Hs.13740	ESTs	2.5	other
129972	AW753185	Hs.180828	dynamin 1-like	1.8	?
129983	U09848	Hs.132390	zinc finger protein 36 (KOX 18)	1.3	other
130010	AA301116	Hs.142838	nucleolar phosphoprotein Nopp34	1.6	other
130081	AA287325	Hs.14713	ESTs	4.1	other
130082	S73265	Hs.1473	gastrin-releasing peptide	1.9	other
130097	AL046962	Hs.14845	forkhead box C3A	2.8	other
130100	AL135561	Hs.14891	hypothetical protein FLJ21047	2.3	other
130111	X53002	Hs.149846	integrin, beta 5	2.3	other
130112	AA918785	Hs.180610	splicing factor proline/glutamine rich (	3	other
130128	L76937	Hs.150477	Werner syndrome	1.8	other
130135	AA311426	Hs.21635	tubulin, gamma 1	6.1	other
130211	NM_003358	Hs.23703	ESTs, Moderately similar to CEGT_HUMAN C	1.8	other
130212	D80001	Hs.152629	KIAA0179 protein	1.3	other
130236	R85367	Hs.51957	splicing factor, arginine/serine-rich 2,	2	other
130241	AL035588	Hs.153203	MyoD family inhibitor	3.2	other
130242	X79201	Hs.153221	synovial sarcoma, translocated to X chro	5.4	?
130249	D81983	Hs.322852	GAS2-related on chromosome 22	4.9	other
130263	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	1.4	other
130287	AA479005	Hs.154036	tumor suppressing subtransferable candid	2.6	other
130310	AB011121	Hs.154248	amyotrophic lateral sclerosis 2 (juvenil	6.3	other
130353	Z19084	Hs.172210	MUF1 protein	6.2	other
130356	AF127577	Hs.155017	nuclear receptor interacting protein 1	2.4	other
130357	AJ224442	Hs.155020	putative methyltransferase	3.5	TM
130359	NM_013449	Hs.277401	bromodomain adjacent to zinc finger doma	8.5	other
130367	AL135301	Hs.8768	hypothetical protein FLJ10849	1.4	other
130372	AI077464	Hs.5011	RNA binding motif protein 9	3.3	?
130393	N89487	Hs.155291	KIAA0005 gene product	1.8	other
130399	AW374106	Hs.155356	hypothetical protein MGC2840 similar to	3.4	other
130407	BE385099	Hs.334727	hypothetical protein MGC3017	2.3	other
130409	NM_001197	Hs.155419	BCL2-interacting killer (apoptosis-induc	2.7	TM
130419	AF037448	Hs.155489	NS1-associated protein 1	1.8	other
130441	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	2.3	other
130448	BE513202	Hs.15589	PPAR binding protein	4	TM
130455	D90041	Hs.155956	N-acetyltransferase 1 (arylamine N-acety	33.6	?
130485	BE245851	Hs.180779	H2B histone family, member B	5	other
130487	U49844	Hs.77613	ataxia telangiectasia and Rad3 related	4.4	other
130498	L38951	Hs.180446	karyopherin (importin) beta 1	1.6	SS,TM
130503	BE208491	Hs.285112	KIAA0618 gene product	16.1	other
130511	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	6.1	other
130526	AW876523	Hs.15928	hypothetical protein FLJ12910	2.1	other
130544	AA321238	Hs.4310	eukaryotic translation initiation factor	1.5	other
130553	AF062649	Hs.252587	pituitary tumor-transforming 1	14.4	?
130556	AI907018	Hs.15977	Empirically selected from AFFX single pr	4.8	other

130567	AA383092	Hs.1608	replication protein A3 (14kD)	8	other
130568	AA232119	Hs.16085	putative G-protein coupled receptor	3.4	other
130574	AF083208	Hs.16178	apoptosis antagonizing transcription fac	1.2	other
130598	AL042210	Hs.16493	hypothetical protein DKFZp762N2316; KIAA	1.4	other
130601	AA609738	Hs.16526	ESTs	1.5	TM
130614	AI354355	Hs.16697	down-regulator of transcription 1, TBP-b	1.3	other
130617	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	12.1	TM
130618	AA383439	Hs.16758	Spir-1 protein	15.9	other
130667	BE246961	Hs.17639	Homo sapiens ubiquitin protein ligase (U	13.9	other
130674	AL048842	Hs.194019	attractin	1.5	other
130675	AA442233	Hs.17731	hypothetical protein FLJ12892	5.4	other
130692	AA652501	Hs.13561	hypothetical protein MGC4692	5	other
130693	R68537	Hs.17862	ESTs	2	other
130712	AJ271881	Hs.279762	bromodomain-containing 7	1.8	TM
130714	AI348274	Hs.18212	DNA segment on chromosome X (unique) 987	2	TM
130730	AB007920	Hs.18586	KIAA0451 gene product	3.8	?
130744	H59696	Hs.18747	POP7 (processing of precursor, S. cerevi	3.2	?
130751	AF052105	Hs.18879	chromosome 12 open reading frame	1.4	other
130757	AL036067	Hs.18925	protein x 0001	5.7	other
130768	AF258627	Hs.211562	ATP-binding cassette, sub-family A (ABC1	5.2	?
130789	AK000355	Hs.8899	sirtuin (silent mating type information	1.6	other
130836	J05068	Hs.2012	transcobalamin I (vitamin B12 binding pr	15.7	SS,
130841	AL157468	Hs.325825	Homo sapiens cDNA FLJ20848 fis, clone AD	2.8	other
130843	AA447492	Hs.20183	ESTs, Weakly similar to AF184793 1 prote	1.5	other
130844	U76248	Hs.20191	seven in absentia (Drosophila) homolog 2	3.5	other
130855	AJ243706	Hs.143323	putative DNA/chromatin binding motif	1.7	other
130861	NM_016578	Hs.20509	HBV pX associated protein-8	1.9	other
130879	NM_003416	Hs.2076	zinc finger protein 7 (KOX 4, clone HF.1	1.4	other
130880	BE514434	Hs.20830	kinesin-like 2	2.1	TM
130892	AL120837	Hs.20993	high-glucose-regulated protein 8	2.5	other
130898	AB033078	Hs.186813	sphingosine-1-phosphate lyase 1	1.7	other
130911	BE409769	Hs.21189	DnaJ (Hsp40) homolog, subfamily A, membe	1.8	other
130919	N79110	Hs.21276	collagen, type IV, alpha 3 (Goodpasture	2.3	TM
130944	BE382657	Hs.21488	signal transducer and activator of trans	5.4	other
130971	N39842	Hs.301444	KIAA1673	2.2	SS,
130993	T97401	Hs.21929	ESTs	1.6	other
131005	AV656308	Hs.2210	thyroid hormone receptor interactor 3	1.6	?
131028	AI879165	Hs.2227	CCAAT/enhancer binding protein (C/EBP),	1.2	other
131042	AI826288	Hs.171637	hypothetical protein MGC2826	1.8	other
131046	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	7.4	?
131060	AA194422	Hs.22564	myosin VI	5.1	other
131070	N53344	Hs.22607	ESTs	7.1	other
131076	AA749230	Hs.26433	dolichyl-phosphate (UDP-N-acetylglucosam	2.1	TM
131099	AL133353	Hs.226581	COX15 (yeast) homolog, cytochrome c oxid	7.1	other
131174	NM_006540	Hs.29131	nuclear receptor coactivator 2	1.9	?
131185	BE280074	Hs.23960	cyclin B1	5.8	?
131206	AW136839	Hs.24210	ESTs	2	other
131213	AA885699	Hs.24332	CGI-26 protein	7.1	TM
131225	H62087	Hs.31659	thyroid hormone receptor-associated prot	7.6	?
131231	N47468	Hs.59757	zinc finger protein 281	2.9	other
131233	D89053	Hs.268012	fatty-acid-Coenzyme A ligase, long-chain	3.5	other
131243	AW383256	Hs.24752	spectrin SH3 domain binding protein 1	2.8	?
131245	AL080080	Hs.24766	thioredoxin domain-containing	2.8	SS,TM
131247	AL043100	Hs.326190	fatty acid amide hydrolase	5.6	other
131281	AA251716	Hs.25227	ESTs	5.8	other
131283	X80038	Hs.339713	Homo sapiens clone F19374 APO E-C2 gene	1.3	other
131305	AV656017	Hs.184325	CGI-76 protein	5	?
131320	AA505691	Hs.145696	splicing factor (CC1.3)	1.8	TM
131339	AF058695	Hs.25812	Nijmegen breakage syndrome 1 (nibrin)	2.8	other
131375	AW293165	Hs.143134	ESTs	5.4	other
131390	BE269388	Hs.182698	mitochondrial ribosomal protein L20	5.3	other
131410	BE259110	Hs.279836	HSPC166 protein	2.2	other
131412	NM_012247	Hs.124027	SELENOPHOSPHATE SYNTHETASE ; Human selen	2	?
131429	AL046302	Hs.26750	hypothetical protein FLJ21908	1.4	other
131458	BE297587	Hs.27047	hypothetical protein FLJ20392	1.7	other
131475	AA992841	Hs.27263	KIAA1458 protein	2	other
131501	AV661958	Hs.8207	GK001 protein	2.6	other

131511	AA732153	Hs.27885	Homo sapiens cDNA: FLJ21333 fis, clone C	2	other
131528	AU076408	Hs.28309	UDP-glucose dehydrogenase	1.8	TM
131532	BE268278	Hs.28393	hypothetical protein MGC2592	7.4	other
131543	AW968881	Hs.41839	programmed cell death 2	2.2	other
131544	AL355715	Hs.28555	programmed cell death 9 (PDCD9)	2.1	other
131562	NM_003512	Hs.28777	H2A histone family, member L	1.7	other
131564	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	5.2	other
131569	AL389951	Hs.271623	nucleoporin 50kD	5	other
131618	BE393822	Hs.29645	Homo sapiens mRNA; cDNA DKFZp761C029 (fr	1.8	other
131622	R78195	Hs.29692	Homo sapiens cDNA FLJ11436 fis, clone HE	1.3	other
131623	AB037791	Hs.29716	hypothetical protein FLJ10980	2.2	TM
131643	AW410601	Hs.30026	HSPC182 protein	3	other
131653	AW960597	Hs.30164	ESTs	1.3	other
131656	AI218918	Hs.30209	KIAA0854 protein	2.8	other
131669	X52486	Hs.3041	uracil-DNA glycosylase 2	2.8	other
131692	BE559681	Hs.30736	KIAA0124 protein	5.6	?
131714	AA642831	Hs.31016	putative DNA binding protein	2.9	?
131722	D13757	Hs.311	phosphoribosyl pyrophosphate amidotransf	3.4	other
131737	AK001641	Hs.31323	inhibitor of kappa light polypeptide gen	3.9	?
131763	AI878932	Hs.317	topoisomerase (DNA) I	3.4	other
131772	AA382590	Hs.170980	KIAA0948 protein	25.5	other
131787	D87077	Hs.196275	KIAA0240 protein	2.4	SS,
131793	AW966127	Hs.32248	Homo sapiens cDNA FLJ14656 fis, clone NT	8	TM
131795	BE501849	Hs.32317	high-mobility group 20B	1.5	other
131798	X86098	Hs.301449	adenovirus 5 E1A binding protein	4.2	other
131817	U20536	Hs.3260	caspase 8, apoptosis-related cysteine pr	4.3	other
131824	U28838	Hs.32935	TATA box binding protein (TBP)-associate	3.5	other
131850	AI251317	Hs.33184	ESTs	5.2	TM
131878	AA083764	Hs.6101	hypothetical protein MGC3178	5.9	other
131885	BE502341	Hs.3402	ESTs	13.7	other
131900	AA099014	Hs.231029	Homo sapiens, clone MGC:15961, mRNA, com	8.7	other
131904	AF078866	Hs.284296	Homo sapiens cDNA: FLJ22993 fis, clone K	5.5	other
131905	AA179298	Hs.3439	stomatin-like 2	11.3	other
131913	AW207440	Hs.185973	degenerative spermatocyte (homolog Droso	1.7	SS,
131916	AA025976	Hs.34569	ESTs	5.2	TM
131925	AF151048	Hs.183180	anaphase promoting complex subunit 11 (y	2.8	other
131929	BE541211	Hs.34804	Homo sapiens cDNA FLJ11472 fis, clone HE	5.4	TM
131941	BE252983	Hs.35086	ubiquitin specific protease 1	2.4	other
131950	AA355113	Hs.35380	x 001 protein	1.5	?
131962	AK000046	Hs.267448	hypothetical protein FLJ20039	2.3	other
131965	W79283	Hs.35962	ESTs	1.4	other
131971	BE567100	Hs.154938	hypothetical protein MDS025	3.5	other
131977	U90441	Hs.3622	procollagen-proline, 2-oxoglutarate 4-di	6.8	TM
131985	AA503020	Hs.36563	hypothetical protein FLJ22418	2.4	?
131991	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	2.2	SS,TM
132019	H56995	Hs.37372	Homo sapiens DNA binding peptide mRNA, p	3.3	TM
132062	BE266155	Hs.3832	clathrin-associated protein AP47	1.5	other
132084	NM_002267	Hs.3886	karyopherin alpha 3 (importin alpha 4)	3.7	other
132103	BE171921	Hs.3991	ESTs	1.5	other
132105	AV646076	Hs.39959	ESTs	5.8	TM
132116	AW960474	Hs.40289	ESTs	1.7	other
132176	AA857025	Hs.8878	kinesin-like 1	3.4	other
132180	NM_004460	Hs.418	fibroblast activation protein, alpha	14.7	SS,
132194	R42432	Hs.4212	ESTs	2.2	other
132207	BE206939	Hs.42287	E2F transcription factor 6	1.5	other
132235	AV658411	Hs.42656	KIAA1681 protein	5.7	other
132252	AI566004	Hs.141269	Homo sapiens cDNA: FLJ21550 fis, clone C	2.1	other
132266	AA301228	Hs.43299	hypothetical protein FLJ12890	1.5	other
132273	AA227710	Hs.43658	DKFZP586L151 protein	10	other
132276	AA653507	Hs.285711	hypothetical protein FLJ13089	2	other
132288	N36110	Hs.305971	solute carrier family 2 (facilitated glu	9.2	other
132294	AB023191	Hs.44131	KIAA0974 protein	2	other
132298	NM_015986	Hs.7120	cytokine receptor-like molecule 9	6.8	SS,
132299	AW405882	Hs.44205	cortistatin	3.8	other
132325	N37065	Hs.44856	hypothetical protein FLJ12116	1.5	other
132370	AW572805	Hs.46845	ESTs	28.3	?
132374	AF155582	Hs.46744	core1 UDP-galactose:N-acetylgalactosamin	1.9	other

132376	AI279892	Hs.46801	sorting nexin 14	2	?
132384	AA312135	Hs.46987	HSPC034 protein	6.1	?
132393	AL135094	Hs.47334	hypothetical protein FLJ14495	1.7	other
132450	AA100012	Hs.48827	hypothetical protein FLJ12085	6.6	other
132452	AW973521	Hs.247324	mitochondrial ribosomal protein S14	5.3	other
132456	AB011084	Hs.48924	KIAA0512 gene product; ALEX2	1.5	other
132470	AI224458	Hs.4934	H.sapiens polyA site DNA	2	other
132484	X16660	Hs.119007	RAB4, member RAS oncogene family	2.9	SS,
132518	AW885606	Hs.5064	ESTs	2.2	other
132530	AA306105	Hs.50785	SEC22, vesicle trafficking protein (S. c	1.7	other
132532	AA454132	Hs.5080	mitochondrial ribosomal protein L16	7.2	TM
132534	BE388673	Hs.5086	hypothetical protein MGC10433	2.2	SS,
132543	BE568452	Hs.5101	protein regulator of cytokinesis 1	2.2	other
132574	AW631437	Hs.5184	TH1 drosophila homolog	14	?
132596	AK001484	Hs.5298	CGI-45 protein	1.9	other
132611	AA345547	Hs.53263	hypothetical protein FLJ13287	2.6	TM
132612	H12751	Hs.5327	PRO1914 protein	2	other
132616	BE262677	Hs.283558	hypothetical protein PRO1855	3.1	other
132638	AI796870	Hs.54277	DNA segment on chromosome X (unique) 992	12.4	TM
132668	AB018319	Hs.5460	KIAA0776 protein	2.8	SS,
132692	AW191962	Hs.249239	collagen, type VIII, alpha 2	3	other
132715	F11875	Hs.5534	Homo sapiens cDNA FLJ12961 fis, clone NT	1.8	other
132718	NM_004600	Hs.554	Sjogren syndrome antigen A2 (60kD, ribon	3.7	other
132724	AI142265	Hs.55498	geranylgeranyl diphosphate synthase 1	1.8	TM
132731	AI189075	Hs.301872	hypothetical protein MGC4840	5.9	other
132744	AA010233	Hs.55921	glutamyl-prolyl-tRNA synthetase	8.7	other
132760	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	3.6	other
132771	Y10275	Hs.56407	phosphoserine phosphatase	2.8	TM
132773	AA459713	Hs.295901	KIAA0493 protein	14.6	other
132784	AI142133	Hs.56845	GDP dissociation inhibitor 2	1.7	other
132788	AI026701	Hs.5716	KIAA0310 gene product	2.5	other
132807	U07418	Hs.57301	mutL (E. coli) homolog 1 (colon cancer,	1.4	other
132810	AB007944	Hs.5737	KIAA0475 gene product	4.3	SS,
132813	BE313625	Hs.57435	solute carrier family 11 (proton-coupled	2.8	other
132815	AI815189	Hs.57475	sex comb on midleg homolog 1	1.6	other
132817	N27852	Hs.57553	tousled-like kinase 2	1.4	other
132821	AJ251595	Hs.169610	CD44 antigen (homing function and Indian	5.4	other
132833	U78525	Hs.57783	eukaryotic translation initiation factor	6.1	?
132842	NM_016154	Hs.279771	Homo sapiens clone PP1596 unknown mRNA	7.2	other
132844	F12200	Hs.5811	chromosome 21 open reading frame 59	2.9	other
132851	U09716	Hs.287912	lectin, mannose-binding, 1	8.1	other
132869	AW963217	Hs.203961	ESTs, Moderately similar to AF116721 89	1.8	other
132873	AW007683	Hs.58598	KIAA1268 protein	2.2	other
132875	NM_004850	Hs.58617	Rho-associated, coiled-coil containing p	5	TM
132891	BE267143	Hs.59271	U2(RNU2) small nuclear RNA auxiliary fac	2.7	?
132897	AW503667	Hs.59545	ring finger protein 15	5.4	?
132902	AI936442	Hs.59838	hypothetical protein FLJ10808	3.2	other
132912	AW732760	Hs.167578	Homo sapiens cDNA FLJ11095 fis, clone PL	1.4	other
132913	W78714	Hs.60257	Homo sapiens cDNA FLJ13598 fis, clone PL	3	other
132940	T79136	Hs.127243	Homo sapiens mRNA for KIAA1724 protein,	10.3	other
132942	AA554458	Hs.197751	KIAA0666 protein	2.1	SS,
132952	AI658560	Hs.61426	Homo sapiens mesenchymal stem cell prote	1.3	other
132962	AA576635	Hs.6153	CGI-48 protein	4.9	other
132972	AA034365	Hs.288924	Homo sapiens cDNA FLJ11392 fis, clone HE	3.6	TM
132973	AA035446	Hs.323277	ESTs	13.1	other
132977	AA093322	Hs.301404	RNA binding motif protein 3	1.3	other
132980	AA040696	Hs.62016	ESTs	2.3	?
132994	AA112748	Hs.279905	clone HQ0310 PRO0310p1	17.1	other
133012	AA847843	Hs.62711	Homo sapiens, clone IMAGE:3351295, mRNA	1.9	other
133015	AJ002744	Hs.246315	UDP-N-acetyl-alpha-D-galactosamine:polyp	5	TM
133062	AW500374	Hs.64056	PRO0149 protein	6.1	other
133069	BE247441	Hs.6430	protein with polyglutamine repeat; calci	1.5	TM
133091	AK001626	Hs.64691	KIAA0483 protein	1.4	other
133110	AA808177	Hs.65228	ESTs	5.6	other
133134	AF198620	Hs.65648	RNA binding motif protein 8A	1.9	other
133145	H94227	Hs.6592	Homo sapiens, clone IMAGE:2981368, mRNA,	4.6	?
133152	Z11695	Hs.324473	mitogen-activated protein kinase 1	5	other

133174	AA431620	Hs.324178	hypothetical protein MGC2745	2.7	other
133175	AW955632	Hs.66658	ESTs, Weakly similar to S19560 proline-r	9.3	other
133177	X97795	Hs.66718	RAD54 (S.cerevisiae)-like	4.5	TM
133208	AI801777	Hs.6774	ESTs	5.5	TM
133226	AW954569	Hs.296287	Homo sapiens, Similar to bromodomain-con	2.7	other
133228	AI492924	Hs.6831	golgi phosphoprotein 1	1.7	?
133254	AI587421	Hs.273330	Homo sapiens, clone IMAGE:3544662, mRNA,	1.3	other
133268	AW956781	Hs.293937	ESTs, Weakly similar to FXD2_HUMAN FORKH	12.2	other
133291	BE297855	Hs.69855	NRAS-related gene	1.2	other
133314	AA102670	Hs.70725	gamma-aminobutyric acid (GABA) A recepto	1.7	TM
133321	T79526	Hs.179516	integral type I protein	11.1	?
133327	AL390127	Hs.7104	Kruppel-like factor 13	2.9	other
133347	BE257758	Hs.71475	acid cluster protein 33	2.5	?
133360	AI016521	Hs.71816	v-akt murine thymoma viral oncogene homo	1.5	other
133366	AA292811	Hs.72050	non-metastatic cells 5, protein expresse	2.1	other
133387	AF231919	Hs.18759	KIAA0539 gene product	1.3	other
133370	AF245505	Hs.72157	DKFZP564I1922 protein	2.2	other
133390	AI950382	Hs.72660	phosphatidylserine receptor	5.7	TM
133391	AW103364	Hs.727	inhibin, beta A (activin A, activin AB a	25.5	other
133394	AA305127	Hs.237225	hypothetical protein HT023	3.3	other
133437	AL031591	Hs.7370	phosphotidylinositol transfer protein, b	1.6	other
133452	NM_002759	Hs.274382	protein kinase, interferon-inducible dou	4.1	other
133453	AI659306	Hs.73826	protein tyrosine phosphatase, non-recept	1.5	other
133500	AW964804	Hs.74280	hypothetical protein FLJ22237	6.3	TM
133529	W45623	Hs.74571	ADP-ribosylation factor 1	4	?
133543	AU077073	Hs.106327	damage-specific DNA binding protein 1 (1	1.8	?
133578	AU077050	Hs.75068	transitin	1.5	other
133579	X75346	Hs.75074	mitogen-activated protein kinase-activat	3.5	TM
133582	BE391579	Hs.75087	Fes-activated serine/threonine kinase	6.8	TM
133594	AW160781	Hs.172589	nuclear phosphoprotein similar to S. cer	2.6	TM
133595	AA393273	Hs.75133	transcription factor 6-like 1 (mitochond	1.4	other
133599	NM_002885	Hs.75151	RAP1, GTPase activating protein 1	8.1	other
133621	NM_004893	Hs.75258	H2A histone family, member Y	13.5	other
133627	NM_002047	Hs.75280	glycyl-tRNA synthetase	2.2	other
133631	NM_000401	Hs.75334	exostoses (multiple) 2	1.8	other
133649	U25849	Hs.75393	acid phosphatase 1, soluble	2	other
133690	AV661185	Hs.75574	mitochondrial ribosomal protein L19	2.8	other
133720	L27841	Hs.75737	pericentriolar material 1	6.8	other
133722	AW969976	Hs.279009	matrix Gla protein	2.5	other
133751	AW402048.comp		Hs.334787	Homo sapiens, Similar to likely ortholog 3.1	TM
133757	T52946	Hs.196209	RAE1 (RNA export 1, S.pombe) homolog	1.4	?
133760	BE271766	Hs.181357	laminin receptor 1 (67kD, ribosomal prot	5.4	other
133765	M62194	Hs.75929	cadherin 11, type 2, OB-cadherin (osteob	5	other
133780	AA557660	Hs.76152	decorin	3.8	other
133797	AL133921	Hs.76272	retinoblastoma-binding protein 2	3.1	?
133822	D50525	Hs.699	peptidylprolyl isomerase B (cyclophilin	9.7	?
133842	AW797466	Hs.285013	putative human HLA class II associated p	2.4	other
133845	AA147026	Hs.76704	ESTs	2.5	other
133865	AB011155	Hs.170290	discs, large (Drosophila) homolog 5	5	other
133867	AW340125	Hs.76989	KIAA0097 gene product	2.5	?
133868	AB012193	Hs.183874	cullin 4A	2.1	other
133922	U30825	Hs.77608	splicing factor, arginine/serine-rich 9	2.8	TM
133924	D86326	Hs.325948	vesicle docking protein p115	1.8	SS,
133929	NM_006306	Hs.211602	SMC1 (structural maintenance of chromoso	2	?
133936	L17128	Hs.77719	gamma-glutamyl carboxylase	2.6	other
133941	BE244332	Hs.77770	adaptor-related protein complex 3, mu 2	2.9	other
133959	X81789	Hs.77897	splicing factor 3a, subunit 3, 60kD	10.4	other
133976	AI908165	Hs.169946	GATA-binding protein 3 (T-cell receptor	1.9	other
133989	AL040328	Hs.78202	SWI/SNF related, matrix associated, acti	2.6	SS,
133997	AI824113	Hs.78281	regulator of G-protein signalling 12	13	other
134010	AB016092	Hs.197114	RNA binding protein; AT-rich element bin	8.8	other
134015	D31764	Hs.278569	sorting nexin 17	1.5	SS,
134070	NM_003590	Hs.78946	cullin 3	8.3	other
134110	U41060	Hs.79136	LIV-1 protein, estrogen regulated	2.7	other
134129	NM_014742	Hs.79305	KIAA0255 gene product	4.2	other
134134	H86504	Hs.173328	protein phosphatase 2, regulatory subuni	1.7	other
134200	BE569598	Hs.197803	KIAA0160 protein	2.6	other

134208	AF107463	Hs.79968	splicing factor 30, survival of motor ne	1.3	other
134219	NM_000402	Hs.80206	glucose-6-phosphate dehydrogenase	1.9	other
134234	BE300078	Hs.80449	Homo sapiens, clone IMAGE:3535294, mRNA,	10.3	SS,
134275	AI878910	Hs.3688	cisplatin resistance-associated overexpr	2.5	other
134292	AI806291	Hs.81234	immunoglobulin superfamily, member 3	1.3	TM
134301	AW502505	Hs.81360	Homo sapiens cDNA: FLJ21927 fis, clone H	1.6	TM
134305	U61397	Hs.81424	ubiquitin-like 1 (sentrin)	2.1	TM
134324	AB029023	Hs.179946	KIAA1100 protein	5.3	?
134326	AW903838	Hs.81800	chondroitin sulfate proteoglycan 2 (vers	2.5	TM
134329	N92038	Hs.81848	RAD21 (S. pombe) homolog	3.9	?
134337	NM_004922	Hs.81964	SEC24 (S. cerevisiae) related gene famil	2.4	TM
134348	AW291946	Hs.82065	interleukin 6 signal transducer (gp130,	6.8	TM
134367	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	2.3	TM
134378	X06560	Hs.82396	2',5'-oligoadenylate synthetase 1 (40-46	5.5	other
134379	AW362124	Hs.323193	hypothetical protein MGC3222	5.9	TM
134384	AI589941	Hs.8254	Homo sapiens, Similar to tumor different	2.2	other
134391	AA417383	Hs.82582	integrin, beta-like 1 (with EGF-like rep	2.1	other
134395	AA456539	Hs.8262	lysosomal	2.3	other
134405	AW067903	Hs.82772	collagen, type XI, alpha 1	72.9	other
134411	BE272095	Hs.167791	reticulocalbin 1, EF-hand calcium bindin	4.4	other
134415	AI750762	Hs.82911	protein tyrosine phosphatase type IVA, m	2.3	other
134421	AU077198	Hs.82985	collagen, type V, alpha 2	6.8	?
134424	Z44190	Hs.83023	peroxisomal biogenesis factor 11B	2.4	other
134446	AA112036	Hs.83419	KIAA0252 protein	2.9	other
134447	M58603	Hs.83428	nuclear factor of kappa light polypeptid	6.7	other
134470	X54942	Hs.83758	CDC28 protein kinase 2	2.4	other
134480	NM_005000	Hs.83916	Empirically selected from AFFX single pr	6.3	?
134485	X82153	Hs.83942	cathepsin K (pycnodysostosis)	1.9	other
134498	AW246273	Hs.84131	threonyl-tRNA synthetase	1.8	other
134513	AA425473	Hs.84429	KIAA0971 protein	1.4	other
134516	AK001571	Hs.273357	hypothetical protein FLJ10709	1.4	other
134520	BE091005	Hs.74861	activated RNA polymerase II transcriptio	5.6	other
134529	AW411479	Hs.848	FK506-binding protein 4 (59kD)	2.8	?
134577	BE244323	Hs.85951	exportin, tRNA (nuclear export receptor	1.7	other
134582	AA927177	Hs.86041	CGG triplet repeat binding protein 1	1.7	TM
134612	AW068223	Hs.171581	ubiquitin C-terminal hydrolase UCH37	2.1	other
134624	AF035119	Hs.8700	deleted in liver cancer 1	1.3	other
134632	X78520	Hs.174139	chloride channel 3	2.1	?
134654	AK001741	Hs.8739	hypothetical protein FLJ10879	2.3	other
134666	BE391929	Hs.8752	transmembrane protein 4	4	other
134687	U62317	Hs.88251	arylsulfatase A	6.2	other
134692	NM_003474	Hs.8850	a disintegrin and metalloproteinase dome	2	other
134705	BE161887	Hs.88799	anaphase-promoting complex subunit 10	1.3	SS,
134714	Y14768	Hs.890	lysosomal	7.2	?
134719	AA852985	Hs.89232	chromobox homolog 5 (Drosophila HP1 alph	3.2	other
134722	AF129536	Hs.284226	F-box only protein 6	2.5	other
134746	X07871	Hs.89476	CD2 antigen (p50), sheep red blood cell	5	other
134751	AW630603	Hs.89497	lamin B1	6.1	other
134790	BE002798	Hs.287850	integral membrane protein 1	5.6	TM
134834	AW451370	Hs.8991	adaptor-related protein complex 1, gamma	5.3	other
134850	AI701162	Hs.90207	hypothetical protein MGC11138	9.1	other
134853	BE268326	Hs.90260	5-aminoimidazole-4-carboxamide ribonucle	2.4	other
134880	AI879195	Hs.90606	15 kDa selenoprotein	2.7	other
134925	AW885909	Hs.6975	PRO1073 protein	1.5	other
134955	AW401361	Hs.91773	protein phosphatase 2 (formerly 2A), cat	4.9	other
134971	AI097346	Hs.286049	phosphoserine aminotransferase	2	other
134975	R50333	Hs.92186	Leman coiled-coil protein	2.6	TM
135011	AB037835	Hs.92991	KIAA1414 protein	1.4	?
135022	NM_000408	Hs.93201	glycerol-3-phosphate dehydrogenase 2 (mi	1.6	?
135032	AW301984	Hs.173685	hypothetical protein FLJ12619	1.4	other
135077	AW503733	Hs.9414	KIAA1488 protein	1.8	other
135083	AB036063	Hs.94262	p53-inducible ribonucleotide reductase s	2.5	other
135095	AF027219	Hs.9443	zinc finger protein 202	1.5	TM
135098	AA081258	Hs.132390	zinc finger protein 36 (KOX 18)	2.1	other
135153	AI093155	Hs.95420	JM27 protein	4.4	?
135181	BE250865	Hs.279529	px19-like protein	14.9	?
135199	AA477514	Hs.96247	transitin-associated factor X	1.3	other

135207	N26427	Hs.9634	ESTs, Highly similar to C10_HUMAN PUTATI	1.7	other
135214	T78802	Hs.96560	hypothetical protein FLJ11656	6.2	other
135243	BE463721	Hs.97101	putative G protein-coupled receptor	2.8	TM
135245	AI028767	Hs.262603	ESTs	12.2	TM
135257	AW291023	Hs.97255	ESTs, Weakly similar to A46010 X-linked	7.7	TM
135263	AI088775	Hs.55498	geranylgeranyl diphosphate synthase 1	1.8	other
135274	AA448460	Hs.112017	GE36 gene	4.2	SS,
135294	AA150320	Hs.8800	protein kinase Njmu-R1	1.2	other
135295	AI090838	Hs.98006	ESTs	4.9	other
135307	AI743770	Hs.88368	ESTs, Weakly similar to KIAA0822 protein	5.9	?
135321	AI652069	Hs.88614	ribosome binding protein 1 (dog 180kD ho	12.3	TM
135354	AA456454	Hs.183418	cell division cycle 2-like 1 (PITSLRE pr	5.8	?
135361	AA373452	Hs.167700	Homo sapiens cDNA FLJ10174 fis, clone HE	6.1	other
135389	U05237	Hs.99872	fetal Alzheimer antigen	1.9	other
135400	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	13.9	TM
302256	AA857131	Hs.171595	HIV TAT specific factor 1	1.6	other
302276	AW057738	Hs.323910	HER2 receptor tyrosine kinase (c-erb-b2,	5.3	other
303135	AW592769	Hs.279474	HSPC070 protein	2.2	TM
303686	AK000714	Hs.109441	MSTP033 protein	1.4	SS,
310085	R43191	Hs.101248	Homo sapiens clone IMAGE:32553, mRNA seq	5.2	other
315518	AA808229	Hs.167771	ESTs	2.3	?
317781	NM_007057	Hs.42650	ZW10 interactor	2.9	?
320836	AI258997	Hs.197289	rab3 GTPase-activating protein, non-cata	2	other
321114	AA902256	Hs.78979	Golgi apparatus protein 1	5.6	SS,
322221	N24236	Hs.179662	nucleosome assembly protein 1-like 1	1.4	?
322474	AF118083	Hs.29494	PRO1912 protein	1.3	other
322556	BE041451	Hs.177507	hypothetical protein	2.9	SS,
323541	AF292100	Hs.104613	RP42 homolog	1.8	other
407827	BE278431	Hs.40323	BUB3 (budding uninhibited by benzimidazo	1.8	other
408198	AL034548	Hs.43627	SRY (sex determining region Y)-box 22	1.6	other
408813	AI580090	Hs.48295	RNA helicase family	6.2	other
409176	R73727	Hs.101617	ESTs, Weakly similar to T32527 hypotheti	5.7	other
409487	H19888		gb:yn57a05.r1 Soares adult brain N2b5HB5	2.7	other
413670	AB000115	Hs.75470	hypothetical protein, expressed in osteo	2.6	?
414108	AI267592	Hs.75761	SFRS protein kinase 1	2.4	TM
414846	AW304454	Hs.77495	UBX domain-containing 1	2.4	other
416040	AW819158	Hs.289044	Homo sapiens cDNA FLJ12048 fis, clone	2.3	other
416980	AA381133	Hs.80684	high-mobility group (nonhistone chromoso	4.2	TM
417378	R57256	Hs.82037	TATA box binding protein (TBP)-associate	23.6	other
418283	S79895	Hs.83942	cathepsin K (pycnodysostosis)	5.8	other
418467	NM_006910	Hs.85273	retinoblastoma-binding protein 6	1.3	other
420269	U72937	Hs.96264	alpha thalassemia/mental retardation syn	1.6	?
420802	U22376	Hs.1334	v-myb avian myeloblastosis viral oncogen	2.3	?
421225	AA463798	Hs.102696	MCT-1 protein	1.6	?
421642	AF172068	Hs.106346	retinoic acid repressible protein	3.5	other
421828	AW891965	Hs.279789	histone deacetylase 3	5	other
421983	AI252640	Hs.110364	peptidylprolyl isomerase C (cyclophilin	3.1	TM
422052	AA302744	Hs.104518	ESTs	1.9	TM
422055	NM_014320	Hs.111029	putative heme-binding protein	2.4	other
423750	AF165883	Hs.298229	profoldin 2	4.2	?
424001	W67883	Hs.137476	paternally expressed 10 (PEG10; KIAA105	7.1	?
425182	AF041259	Hs.155040	zinc finger protein 217	2.3	other
425284	AF155568	Hs.155489	NS1-associated protein 1	3.5	other
426372	BE304680	Hs.169531	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	1.9	?
428049	AW183765	Hs.182238	GW128 protein	7.8	?
428477	AW500533	Hs.11482	splicing factor, arginine/serine-rich 11	1.7	other
437562	AB001638	Hs.5683	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	2.4	other
438449	AK001333	Hs.6216	Homo sapiens hepatocellular carcinoma-as	3.8	other
441560	F13388	Hs.7888	Homo sapiens clone 23736 mRNA sequence	5.8	other
445580	AF167572	Hs.12912	skb1 (S. pombe) homolog	2	TM
446999	AA151520	Hs.334822	hypothetical protein MGC4485	7.5	other
447111	AI017574	Hs.17409	cysteine-rich protein 1 (intestinal)	2.2	other
447778	BE620592	Hs.71190	ESTs, Weakly similar to S16508 hypotheti	2.9	other
448873	NM_003677	Hs.22393	density-regulated protein	1.8	other
449687	W68520	Hs.331328	intermediate filament protein syncoilin	5.9	other
450701	H39960	Hs.288467	Homo sapiens cDNA FLJ12280 fis, clone MA	5.7	other
450703	AA011202	Hs.184771	nuclear factor I/C (CCAAT-binding transc	1.4	other

452461	N78223	Hs.108106	transcription factor	4.8	?
452511	BE408178	Hs.285165	Homo sapiens cDNA FLJ20845 fis, clone AD	2.9	other
453157	AF077038	Hs.31989	DKFZP586G1722 protein	12.1	SS,TM
453658	BE541906	Hs.87819	Homo sapiens, clone MGC:2492, mRNA, comp	4.8	other
100585	AA328229	Hs.184582	ribosomal protein L24	1.8	TM
100690	AA383256	Hs.1657	estrogen receptor 1	1.6	other
100833	AF135168	Hs.108802	N-ethylmaleimide-sensitive factor	1.3	other
100850	AA836472	Hs.297939	cathepsin B	1.7	?
101161	NM_006262	Hs.37044	periphertn	16.9	other
102481	U50360		gb:Human calcium, calmodulin-dependent p	3.2	other
102831	AA262170	Hs.80917	adaptor-related protein complex 3, sigma	2	?
103549	BE270465	Hs.78793	protein kinase C, zeta	8	other
103749	AL135301	Hs.8768	hypothetical protein FLJ10849	1.8	other
104331	AB040450	Hs.279862	cdk inhibitor p21 binding protein	2	?
104532	AI498763	Hs.203013	hypothetical protein FLJ12748	2.1	other
104563	AL117403	Hs.306189	DKFZP434F1735 protein	1.2	other
105032	AA127818		gb:zl12a02.s1 Soares_pregnant_uterus_NbH	7	?
105039	AA907305	Hs.36475	ESTs	2.6	?
106531	AA454038	Hs.8832	ESTs	1.6	other
106977	AL043152	Hs.50421	KIAA0203 gene product	4.9	other
107298	N95657	Hs.6820	ESTs, Moderately similar to YOJ1_CAEEL H	2.5	TM
108717	AA122393	Hs.70811	hypothetical protein FLJ20516	1.3	other
110018	AW579842	Hs.104557	hypothetical protein FLJ10697	5.3	TM
110330	AI288666	Hs.16821	DKFZP434I118 protein	6.3	other
111391	NM_003896	Hs.225939	alatyltransferase 9 (CMP-NeuAcfactosyic	5.1	SS,
111392	W46342	Hs.325081	Homo sapiens, clone IMAGE:3859680, mRNA,	8.4	other
113554	AW503990	Hs.142442	HP1-BP74	3.7	TM
113722	AV653556	Hs.184411	albumin	1.3	other
115008	AK001827	Hs.87889	helicase-moi	2	other
115062	AA253314	Hs.154103	LIM protein (similar to rat protein kina	1.5	other
115121	AI634549	Hs.88155	ESTs	2.6	other
117881	AF161470	Hs.260622	butyrate-induced transcript 1	5.8	TM
119075	M10905	Hs.287820	fibronectin 1	5.7	other
119615	AL034423	Hs.75875	ubiquitin-conjugating enzyme E2 variant	1.3	other
120253	AA131376	Hs.326401	fibroblast growth factor 12B	38.9	other
125006	BE065136	Hs.145696	splicing factor (CC1.3)	2.9	?
127609	X80031	Hs.530	collagen, type IV, alpha 3 (Goodpasture	1.6	other
128868	AA419008	Hs.108730	chromosome 22 open reading frame 3	3	other
128891	F34856	Hs.292457	Homo sapiens, clone MGC:16362, mRNA, com	13.3	other
128959	AI580127	Hs.107381	hypothetical protein FLJ11200	10.9	other
129209	R62678	Hs.17820	Rho-associated, coiled-coil containing p	2.4	other
129449	AI096988	Hs.111554	ADP-ribosylation factor-like 7	8.2	TM
129453	AW974265	Hs.111632	Lsm3 protein	3.3	?
129629	AK000398	Hs.11747	hypothetical protein FLJ20391	3.9	other
129917	M30773	Hs.278540	protein phosphatase 3 (formerly 2B), reg	5.3	TM
129922	AF042379	Hs.13386	gamma-tubulin complex protein 2	4.6	other
129989	AB015856	Hs.247433	activating transcription factor 6	4	SS,
130182	BE267033	Hs.192853	ubiquitin-conjugating enzyme E2G 2 (homo	4.6	other
130365	W56119	Hs.155103	eukaryotic translation initiation factor	11	other
130471	AL121438	Hs.183706	adducin 1 (alpha)	2.7	other
130542	U64675	Hs.179825	RAN binding protein 2-like 1	7.9	other
130586	AB007891	Hs.16349	KIAA0431 protein	5.6	TM
130768	AF258627	Hs.211562	ATP-binding cassette, sub-family A (ABC1	5.2	other
130992	BE398091	Hs.74316	desmoplakin (DPI, DPII)	1.8	TM
131047	H23230	Hs.22481	ESTs, Moderately similar to A46010 X-lin	1.7	?
131135	NM_016569	Hs.267182	TBX3-iso protein	3.3	TM
131339	AF058696	Hs.25812	Nijmegen breakage syndrome 1 (nibrin)	2.6	other
131760	X76732	Hs.3164	nucleobindin 2	2.9	TM
131774	BE267158	Hs.169474	DKFZP586J0119 protein	5.6	other
131853	AI681917	Hs.3321	ESTs, Highly similar to IRX1_HUMAN IROQU	1.3	other
131881	AW361018	Hs.3383	upstream regulatory element binding prot	3.2	TM
131887	W17064	Hs.332848	SWI/SNF related, matrix associated, acti	3.2	other
132031	AF193844	Hs.3758	COP9 complex subunit 7a	5.9	?
132192	AA206153	Hs.4209	mitochondrial ribosomal protein L37	2.2	TM
132203	NM_004782	Hs.194714	synaptosomal-associated protein, 29kD	7.9	?
132240	AB018324	Hs.42676	KIAA0781 protein	4.3	other
132348	AW067708	Hs.170311	heterogeneous nuclear ribonucleoprotein	12.5	other

132528	T78736	Hs.50756	SMC4 (structural maintenance of chromoso	7.4	?	
132571	AW674699	Hs.5169	suppressor of G2 allele of SKP1, S. cere	6.9	other	
132726	N52268	Hs.55608	hypothetical protein MGC955	14.3	?	
132863	BE268048	Hs.236494	RAB10, member RAS oncogene family	10.3	other	
133016	AI439588	Hs.6289	hypothetical protein FLJ20888	4.4	other	
133053	AI065016	Hs.6390	Homo sapiens clone FLB3344 PRO0845 mRNA,	1.8	SS,TM	
133197	AI275243	Hs.180201	hypothetical protein FLJ20671	1.8	other	
133240	AK001489	Hs.242894	ADP-ribosylation factor-like 1	1.8	other	
133266	AI160873	Hs.69233	zinc finger protein	16.1	other	
133285	M76477	Hs.289082	GM2 ganglioside activator protein	10.4	SS,	
133383	BE313555	Hs.7252	KIAA1224 protein	1.5	?	
133540	AL037159	Hs.74819	proteasome (prosome, macropain) 26S subu	1.7	other	
133784	BE622743	Hs.301084	ariaptin 1	12.1	other	
133791	M34338	Hs.76244	spermidine synthase	9.7	other	
133850	W29092	Hs.7678	cellular retinoic acid-binding protein 1	4.2	SS,	
133859	U88782	Hs.178761	26S proteasome-associated pad1 homolog	2.2	other	
133881	U30872	Hs.77204	centromere protein F (350/400kD, mitosin	9.1	other	
134208	NM_000288	Hs.79993	peroxisomal biogenesis factor 7	3.2	other	
134403	AA334551	Hs.82767	sperm specific antigen 2	1.4	other	
134724	AF045239	Hs.321576	ring finger protein 22	1.4	other	
134806	AD001528	Hs.89718	spermine synthase	2.8	other	
134859	D26488	Hs.90315	KIAA0007 protein	13.3	other	
135193	X95525	Hs.96103	TATA box binding protein (TBP)-associate	3.1	other	
	AA243007		ESTs	1.6	?	
	T70541		ESTs	2.5	SS,	
	X57766		Human stromelysin-3 mRNA	4.5	other	
	S66431		Homo sapiens clone 23592 mRNA sequence	3.1	other	
	AA453483		ESTs	4.6	TM	
	R63925		ESTs	1.4	other	
	AA173417		ESTs	1.9	other	
	AA280588		ESTs	2.2	other	
	AA504223		ESTs Highly similar to CHROMOSOME	2.4	other	
	AA609996		ESTs Highly similar to Surf-4 protein [M.musculus]	5.5	?	
	F02907		ESTs	2.3	TM	
	AA480103		ESTs Weakly similar to !!!! ALU SUBFAMILY J	2.8	TM	
	AA024664		Human NADH:ubiquinone oxidoreductase subunit	6.2	other	
	AA251776		ESTs	2.3	other	
	AA399047		ESTs	2.4	other	
	N34059		EST - RC_N34059	3.3	other	
	U85367		Human GABA-A receptor pi subunit mRNA complete cds	1.7	TM	
	AA480899		ESTs	3.3	other	
	T54762		ESTs	2.9	?	
	Z41963		Homo sapiens HP protein (HP) mRNA complete cds	1.3	?	
	AA521186		ESTs	1.6	TM	
	AA400195		ESTs	1.3	other	
	AA045083		VITAMIN K-DEPENDENT GAMMA-CARBOXYLASE	2.5	other	
	AA099589		Homo sapiens mRNA for GDP dissociation inhibitor beta	1.8	TM	
	W85712		ESTs Weakly similar to PROCOLLAGEN ALPHA 2(IV	2.6	TM	
	W45728		ESTs Highly similar to HETEROGENEOUS	3.7	other	
	U61232		Human tubulin-folding cofactor E mRNA complete cds	2.1	other	
	AA425154		ESTs	5.3	other	
	T39176		ESTs Weakly similar to ZK1058.4 [C.elegans]	2.6	SS,TM	
	AA496000		ESTs	1.9	SS,	
	W38150		EST - RC_W38150	1.7	?	
	T96595		EST - RC_T96595	1.8	TM	
	AA227463		ESTs Weakly similar to No definition line found [C.elegans]	1.9	?	
	R46025		ESTs	2.8	SS,	
	AA233177		ESTs	2	other	
	AA338760		ESTs	1.3	?	
	AA412106		ESTs	6.2	other	
	L47276		EST - L47276	3.4	other	
	D82307		ESTs Weakly similar to TH1 protein [D.melanogaster]	11.4	other	
	AA293568		ESTs	1.5	other	
	R37778		ESTs	2.4	other	
	AA250843		Interferon regulatory factor 5	14.8	?	
	W49521		Human prolyl 4-hydroxylase alpha (II) subunit	6.5	?	
	D80000		Human mRNA for KIAA0178 gene partial cds	2	other	

R99978	ESTs Weakly similar to line-1 protein ORF2 [H.sapiens]	6.1	?		
AA195036	Human Ro/SSA ribonucleoprotein homolog (RoRet	5.3	?		
Z38501	ESTs Weakly similar to PROBABLE E5	1.4	other		
U37547	Human IAP homolog B (MIHB) mRNA complete cds	3.2	other		
AA479961	ESTs	1.7	other		
X57579	Inhibin beta A (activin A activin AB alpha polypeptide)		15.6	?	
AA449071	ESTs	1.3	TM		
N51855	ESTs Moderately similar to NAD(+) ADP-	1.3	other		
AA421213	ESTs Weakly similar to F28F8.3 [C.elegans]	3.2	other		
AA355201	ESTs	1.2	SS,TM		
N78717	H.sapiens mRNA for transiin	1.5	?		
N73808	ESTs	5	?		
U86782	Human 26S proteasome-associated pad1	2.2	other		
AA234817	ESTs	1.3	other		
D13666	Homo sapiens mRNA for osteoblast specific	7.5	SS,		
AA236177	ESTs	7.1	?		
U50848	Protein kinase interferon-inducible double	4.1	?		
M28211	Homo sapiens GTP-binding protein (RAB4)	2.9	other		
AA446949	ESTs	2.2	other		
W03007	ESTs	1.2	other		
W81011	ESTs	1.2	other		
W87544	ESTs	1.2	other		
X02751	Neuroblastoma RAS viral (v-ras) oncogene homolog	1.2	?		
Z14077	YY1 transcription factor	1.2	other		
Z38839	ESTs	1.2	?		
AA410894	ESTs	1.7	other		
AA504499	ESTs Highly similar to probable chloride channel 3 [H.sap	1.3	other		

TABLE 7A

Table 7 A shows the accession numbers for those pkeys lacking unigeneID's for Table 7. For each probeset, we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT number	Accession
102481	31281_-28	U50360
105032	genbank_AA127818	AA127818
409487	1134778_1	H19886 AW402806 T10231

TABLE 8: Figure 8 from BRCA 001-1 US

Table 8 shows genes upregulated in tumor tissue compared to normal breast tissue. Specifically, one column shows the ratio of expression of the indicated gene in breast tumor tissue compared to other body tissues, and another column shows the ratio of expression of the indicated gene in breast tumor tissue compared to normal breast tissue.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of tumor to normal body tissue
R2: Ratio of tumor to normal breast tissue

Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2
100075	AF152333	Hs.284160	protocadherin gamma subfamily B, 4	1	3.8
100229	AV652249	Hs.180107	polymerase (DNA directed), beta	1.7	5.3
100262	D38500	Hs.278468	postmeiotic segregation increased 2-like	0.8	4.8
100271	BE160081	Hs.256280	S100 calcium-binding protein A11 (calgiz	3.2	2.3
100355	AI907114	Hs.71465	squalene epoxidase	3.3	1.4
100522	X51501	Hs.99949	prolactin-induced protein	11.9	0.4
100552	AA019521	Hs.301946	lysosomal	3.8	1.2
100599	X77343	Hs.334334	transcription factor AP-2 alpha (activat	9.4	9.4
100676	X02761	Hs.287820	fibronectin 1	3	7.8
100690	AA383256	Hs.1657	estrogen receptor 1	4.4	4.4
100895	U01351	Hs.75772	nuclear receptor subfamily 3, group C, m	1	3.9
101046	K01160		NM_002122:Homo sapiens major histocompat	1.7	4
101086	AA382524	Hs.250959	histatin 1	0.8	4.1
101148	NM_002923	Hs.78944	regulator of G-protein signaling 2, 24k	1.2	12
101161	NM_006262	Hs.37044	periphertn	3.1	1.1
101201	L22524	Hs.2256	matrix metalloproteinase 7 (MMP7; uterin	4.4	0.6
101212	AI186220	Hs.83164	collagen, type XV, alpha 1	3.1	3.4
101441	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran	0.9	4.2
101447	M21305		gb:Human alpha satellite and satellite 3	29.9	0.3
101469	AA310162	Hs.169248	cytochrome c	0.8	4.9
101567	M33552	Hs.56729	lysosomal	1	5.9
101600	BE561617	Hs.119192	H2A histone family, member Z	2.8	4
101624	M55998		gb:Human alpha-1 collagen type I gene, 3	3.1	1.7
101674	NM_002291	Hs.82124	laminin, beta 1	1.5	4.1
101861	AA350659	Hs.83347	angio-associated, migratory cell protein	3.1	1.4
101977	AF112213	Hs.184062	putative Rab5-interacting protein	1.3	6.9
102193	AL036335	Hs.313	secreted phosphoprotein 1 (osteopontin,	1.9	4.9
102199	AA334592	Hs.79914	lumican	2.2	3.8
102304	AF015224	Hs.46452	mammaglobin 1	4.2	0.7
102345	NM_003480	Hs.300946	Microfibril-associated glycoprotein-2	1.1	4.2
102457	NM_001394	Hs.2359	dual specificity phosphatase 4	4.5	0.5
102534	U96759	Hs.198307	von Hippel-Lindau binding protein 1	1.4	4.2
102541	AI379954	Hs.79025	KIAA0096 protein	0.9	3.9
102827	BE244588	Hs.6458	chaperonin containing TCP1, subunit 2 (b	1.5	10.9
102952	R50032	Hs.159263	collagen, type VI, alpha 2	2.2	6.2
102991	AW293542	Hs.75309	eukaryotic translation elongation factor	5.6	5.7
103119	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	3.7	0.5
103175	X69089	Hs.79227	myomesin (M-protein) 2 (165kD)	1.3	4
103286	D38616	Hs.54941	phosphorylase kinase, alpha 2 (liver)	1.3	3.8
103319	X83492	Hs.82359	tumor necrosis factor receptor superfami	0.8	4.6
103372	BE536700	Hs.4688	seryl-tRNA synthetase	0.9	8
103419	T34708	Hs.272927	Sec23 (S. cerevisiae) homolog A	1.1	5.1
103471	Y00815	Hs.75216	protein tyrosine phosphatase, receptor t	3.7	1.2
103546	Z14244	Hs.75752	cytochrome c oxidase subunit VIIb	0.9	4.4

103658	NM_000088	Hs.172928	collagen, type I, alpha 1	3.2	3	
103758	AA084874		gb:zn13e04.r1 Stratagene hNT neuron (937	0.9	10	
103774	H24185	Hs.92918	hypothetical protein	1.9	15.9	
103821	AA095971	Hs.198783	Homo sapiens cDNA: FLJ22463 fis, clone H	1.2	3.9	
103869	BE439604	Hs.24322	ATPase, H+ transporting, lysosomal (vacu	1.4	3.9	
103980	AW130242	Hs.293476	hypothetical protein FKSG44	1.6	4.1	
104054	AK001913	Hs.7100	hypothetical protein	1.5	4.3	
104115	AF183810	Hs.26102	opposite strand to trichorhinophalangeal	7	7	
104189	AB040927	Hs.301804	KIAA1494 protein	2	4.6	
104230	AB002347	Hs.15303	KIAA0349 protein	0.7	4.5	
104278	AW563693	Hs.109253	N-terminal acetyltransferase complex ard	3.3	3.3	
104295	AW365522	Hs.103657	hypothetical protein PRO2219	2.3	4.2	
104319	AW804296	Hs.9950	Sec61 gamma	3.1	7	
104425	AF283775	Hs.35380	x 001 protein	4	1.3	
104432	X51501	Hs.99949	prolactin-induced protein	3.8	0.6	
104464	AW966728	Hs.54642	methionine adenosyltransferase II, beta	0.8	6.7	
104479	AK001731	Hs.106390	Homo sapiens mRNA; cDNA DKFZp586H0924 (I	1.7	4.8	
104505	W94824	Hs.11565	RIKEN cDNA 2010100O12 gene	2	7.5	
104592	AW630488	Hs.325820	protease, serine, 23	1.9	7.4	
104613	AF123303	Hs.24713	hypothetical protein	1.1	6.3	
104636	R82252	Hs.106106	protein kinase (cAMP-dependent, catalyt	1.2	4	
104782	AW270555	Hs.171774	hypothetical protein	1.4	3.9	
104792	AA960961	Hs.305953	zinc finger protein 83 (HPF1)	1.5	4.2	
104848	AA305351	Hs.274369	uncharacterized hypothalamus protein HAR	1.1	4.1	
104849	AI279065	Hs.241507	ribosomal protein S6	1.3	4.6	
104850	AL133035	Hs.8728	hypothetical protein DKFZp434G171	1.2	3.6	
104852	W70164	Hs.20107	ESTs	0.8	4.2	
104861	AA058630	Hs.29759	RNA POLYMERASE I AND TRANSCRIPT RELEASE	1.7	5.1	
104873	W03831	Hs.20597	host cell factor homolog	0.8	5.4	
104891	W44626	Hs.30627	ESTs	0.7	6.8	
104920	AW965089	Hs.306083	Novel human gene mapping to chomosome 22		1	3.9
104926	BE298808	Hs.33363	DKFZP434N093 protein	3.3	3.3	
104952	AW076098	Hs.74316	desmoplakin (DPI, DPII)	1.2	3.7	
104963	AB029020	Hs.173694	KIAA1097 protein	1.1	5.5	
104977	AI392640	Hs.18272	amino acid transporter system A1	3.2	1.4	
105030	BE613061	Hs.337772	Homo sapiens, Similar to RIKEN cDNA 0610	1.6	11.4	
105035	N39760	Hs.8859	Homo sapiens, Similar to RIKEN cDNA 5830	1.5	7.2	
105068	BE410438	Hs.9006	VAMP (vesicle-associated membrane protei	1.1	3.5	
105159	AF146277	Hs.265561	CD2-associated protein	1.2	10	
105178	AA313825	Hs.21941	AD036 protein	3.6	8.3	
105182	BE407961	Hs.18271	golgi phosphoprotein 3	1.7	6.8	
105274	AI554929	Hs.281866	ATPase, H+ transporting, lysosomal (vacu	1.1	3.7	
105303	BE243327	Hs.182626	chromosome 22 open reading frame 5	1.5	4	
105413	AI015709	Hs.172089	Homo sapiens mRNA; cDNA DKFZp586I2022 (I	1.5	14	
105426	W20027	Hs.23439	ESTs	4.3	2.9	
105432	W03516	Hs.76698	stress-associated endoplasmic reticulum	1.5	5	
105443	AA252372	Hs.12144	KIAA1033 protein	1.2	3.6	
105483	AL137257	Hs.23458	Homo sapiens cDNA: FLJ23015 fis, clone L	1.7	15.8	
105492	AI805717	Hs.289112	CGI-43 protein	2	4.8	
105495	AL037715	Hs.28785	microfibrillar-associated protein 3	1.3	3.9	
105539	AB040884	Hs.109694	KIAA1451 protein	2.7	11.4	
105594	AB024334	Hs.25001	tyrosine 3-monooxygenase/tryptophan 5-mo	1.3	6.1	
105623	BE504200	Hs.30127	hypothetical protein	1.7	4.5	
105807	AA788946	Hs.16889	ESTs, Moderately similar to CA1C RAT COL	3.9	24.6	
105812	BE614149	Hs.20814	CGI-27 protein	1.8	3.6	
105823	AI559444	Hs.293960	ESTs	1.9	6.6	
105831	AA329449	Hs.247302	twisted gastrulation	1.5	4.3	
105851	AI827976	Hs.24391	hypothetical protein FLJ13612	3.8	1.9	
105879	BE392914	Hs.30503	Homo sapiens cDNA FLJ11344 fis, clone PL	1.7	4	
105918	AW028485	Hs.26136	hypothetical protein MGC14156	1.7	7.4	
105939	AL137728	Hs.12258	Homo sapiens mRNA; cDNA DKFZp434B0920 (I	1.2	3.8	
105941	AB033075	Hs.10669	development and differentiation enhancin	1.3	4.6	
105969	AB030656	Hs.17377	coronin, actin-binding protein, 1C	1.1	5.9	
105990	AI690586	Hs.29403	hypothetical protein FLJ22060	2	4.6	
106012	AI240655	Hs.8895	ESTs	4.1	1.2	
106060	NM_001329	Hs.171391	C-terminal binding protein 2	2.6	7	
106070	T74445	Hs.5957	Homo sapiens clone 24416 mRNA sequence	1.4	10.7	

106083	H62087	Hs.31659	thyroid hormone receptor-associated prot	1.5	3.6	
106155	AA425414	Hs.33287	nuclear factor I/B	5.4	1.2	
106255	BE613206	Hs.279607	calpastatin	1.8	4	
106414	BE568205	Hs.28827	mitogen-activated protein kinase kinase	5.1	6.1	
106538	AK000274	Hs.278635	HDCMA18P protein	1.2	5.9	
106568	AW051564	Hs.28285	patched related protein translocated in	1.8	5.4	
106574	BE044325	Hs.227280	U6 snRNA-associated Sm-like protein	2.3	11.2	
106613	N38604	Hs.30212	thyroid receptor interacting protein 15	1.2	3.6	
106617	H09548	Hs.5367	ESTs, Weakly similar to I38022 hypotheti	0.9	4.4	
106619	AA459480	Hs.23956	hypothetical protein FLJ20502	1.3	3.6	
106701	BE387614	Hs.25797	splicing factor 3b, subunit 4, 49kD	1.6	7.3	
106721	AA741038	Hs.6570	ESTs	1.7	6.1	
106776	AA208079	Hs.6693	hypothetical protein FLJ20420	1	5.4	
106866	AA487416	Hs.268231	Homo sapiens cDNA: FLJ23111 fis, clone L	1.6	5.4	
106868	BE185536	Hs.301183	molecule possessing ankyrin repeats indu	3.3	1.2	
106887	BE503373	Hs.334335	hypothetical protein FLJ13576	1.4	6.3	
106940	T85594	Hs.339808	hypothetical protein FLJ10120	3.3	1.8	
106968	AF216751	Hs.26813	CDA14	3	3	
107052	BE391904	Hs.12482	glyceronephosphate O-acyltransferase	1.7	7.6	
107061	BE147611	Hs.6354	stromal cell derived factor receptor 1	1.2	4.3	
107149	AI289507	Hs.299883	hypothetical protein FLJ23399	1.8	6.5	
107222	BE172058	Hs.82689	tumor rejection antigen (gp96) 1	1.2	6.9	
107233	BE267795	Hs.22595	hypothetical protein FLJ10837	1.4	3.5	
107295	AA186629	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp	2.6	4.3	
107679	AA011510	Hs.60512	ESTs	1.8	4	
107914	AA027229	Hs.61329	ESTs, Weakly similar to T16370 hypotheti	1.3	3.5	
107965	AF109219	Hs.108787	phosphatidylinositol glycan, class N	1.6	3.5	
108033	AW368993	Hs.323748	Homo sapiens clone CDABP0086 mRNA sequen	1.8	8.1	
108060	AA291440	Hs.73149	paired box gene 6	1.1	3.5	
108081	AA093668	Hs.28578	muscleblind (Drosophila)-like	0.7	5.8	
108137	AI283611	Hs.283479	ESTs, Weakly similar to HMG1_HUMAN HIGH		1.2	6.6
108186	AW058579	Hs.7780	Homo sapiens mRNA; cDNA DKFZp564A072 (fr		3.1	6.9
108215	AI879238	Hs.299315	collapsin response mediator protein-5; C	1.5	4.6	
108297	AA333660	Hs.71331	hypothetical protein MGC5350	1.5	4	
108339	AW151340	Hs.51615	ESTs, Weakly similar to ALU7_HUMAN ALU S		6.3	4.7
108371	AA074374	Hs.67639	ESTs	1.3	3.8	
108399	AF086070	Hs.237519	EST	1	3.6	
108469	AA079487		gb:zm97f08.s1 Stratagene colon HT29 (937	1.5	3.6	
108470	AA079500		gb:zm96h10.s1 Stratagene colon HT29 (937	1.1	4.3	
108564	M23114	Hs.1526	ATPase, Ca++ transporting, cardiac muscl	2	4.9	
108641	AA112059	Hs.429	ATP synthase, H+ transporting, mitochond	1.1	3.5	
108668	AA058522	Hs.185751	ESTs	1.2	3.6	
108694	AA036725	Hs.61847	ESTs	1.4	3.8	
108824	AK001332	Hs.44672	hypothetical protein FLJ10470	1.4	3.5	
108863	AA133456	Hs.102548	glucocorticoid receptor DNA binding fact	1.2	4	
108893	BE276891	Hs.194691	retinoic acid induced 3	1.3	3.6	
108992	AA152312	Hs.72047	ESTs	1.1	4.1	
109072	AI732585	Hs.22394	hypothetical protein FLJ10893	1.2	3.5	
109097	AA167512		gb:zp10f12.s1 Stratagene fetal retina 93	1.3	5	
109160	BE220601	Hs.301997	hypothetical protein FLJ13033	4	6.1	
109244	BE179030	Hs.84239	Human DNA sequence from clone RP5-1174N9		1.7	7.4
109481	AA878923	Hs.289069	hypothetical protein FLJ21016	3.8	7.7	
109484	AA368263	Hs.72531	hypothetical protein FLJ11838	1.9	4	
109795	AA173942	Hs.326418	Homo sapiens mRNA; cDNA DKFZp564H1916 (I	3.7	1.3	
110009	BE075297	Hs.8614	ESTs, Weakly similar to A43932 mucin 2 p	4.6	7.4	
110107	AW151660	Hs.31444	ESTs	1.2	3.5	
110411	AW001579	Hs.9645	Homo sapiens mRNA for KIAA1741 protein,	3.7	3.3	
110731	NM_014899	Hs.188006	KIAA0878 protein	2.8	3.7	
110758	N21207	Hs.182999	ESTs	1.6	3.5	
110930	BE242691	Hs.14947	ESTs	3.1	1.2	
110935	AI753230	Hs.323562	hypothetical protein DKFZp564K142	1.9	7.5	
111051	AI681293	Hs.12186	hypothetical protein FLJ22558	2	4	
111110	AK001568	Hs.23618	hypothetical protein FLJ10704	1.1	3.8	
111356	BE301671	Hs.4867	mannosyl (alpha-1,3-)-glycoprotein beta-	1	8.2	
111357	BE314949	Hs.87128	hypothetical protein FLJ23309	3.3	6.1	
111770	R27975	Hs.269401	ESTs, Moderately similar to S65657 alpha	1.2	5.4	
111900	AF131784	Hs.25318	Homo sapiens clone 25194 mRNA sequence	3.2	0.8	

111903	NM_014906	Hs.166351	KIAA1072 protein	1	5.4	
111951	NM_014927	Hs.100527	KIAA0902 protein	1	3.8	
112141	AW137198	Hs.278682	Phosphatidylglycerophosphate Synthase	1.4	3.5	
112193	R49499	Hs.138238	ESTs	1.5	3.6	
112197	NM_003655	Hs.5637	ESTs	4.6	2	
112610	AW500106	Hs.23643	serine/threonine protein kinase MASK	3.3	10.5	
112971	Z42387	Hs.83885	transmembrane, prostate androgen induced	3.2	3	
112984	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	3.7	10.8	
113056	AF019226	Hs.8036	glioblastoma overexpressed	4.5	3.7	
113449	AW160683	Hs.158006	hypothetical protein	1.2	4.4	
113497	AF143321	Hs.15572	hypothetical protein IMAGE 109914	0.9	3.6	
113508	AL042936	Hs.211571	holocytochrome c synthase (cytochrome c	1.1	3.5	
113531	AK001898	Hs.16740	hypothetical protein FLJ11036	1.2	3.9	
113604	AI075407	Hs.296083	ESTs, Moderately similar to I54374 gene	1.7	5.3	
113674	NM_014214	Hs.5753	inositol(myo)-1(or 4)-monophosphatase 2	0.8	6.1	
113841	W30681	Hs.146233	Homo sapiens cDNA: FLJ22130 fis, clone H	1.7	6.2	
113857	AW243158	Hs.5297	DKFZP564A2418 protein	1.2	4.6	
113931	BE255499	Hs.3498	hypothetical protein MGC15749	1.5	4	
113936	W17056	Hs.83623	nuclear receptor subfamily 1, group I, m	3.8	1	
113987	AA345519	Hs.9641	complement component 1, q subcomponent,	1.2	4.7	
114132	AI342493	Hs.24192	Homo sapiens cDNA FLJ20767 fis, clone CO	0.3	4.3	
114156	BE179882	Hs.336920	glutathione peroxidase 3 (plasma)	1.1	4.3	
114213	N58309	Hs.19575	CGI-11 protein	1.6	9.2	
114638	AA075488		gb:zm88d01.s1 Stratagene ovarian cancer	1.6	3.7	
114760	AI929382	Hs.252692	hypothetical protein FLJ20343	1.4	4	
114781	T10446	Hs.95388	ESTs	1	4.3	
114795	AB037858	Hs.173484	hypothetical protein FLJ10337	1.6	9.2	
114901	AV660012	Hs.196437	hypothetical protein FLJ10788	1.4	5.2	
115096	AI683089	Hs.175319	ESTs	3.7	1	
115518	BE541042	Hs.23240	Homo sapiens cDNA: FLJ21848 fis, clone H	3.2	4.2	
115646	N36110	Hs.305971	solute carrier family 2 (facilitated glu	1.5	3.9	
115764	AW582258	Hs.91011	anterior gradient 2 (Xenopus laevis) hom	1.3	5.9	
115802	AW410233	Hs.206521	YME1 (S.cerevisiae)-like 1	1.7	6.6	
115994	AB037836	Hs.109315	KIAA1415 protein	1.5	9.1	
116032	BE383658	Hs.42484	hypothetical protein FLJ10618	0.9	4.3	
116048	BE395293	Hs.94491	hypothetical protein FLJ20297	1.6	5.5	
116274	AI129767	Hs.182874	guanine nucleotide binding protein (G pr	3.2	2.4	
116310	Z24854	Hs.42299	ESTs	0.8	4.7	
116356	AI371223	Hs.288671	Homo sapiens cDNA FLJ11997 fis, clone HE	2.4	3.9	
116429	AF191018	Hs.279923	putative nucleotide binding protein, est	5.5	5.5	
116461	AA313607	Hs.58633	Homo sapiens cDNA: FLJ22145 fis, clone H	5	1.3	
116470	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	8.7	4.5	
116578	D21262	Hs.75337	nucleolar and coiled-body phosphprotein	3.2	8.9	
116579	AW388411	Hs.81915	leukemia-associated phosphoprotein p18 (	3.2	3	
116589	AI557212	Hs.17132	ESTs, Moderately similar to I54374 gene	3.1	8.3	
116786	H25836	Hs.301527	ESTs, Moderately similar to unknown [H.s	3.2	4.5	
117170	N25929	Hs.42500	ADP-ribosylation factor-like 5	7	5.5	
117215	N20068	Hs.133207	PTPRF interacting protein, binding prote	1.2	6.2	
117280	M18217	Hs.172129	Homo sapiens cDNA: FLJ21409 fis, clone C	4.5	2.4	
117576	AI383467	Hs.44597	ESTs	1.4	4.2	
117667	U59305	Hs.44708	Ser-Thr protein kinase related to the my	4.3	0.5	
117881	AF161470	Hs.260622	butyrate-induced transcript 1	2.1	5.7	
118338	BE327311	Hs.47166	HT021	3.6	7.7	
118475	N56845		gb:za48c11.s1 Soares fetal liver spleen	4.2	0.5	
118493	AL353944	Hs.50115	Homo sapiens mRNA; cDNA DKFZp761J1112 (f	3.5	3.3	
118505	N67343		gb:yz50b07.s1 Morton Fetal Cochlea Homo	2.1	3.8	
119159	AF142419	Hs.15020	homolog of mouse quaking QKI (KH domain	3.7	1.5	
119307	BE048061	Hs.37054	ephrin-A3	3	1.1	
119355	BE218319	Hs.5807	GTPase Rab14	1.1	5.6	
119452	BE041667	Hs.314544	Homo sapiens cervical cancer suppressor-	1.4	4.3	
119771	AI905687	Hs.2533	EST	3.2	1	
119940	AL050097	Hs.272531	DKFZP586B0319 protein	4.3	0.7	
119943	BE565849	Hs.14158	copine III	3.5	1.9	
120407	AA235207	Hs.250456	hypothetical protein DKFZp762F2011	1.5	3.7	
120493	AW968080	Hs.152939	Homo sapiens clone 24630 mRNA sequence	4	1.4	
120877	AF150208	Hs.108327	damage-specific DNA binding protein 1 (1	1.6	6.8	
120887	AA350781	Hs.96987	ESTs	1.1	3.6	

121368	BE262956	Hs.178292	KIAA0180 protein	1.5	4.1	
121603	AA416785	Hs.249495	heterogeneous nuclear ribonucleoprotein	2.2	5.5	
121723	AA243499	Hs.104800	hypothetical protein FLJ10134	3.4	3.2	
122223	AF169797	Hs.27413	adaptor protein containing pH domain, PT	3.9	3.9	
122378	AB032948	Hs.21356	hypothetical protein DKFZp762K2015	1.4	7.1	
122946	AI718702	Hs.308026	major histocompatibility complex, class	1.4	3.7	
123155	AF121856	Hs.284291	sorting nexin 6	1.2	4.9	
123158	AF161426	Hs.218329	hypothetical protein	2.4	3.6	
123327	AA421581	Hs.178443	ESTs	0.9	5.2	
123495	W28673	Hs.106747	serine carboxypeptidase 1 precursor prot	1.3	5.1	
123526	AA608657		gb:ae55d04.s1 Stratagene lung carcinoma	2.1	5.2	
123533	AA608751		gb:ae56h07.s1 Stratagene lung carcinoma	2.1	9.3	
123768	AI932318	Hs.188762	ESTs, Moderately similar to H2BL_HUMAN H	1.1	3.6	
123961	AL050184	Hs.21810	DKFZP434B203 protein	1.1	3.5	
123999	AF084555	Hs.7351	cyclic AMP phosphoprotein, 19 kD	1.4	3.8	
124000	BE563957	Hs.74861	activated RNA polymerase II transcriptio	1.9	11.2	
124038	AB037860	Hs.173933	nuclear factor I/A	1.5	4.4	
124059	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypothet	14.8	11.5	
124083	AW195237	Hs.7734	hypothetical protein FLJ22174	1.2	6.2	
124148	BE300094	Hs.227751	lectin, galactoside-binding, soluble, 1	2.5	12.7	
124153	AU077333	Hs.160483	erythrocyte membrane protein band 7.2 (s	1	4.1	
124252	BE613340	Hs.334725	Homo sapiens, Similar to RIKEN cDNA 9430	1.5	8.4	
124314	AK001552	Hs.215766	GTP-binding protein	1.8	10.2	
124375	D87454	Hs.192966	KIAA0265 protein	1.1	4.8	
124432	N39016	Hs.268869	ESTs, Weakly similar to ALUC_HUMAN !!!!	1.3	4.1	
124447	N48000		gb:yy98e12.s1 Soares_multiple_sclerosis_	2.7	4.3	
124539	D54120	Hs.148409	cell division cycle 42 (GTP-binding prot	2.1	5.7	
124543	AI393320	Hs.104573	ESTs	1	4.1	
124564	H68409	Hs.108275	ESTs	1.4	4	
124574	AL036596	Hs.42322	A kinase (PRKA) anchor protein 2	0.7	4	
124605	AA749315	Hs.77171	minichromosome maintenance deficient (S.	1.1	3.5	
124639	H60193	Hs.21143	DKFZP586C1324 protein	1.4	3.6	
124659	AI680737	Hs.289068	Homo sapiens cDNA FLJ11918 fis, clone HE	1.5	9.9	
124737	BE270465	Hs.78793	protein kinase C, zeta	0.7	4	
124760	AW408586	Hs.91052	ESTs, Moderately similar to ALU5_HUMAN A	0.9	3.6	
124763	BE410405	Hs.76288	calpain 2, (m/II) large subunit	1.3	3.9	
124792	R44357	Hs.48712	hypothetical protein FLJ20736	1.6	4.2	
124842	R56485		gb:yg93h09.s1 Soares infant brain 1NIB H	1	3.6	
124940	AF068848	Hs.103804	heterogeneous nuclear ribonucleoprotein	3.2	3.4	
124949	AI903210	Hs.336780	tubulin, beta polypeptide	1	4.4	
124960	AL023513	Hs.194766	seizure related gene 6 (mouse)-like	0.9	5.2	
124995	T52700	Hs.110044	ESTs	0.9	3.5	
125030	AA610577	Hs.187775	ESTs	1.2	5	
125034	BE548446	Hs.5187	Homo sapiens mRNA; cDNA DKFZp434F152 (fr	1.5	3.7	
125058	T83731	Hs.3343	phosphoglycerate dehydrogenase	0.9	6	
125076	AA973971		gb:oq02h08.s1 NCI_CGAP_Lu5 Homo sapiens	1	3.7	
125090	T91518		gb:ye20i05.s1 Stratagene lung (937210) H	3.2	2.5	
125103	AA570056	Hs.122730	ESTs, Moderately similar to KIAA1215 pro	5.3	6.6	
125154	W38419		gb:zc78a07.s1 Pancreatic Islet Homo sapi	0.9	6.1	
125155	AA837043	Hs.143669	ESTs	1.1	4.3	
125159	AK000669	Hs.274428	TRF2-interacting telomeric RAP1 protein	1.1	4.1	
125170	AL020996	Hs.8518	selenoprotein N	1.1	3.8	
125181	R40815	Hs.12396	ESTs, Weakly similar to 2004399A chromos	1	3.6	
125193	W87577	Hs.84298	CD74 antigen (invariant polypeptide of m	1.2	7.8	
125260	H05635	Hs.294030	topoisomerase-related function protein 4	1	4.9	
125262	AW884980	Hs.171957	triple functional domain (PTPRF interact	1.3	4.8	
125272	BE612888	Hs.180224	myosin regulatory light chain	1.1	16.1	
125388	W27235	Hs.64311	a disintegrin and metalloproteinase doma	1.4	5.3	
125824	Z45258	Hs.286013	short coiled-coil protein	2.4	8.7	
125852	AW630088	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (f	1.8	4.6	
125970	AW504721	Hs.177516	high density lipoprotein binding protein	1.9	3.8	
126192	AW160399	Hs.30376	hypothetical protein	1.4	4.1	
126469	BE384361	Hs.182885	ESTs, Weakly similar to JC5024 UDP-galac	2	3.7	
126510	AA057593	Hs.334762	hypothetical protein FLJ14735	1.3	4.1	
127095	AA340277	Hs.10248	Homo sapiens cDNA FLJ20167 fis, clone CO	1.3	5	
127524	AI243596	Hs.94830	ESTs, Moderately similar to T03094 A-kin	4.3	0.9	
128312	J04182	Hs.150101	lysosomal	1.5	4.7	

128453	X02761	Hs.287820	fibronectin 1	1.2	4.3
128460	T16206	Hs.237164	ESTs, Highly similar to LDHH_HUMAN L-LAC	3.1	44.4
128491	H08379	Hs.165563	hypothetical protein DKFZp434N1429	0.6	13.1
128495	NM_005904	Hs.100602	MAD (mothers against decapentaplegic, Dr	1.3	4
128548	NM_003478	Hs.101299	cullin 5	1	5.1
128574	AI185977	Hs.38260	ubiquitin specific protease 18	0.8	4
128611	NM_014721	Hs.102471	KIAA0580 gene product	1.3	3.7
128652	AA432202	Hs.103147	hypothetical protein FLJ21347	1.4	3.9
128653	D87432	Hs.10315	solute carrier family 7 (cationic amino	1.2	3.6
128655	AI246669	Hs.324275	WW domain-containing protein 1	0.8	4.1
128684	BE248444	Hs.283685	hypothetical protein FLJ20396	3	1.6
128717	AK001564	Hs.104222	hypothetical protein FLJ10702	2.8	4.8
128774	AA476220	Hs.54457	CD81 antigen (target of antiproliferativ	1.1	10.6
128780	AF026692	Hs.105700	secreted frizzled-related protein 4	1	3.8
128805	AA194554	Hs.183434	ATPase, H+ transporting, lysosomal (vacu	5.3	5.3
128827	AI638184	Hs.106334	Homo sapiens clone 23836 mRNA sequence	2.2	5.3
128840	AI917602	Hs.106440	ESTs	1	4.5
128869	AA768242	Hs.80618	hypothetical protein	0.8	3.6
128889	D60985	Hs.106909	DKFZP566D193 protein	4.6	3.7
128890	AI222020	Hs.182364	CocoaCrisp	3	1.5
128915	AK000140	Hs.107139	hypothetical protein	0.2	3.9
128920	AA622037	Hs.166468	programmed cell death 5	2.5	15.2
128926	AF155096	Hs.107213	hypothetical protein FLJ20585	4	4
128930	AA298958	Hs.10724	MDS023 protein	1.2	4.5
128942	AW247536	Hs.10729	hypothetical protein	1.4	5
128948	AW953622	Hs.223025	RAB31, member RAS oncogene family	2.3	5.6
128953	AB020716	Hs.107362	KIAA0909 protein	0.9	3.9
128979	AW271217	Hs.281434	Homo sapiens cDNA FLJ14028 fis, clone HE	1.5	3.6
128980	AA258924	Hs.10758	NM_002495*:Homo sapiens NADH dehydrogena	0.8	3.8
129005	AI770025	Hs.13323	hypothetical protein FLJ22059	1.2	5.7
129009	C15105	Hs.330716	Homo sapiens cDNA FLJ14368 fis, clone HE	2.1	9.9
129013	AA371158	Hs.107942	DKFZP564M112 protein	2.4	3.8
129068	AI634522	Hs.152925	KIAA1268 protein	1.2	3.8
129106	AW504486	Hs.108689	sterol regulatory element binding transc	1.2	5.5
129113	BE543205	Hs.288771	DKFZP586A0522 protein	0.5	3.7
129125	AB002450	Hs.278391	CGI-109 protein	1	5.2
129126	AW881089	Hs.108806	Homo sapiens mRNA; cDNA DKFZp566M0947 (f	1.5	7
129151	N23018	Hs.171391	C-terminal binding protein 2	2.1	9.7
129230	AA335362	Hs.109646	Empirically selected from AFFX single pr	0.9	8.6
129234	M18916	Hs.282997	glucosidase, beta; acid (includes glucos	1.1	3.5
129238	BE542214	Hs.109697	ESTs	1.1	12.8
129239	W57656	Hs.109701	ubiquitin-like 5	3.2	5.1
129241	AI878857	Hs.109706	hematological and neurological expressed	1.9	5.7
129243	BE169531	Hs.109727	TAK1-binding protein 2; KIAA0733 protein	1.2	6.6
129247	R49920	Hs.109733	CGI-131 protein	1.5	3.5
129250	AA344367	Hs.109760	Empirically selected from multiple AFFX	1	5.4
129258	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-l	1.3	4.1
129260	AF077200	Hs.279813	hypothetical protein	1.6	3.9
129270	AA357185	Hs.109918	ras homolog gene family, member H	1.8	4.2
129277	AB007896	Hs.110	putative L-type neutral amino acid trans	1.1	6.1
129284	AA318224	Hs.296141	ESTs	2.5	4.8
129300	W94197	Hs.110165	ribosomal protein L26 homolog	1.6	5.1
129318	AF189062	Hs.285976	tumor metastasis-suppressor	1.8	6.5
129352	AW511656	Hs.170177	Mels1 (mouse) homolog	0.9	4
129362	U30246	Hs.110736	solute carrier family 12 (sodium/potassi	1.4	9.2
129379	BE278984	Hs.11085	CGI-111 protein	1	4.8
129390	AA318271	Hs.250905	hypothetical protein	1	4.1
129416	AA018188	Hs.111244	hypothetical protein	1.8	10.7
129427	AI498631	Hs.111334	ferritin, light polypeptide	1.1	4.8
129470	W92931	Hs.250899	heat shock factor binding protein 1	1.8	9.3
129472	AL050260	Hs.323817	DKFZP547E1010 protein	1	5
129475	NM_004477	Hs.203772	FSHD region gene 1	1.1	4.2
129498	AA449789	Hs.75511	connective tissue growth factor	1.9	6.6
129501	AI631811	Hs.180403	STRIN protein	1.1	9.7
129527	AA769221	Hs.270847	delta-tubulin	1.1	4.3
129545	R18087	Hs.323769	cisplatin resistance related protein CRR	1	4.2
129579	AW517695	Hs.285218	junctional adhesion molecule 1	2.3	3.5

129606	AW968941	Hs.166254	hypothetical protein DKFZp566I133	2.4	4.4
129619	AA209534	Hs.284243	tetraspan NET-6 protein	3.2	13
129620	D79338	Hs.239720	CCR4-NOT transcription complex, subunit	1.6	4.6
129621	AL110212	Hs.301005	purine-rich element binding protein B	1.1	5.7
129634	AB020335	Hs.181300	sel-1 (suppressor of lin-12, C.elegans)-	0.9	4.3
129663	AI207406	Hs.11866	translocase of inner mitochondrial membr	1.9	4.8
129679	AW889132	Hs.11916	ribokinase	0.9	4.1
129688	U53209	Hs.24937	transformer-2 alpha (htra-2 alpha)	1.3	4.7
129691	M26939	Hs.119571	collagen, type III, alpha 1 (Ehlers-Dan	4.7	3.7
129712	U46386	Hs.12102	sorting nexin 3	1.2	3.6
129747	AL050272	Hs.12305	DKFZP566B183 protein	1	8.9
129788	BE397454	Hs.124969	Homo sapiens clone 24707 mRNA sequence	1.4	3.6
129796	BE218319	Hs.5807	GTPase Rab14	2.9	5.1
129797	M62839	Hs.1252	apolipoprotein H (beta-2-glycoprotein I)	0.3	5.1
129800	AF052112	Hs.12540	lysosomal	1.6	8.8
129834	AL080084	Hs.298155	CGI-100 protein	0.9	5.3
129836	AW410233	Hs.206521	YME1 (S.cerevisiae)-like 1	1.8	9.9
129843	NM_014840	Hs.200598	KIAA0537 gene product	0.9	3.6
129874	AA626837	Hs.181551	hypothetical protein MGC2594	1.4	9.5
129878	Z43161	Hs.283714	30 kDa protein	1.1	6.3
129904	AL119499	Hs.13285	neuronal potassium channel alpha subunit	1	3.5
129917	M30773	Hs.278540	protein phosphatase 3 (formerly 2B), reg	2	5.1
129976	X14008	Hs.234734	lysosomal	0.9	4.9
129982	Z14221		gb:H.sapiens germline transcript of Ig h	1.2	3.8
130007	R15917	Hs.142570	Homo sapiens clone 24629 mRNA sequence	4.3	1.3
130060	BE277024	Hs.146381	RNA binding motif protein, X chromosome	1.6	3.8
130064	X57815.comp		Empirically selected from AFFX single pr	1.2	8.2
130068	M93143	Hs.262869	plasminogen-like	1.4	7.9
130090	H97878	Hs.132390	zinc finger protein 38 (KOX 18)	1.4	12.3
130095	AK001635	Hs.14838	hypothetical protein FLJ10773	0.2	4.6
130102	W61005	Hs.14898	DHHC1 protein	1	4.1
130112	AA916785	Hs.180610	splicing factor proline/glutamine rich (	1.2	5.3
130115	T47294	Hs.149923	X-box binding protein 1	3.8	0.8
130123	NM_005095	Hs.150390	zinc finger protein 262	1	4.2
130150	BE094846	Hs.15113	homogentisate 1,2-dioxygenase (homogenti	0.5	4
130161	R42678	Hs.151385	KIAA0564 protein	1	3.7
130210	M23115	Hs.1526	ATPase, Ca++ transporting, cardiac muscl	0.4	4.4
130213	BE278370	Hs.15265	heterogeneous nuclear ribonucleoprotein	1.7	7.5
130215	BE301883	Hs.152707	glioblastoma amplified sequence	1	6.6
130232	U29463		gb:Human cytochrome b561 gen	1.2	4.2
130252	U92014	Hs.153527	Homo sapiens pTM5 mariner-like transposo	1.3	3.6
130281	W78907	Hs.15395	similar to arginyl-tRNA synthetase (arg)	1.5	4.4
130343	AB040914	Hs.278628	KIAA1481 protein	2.9	7.5
130385	AW067800	Hs.155223	stanniocalcin 2	3.2	0.2
130414	AW842182	Hs.241392	small inducible cytokine A5 (RANTES)	1.4	10.6
130417	AW163518	Hs.155485	huntingtin interacting protein 2	1.7	11.7
130440	AA852868	Hs.132853	KIAA0171 gene product	1.1	5
130442	NM_006245	Hs.118244	protein phosphatase 2, regulatory subuni	1.4	4.3
130465	AW362955	Hs.15641	Homo sapiens cDNA FLJ14415 fis, clone HE	1.6	7.6
130479	R44163	Hs.12457	hypothetical protein FLJ10814	0.9	4.1
130499	AB007915	Hs.158286	KIAA0446 gene product	1	3.8
130546	AI598022	Hs.193589	TAR DNA binding protein	1.3	4.7
130568	AA232119	Hs.16085	putative G-protein coupled receptor	1.2	9.4
130606	AI652143	Hs.288382	hypothetical protein FLJ13111	1	4.1
130612	BE242873	Hs.16677	WD repeat domain 15	1.1	3.6
130616	AL049963	Hs.284205	up-regulated by BCG-CWS	0.6	3.8
130623	AL045128	Hs.1691	glucan (1,4-alpha-), branching enzyme 1	0.9	6.6
130629	AL042896	Hs.1697	ATPase, H+ transporting, lysosomal (vacu	0.9	3.9
130632	AW073971	Hs.238954	ESTs, Weakly similar to KIAA1204 protein	0.9	6.9
130639	AI557212	Hs.17132	ESTs, Moderately similar to I54374 gene	2.6	3.9
130641	AF158555	Hs.239169	glutaminase	1.2	13.6
130653	AI861791	Hs.278479	TSPY-like	1.3	4
130655	AI831962	Hs.17409	cysteine-rich protein 1 (intestinal)	2.5	4
130666	AL117506	Hs.194035	KIAA0737 gene product	1.3	6.2
130669	AI928985	Hs.17680	hypothetical protein MGC1314 similar to	1.4	3.9
130693	R68537	Hs.17962	ESTs	3.2	0.8
130694	NM_014827	Hs.17969	KIAA0663 gene product	1.1	4.8

130696	AA325308	Hs.18016	Homo sapiens mRNA; cDNA DKFZp586H0324 (f	1.8	5
130701	Z98883	Hs.18079	phosphatidylinositol glycan, class Q	1.1	6.7
130707	AW190925	Hs.203559	hypothetical protein FLJ12701	1.2	4.1
130731	AI932971	Hs.18593	Homo sapiens cDNA: FLJ21449 fis, clone C	1.4	6.9
130787	AF072813	Hs.252831	reticulon 3	1.2	11.2
130796	AA088809	Hs.19525	hypothetical protein FLJ22794	1.8	6.8
130808	NM_001761	Hs.1973	cyclin F	1.3	4.1
130863	Y10805	Hs.20521	HMT1 (hnRNP methyltransferase, S. cerevi	3.2	5.9
130902	AB037750	Hs.21061	KIAA1329 protein	1	3.8
130908	AW195747	Hs.21122	hypothetical protein FLJ11830 similar to	1.3	7.9
130911	BE409769	Hs.21189	DnaJ (Hsp40) homolog, subfamily A, membe	2.7	3.7
130913	BE390905	Hs.21198	translocase of outer mitochondrial membr	1.9	4
130923	H96115	Hs.21293	UDP-N-acetylglucosamine pyrophosphorylas	1.9	10.3
130959	AB023182	Hs.184523	KIAA0965 protein	1.5	6.8
130967	AA393071	Hs.182579	leucine aminopeptidase	1.4	5.5
130975	AA099923	Hs.283728	PEST-containing nuclear protein	1.3	3.8
131037	BE243101	Hs.22391	chromosome 20open reading frame 3	1.9	4.1
131039	D87436	Hs.166318	ffpin 2	1.8	3.5
131060	AA194422	Hs.22584	myosin VI	4.5	5
131097	AL137682	Hs.22937	I-kappa-B-interacting Ras-like protein 2	2	3.7
131101	BE387561	Hs.22981	DKFZP586M1523 protein	1.6	4.5
131104	W27770	Hs.301756	ESTs, Weakly similar to T31475 hypotheti	0.9	3.5
131107	BE620886	Hs.75354	GCN1 (general control of amino-acid synt	2.1	4.5
131109	BE564123	Hs.23060	DKFZP564F0522 protein	1.1	4.6
131136	AB033099	Hs.23413	KIAA1273 protein	1.2	4.2
131148	AW953575	Hs.303125	p53-induced protein PIGPC1	4.5	13.5
131150	X77753	Hs.23582	tumor-associated calcium signal transduc	3.4	0.4
131156	AI472209	Hs.323117	ESTs	0.8	4.9
131164	AW013807	Hs.182255	keratin 19	3.3	2.4
131181	H25094	Hs.293663	ESTs, Moderately similar to I38022 hypot	0.6	4
131194	AW884222	Hs.24083	KIAA0997 protein	1.4	3.8
131199	AW979155	Hs.298275	amino acid transporter 2	1.2	8.5
131215	AL050107	Hs.24341	transcriptional co-activator with PDZ-bi	0.7	4.7
131216	AI815486	Hs.243901	Homo sapiens cDNA FLJ20738 fis, clone HE	2.1	8.2
131233	D89053	Hs.268012	fatty-acid-Coenzyme A ligase, long-chain	1.7	3.5
131237	AW956868	Hs.24608	DKFZP564D177 protein	1.3	5.4
131262	AU077158	Hs.24930	tubulin-specific chaperone a	1.6	4.8
131263	AU077002	Hs.24950	regulator of G-protein signalling 5	1.4	4.4
131367	AI750575	Hs.173933	nuclear factor I/A	3.3	2.2
131372	AW293399	Hs.144904	nuclear receptor co-repressor 1	1.6	3.9
131373	NM_006052	Hs.26146	Down syndrome critical region gene 3	1	11.1
131388	NM_014810	Hs.92200	KIAA0480 gene product	5	2
131492	AI452601	Hs.288869	nuclear receptor subfamily 2, group F, m	0.9	3.5
131493	AW960146	Hs.284137	hypothetical protein FLJ12888	1	3.5
131514	BE270734	Hs.2795	lactate dehydrogenase A	2	6.5
131524	AB040927	Hs.301804	KIAA1494 protein	1.5	10.7
131528	AU076408	Hs.28309	UDP-glucose dehydrogenase	1.3	4.7
131534	AF157326	Hs.184786	TBP-interacting protein	1.3	4.9
131555	T47364	Hs.278613	interferon, alpha-inducible protein 27	1.5	8
131578	AA936296	Hs.234265	DKFZP586G011 protein	1.8	3.5
131589	C18825	Hs.29191	epithelial membrane protein 2	1.3	8.2
131609	D83032	Hs.169984	nuclear protein	2.8	3.9
131628	BE514605	Hs.289092	Homo sapiens cDNA: FLJ22380 fis, clone H	1.3	11.2
131670	H03514	Hs.10130	ESTs	1.3	4.8
131697	C19034	Hs.288613	Homo sapiens cDNA FLJ14175 fis, clone NT	3.2	9.7
131701	AF103798	Hs.30819	hypothetical protein	1.3	5.2
131703	AW160885	Hs.30888	cytochrome c oxidase subunit VIIa polype	1.3	7.8
131739	AF017986	Hs.31386	secreted frizzled-related protein 2	10.6	14.7
131764	AI805664	Hs.31731	peroxiredoxin 5	1.1	3.6
131781	AF077036	Hs.31989	DKFZP586G1722 protein	1.6	3.7
131791	X62111		gb:H.sapiens VII-5 gene for immunoglobul	1.1	3.5
131853	AI581917	Hs.3321	ESTs, Highly similar to IRX1_HUMAN IROQU	5.3	1.2
131870	NM_014874	Hs.3363	KIAA0214 gene product	0.6	4.2
131903	NM_004642	Hs.3436	deleted in oral cancer (mouse, homolog)	2.4	4.9
131913	AW207440	Hs.185973	degenerative spermatocyte (homolog Droso	2.4	6
131930	AA772603	Hs.69476	Homo sapiens cDNA FLJ12758 fis, clone NT	1.7	9.2
131941	BE252983	Hs.35088	ubiquilin specific protease 1	0.5	5.2

131947	AI123939	Hs.182997	ESTs	0.7	4.1
131961	AA129782	Hs.3576	Homo sapiens mRNA full length insert cDN	0.9	4.8
131964	AW381148	Hs.198365	2,3-bisphosphoglycerate mutase	1.1	6.1
131974	AF208858	Hs.268122	hypothetical protein	1.3	3.9
131983	AF119665	Hs.184011	pyrophosphatase (inorganic)	3.3	6.9
131997	AF229181	Hs.136644	CS box-containing WD protein	0.9	5.2
132006	AW162336	Hs.3709	low molecular mass ubiquinone-binding pr	1.2	3.6
132053	BE277910	Hs.3833	3'-phosphoadenosine 5'-phosphosulfate sy	3.2	1.8
132055	BE379335	Hs.211594	proteasome (prosome, macropain) 26S subu	1.2	3.6
132071	AF217798	Hs.3850	LIS1-interacting protein NUDEL; endoolig	0.7	5.2
132078	AI701457	Hs.38694	ESTs	2	5.3
132094	NM_016045	Hs.3945	CGI-107 protein	1.2	4.3
132116	AW960474	Hs.40289	ESTs	3.1	3.1
132164	AI752235	Hs.41270	procollagen-lysine, 2-oxoglutarate 5-dio	1.8	3.7
132181	AW961231	Hs.16773	Homo sapiens clone TCCCIA00427 mRNA sequ	1.2	5
132208	AL031709	Hs.241575	hypothetical protein CAB56184	1.4	4.2
132258	AA306325	Hs.4311	SUMO-1 activating enzyme subunit 2	2	10.3
132303	BE177330	Hs.325093	Homo sapiens cDNA: FLJ21210 fis, clone C	1.2	4.1
132316	U28831	Hs.44566	KIAA1841 protein	5.9	1.6
132358	NM_003542	Hs.46423	H4 histone family, member G	5.8	1.5
132384	AA312135	Hs.46967	HSPCO34 protein	2.1	9.3
132397	AA021160	Hs.4750	hypothetical protein DKFZp564K0822	1.3	4.6
132413	AW361383	Hs.260116	metalloprotease 1 (pitrilysin family)	2	4.9
132442	AW970859	Hs.313503	ESTs	1.2	6
132534	BE388673	Hs.5086	hypothetical protein MGC10433	2	3.9
132540	BE396290	Hs.5097	synaptogyrin 2	1.4	5.1
132554	AF065391	Hs.194718	zinc finger protein 265	1.2	4
132575	AV660538	Hs.284182	60S ribosomal protein L30 isolog	3	1.7
132585	AF029750	Hs.179600	TAP binding protein (tapasin)	1.8	4.7
132602	AW606927	Hs.5308	hypothetical protein DKFZp586F1122 simil	1.6	4.9
132608	AA353044	Hs.5321	ARP3 (actin-related protein 3, yeast) ho	1.8	6.1
132718	NM_004800	Hs.554	Sjogren syndrome antigen A2 (60kD, ribon	4.2	2
132719	AI264357	Hs.55405	hypothetical protein MGC16212	1.1	5.3
132730	AK000868	Hs.5570	hypothetical protein FLJ10006	1.4	5.2
132765	BE222975	Hs.56205	insulin induced gene 1	1.1	5.8
132782	F07424	Hs.279840	zinc finger protein 222	1.3	3.7
132793	AB020713	Hs.56966	KIAA0906 protein	2.3	6.3
132805	AW975748	Hs.5724	sclerostin	0.7	7.7
132863	BE268048	Hs.236494	RAB10, member RAS oncogene family	1.8	6.2
132894	D83209	Hs.5944	solute carrier family 11 (proton-coupled	1.5	20.8
132930	AA579258	Hs.6083	Homo sapiens cDNA: FLJ21028 fis, clone C	1	3.8
132932	AW118826	Hs.6093	Homo sapiens cDNA: FLJ22783 fis, clone K	0.7	5.4
132933	BE263252	Hs.6101	hypothetical protein MGC3178	1.6	4.1
132965	AI248173	Hs.191460	hypothetical protein MGC12936	1	4.2
132984	BE539199	Hs.62112	zinc finger protein 207	1.5	4.4
132990	X77343	Hs.334334	transcription factor AP-2 alpha (activat	13.9	0.8
132998	Y00062	Hs.170121	protein tyrosine phosphatase, receptor t	0.6	4.8
133002	AW499985	Hs.42915	ARP2 (actin-related protein 2, yeast) ho	1.5	11.1
133011	NM_006379	Hs.171921	sema domain, immunoglobulin domain (Ig),	3.5	1
133012	AA847843	Hs.62711	Homo sapiens, clone IMAGE:3351295, mRNA	1	4.5
133040	AW502761	Hs.30909	KIAA0430 gene product	0.9	5.5
133056	H12026	Hs.6396	jumping translocation breakpoint	1.7	5.3
133063	AI654133	Hs.30212	thyroid receptor interacting protein 15	0.6	4.9
133067	AK000708	Hs.169764	hypothetical protein FLJ20701	1.2	3.5
133080	AF089816	Hs.6454	chromosome 19 open reading frame 3	1.2	17.5
133110	AA808177	Hs.65228	ESTs	0.9	5.1
133150	AV655783	Hs.661	Empirically selected from AFFX single pr	1.1	4.5
133175	AW955532	Hs.66668	ESTs, Weakly similar to S19560 proline-r	1.5	4.8
133199	AF231981	Hs.250175	homolog of yeast long chain polyunsatura	5.5	5.9
133203	AA464362	Hs.6748	hypothetical protein PP1565	1.2	3.7
133206	AB037773	Hs.6762	hypothetical protein	1.6	8.6
133221	W32474	Hs.301746	RAP2A, member of RAS oncogene family	2.4	4.8
133229	AL137480	Hs.6834	KIAA1014 protein	1	4.2
133241	AW796524	Hs.68644	Homo sapiens microsomal signal peptidase	1.3	3.9
133257	BE617892	Hs.6895	actin related protein 2/3 complex, subun	1.4	5.4
133271	Z48633	Hs.283742	H.sapiens mRNA for retrotransposon	3.1	0.7
133273	N27672	Hs.69469	dendritic cell protein	2.5	6.5

133287	AW797437	Hs.69771	B-factor, properdin	1.3	4	
133291	BE297855	Hs.69855	NRAS-related gene	1.4	5	
133292	AA304961	Hs.699	peptidylprolyl isomerase B (cyclophilin	2.2	6.8	
133294	AJ001388	Hs.69997	zinc finger protein 238	1.5	4.3	
133300	AF116666	Hs.70333	hypothetical protein MGC10753	1.4	6.3	
133302	X04898	Hs.237658	apolipoprotein A-II	0.2	3.6	
133308	U56979	Hs.250651	H factor 1 (complement)	0.6	5	
133347	BE257758	Hs.71475	acid cluster protein 33	1.2	4.2	
133370	AF245505	Hs.72157	DKFZP564I1922 protein	3.7	5.8	
133404	AB007916	Hs.214646	KIAA0447 gene product	1.4	5.1	
133408	AI738719	Hs.198427	hexokinase 2	0.9	6.3	
133422	AB033061	Hs.73287	KIAA1235 protein	1.2	3.7	
133442	AL137663	Hs.7378	Homo sapiens mRNA; cDNA DKFZp434G227 (fr	0.7	4.8	
133448	M27749	Hs.288168	immunoglobulin lambda-like polypeptide 1	1.1	4.3	
133449	AF038962	Hs.7381	voltage-dependent anion channel 3	0.7	4.2	
133501	AI962602	Hs.74284	hypothetical protein MGC2714	3.1	5.9	
133504	NM_004415	Hs.74316	desmoplakin (DPI, DPII)	4.3	11.5	
133506	BE562958	Hs.74346	hypothetical protein MGC14353	1.8	19.7	
133532	D87452	Hs.74579	KIAA0263 gene product	1.2	5.4	
133574	H97991	Hs.193313	Empirically selected from AFFX single pr	1.4	3.9	
133586	AI929645	Hs.225938	synapsin I	0.6	4.9	
133589	L37368	Hs.75104	RNA-binding protein S1, serine-rich doma	2	10.8	
133591	AI423369	Hs.75111	protease, serine, 11 (IGF binding)	2.1	4.5	
133606	U10564	Hs.75188	wee1+ (S. pombe) homolog	3.3	1.1	
133817	BE244334	Hs.75249	ADP-ribosylation factor-like 6 interacti	2.3	5.6	
133651	AI301740	Hs.173381	dihydropyrimidinase-like 2	0.8	13.5	
133660	H14843	Hs.303154	popeye protein 3	1	9.1	
133663	AJ006239	Hs.75438	quinoid dihydropteridine reductase	0.5	5.8	
133668	L77964	Hs.271980	mitogen-activated protein kinase 6	1.1	6.9	
133671	AW503116	Hs.301819	zinc finger protein 146	1.8	3.8	
133681	AI352558	Hs.75544	tyrosine 3-monooxygenase/tryptophan 5-mo	1.5	11.1	
133694	W17187.comp	Hs.232400	heterogeneous nuclear ribonucleoprotein	2	3.9	
133708	AI018666	Hs.75687	synaptophysin	0.6	3.5	
133737	AW001130	Hs.75824	KIAA0174 gene product	1.2	7.2	
133743	AI929587	Hs.75847	CREBBP/EP300 inhibitory protein 1	1.5	5	
133750	BE410769	Hs.75873	zyxin	1.2	4.8	
133765	M62194	Hs.75929	cadherin 11, type 2, OB-cadherin (osteob	3.2	4.1	
133776	BE268649	Hs.177766	ADP-ribosyltransferase (NAD+; poly (ADP-	2.1	3.8	
133799	W24087	Hs.76285	DKFZP564B167 protein	1.9	12.6	
133800	AF075337	Hs.76293	thymosin, beta 10	2.6	6.6	
133802	AW239400	Hs.76297	G protein-coupled receptor kinase 6	1	4.9	
133808	D25969	Hs.76325	step II splicing factor SLU7	0.5	3.8	
133817	AW578716	Hs.7644	H1 histone family, member 2	1.5	4.5	
133829	AW630088	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (f	3.7	5.6	
133841	AA345824	Hs.76688	carboxylesterase 1 (monocyte/macrophage	0.3	4.4	
133845	AA147026	Hs.76704	ESTs	5.5	2.9	
133883	AI815523	Hs.76930	synuclein, alpha (non A4 component of am	0.6	4.8	
133887	X07767	Hs.77271	protein kinase, cAMP-dependent, catalyti	1	10.2	
133892	AW859528	Hs.301497	arginyltransferase 1	0.9	4.8	
133913	AU076964	Hs.7753	calumenin	2.8	10.5	
133914	AI458213	Hs.77542	ESTs	1.8	5.6	
133917	AL031177	Hs.7756	proteasome (prosome, macropain) 26S subu	1.5	6.6	
133947	L41066	Hs.77810	nuclear factor of activated T-cells, cyt	1.5	3.8	
133986	M54968	Hs.184050	v-Ki-ras2 Kirsten rat sarcoma 2 viral on	0.9	4.3	
133987	L15409	Hs.174007	von Hippel-Lindau syndrome	2.3	4.3	
133989	AL040328	Hs.78202	SWI/SNF related, matrix associated, acti	3.3	3.4	
133990	R48316	Hs.7822	Homo sapiens mRNA; cDNA DKFZp564C1216 (f	1.3	5.7	
134029	BE150882	Hs.143501	hypothetical protein hCLA-iso	1	6.5	
134040	NM_003470	Hs.78683	ubiquitin specific protease 7 (herpes vi	1.7	3.6	
134042	AI027881	Hs.7869	lysosomal	1	7.5	
134049	AF117236	Hs.78825	matrin 3	1.2	4	
134095	NM_004354	Hs.79069	cyclin G2	2.7	4.8	
134098	BE513171	Hs.79086	mitochondrial ribosomal protein L3	3.3	2.1	
134207	Z43039	Hs.170198	KIAA0009 gene product	1.3	3.5	
134210	AF035606	Hs.80019	programmed cell death 6	1.7	6.9	
134218	U77735	Hs.80205	pim-2 oncogene	0.8	5.3	
134270	X68194	Hs.80919	synaptophysin-like protein	1.4	11.4	

134277	NM_004369	Hs.80988	collagen, type VI, alpha 3	2.6	3.5
134280	NM_000712	Hs.81029	biliverdin reductase A	1.8	5.8
134288	AI022650	Hs.8117	erbb2-interacting protein ERBIN	1.1	3.6
134296	R00603	Hs.8128	phosphatidylserine decarboxylase	1.1	5.9
134300	NM_001430	Hs.8138	endothelial PAS domain protein 1	0.5	4.8
134310	AL037800	Hs.8146	selenoprotein T	1.7	7.9
134343	D50683	Hs.82026	transforming growth factor, beta recepto	0.8	7.8
134364	X76534	Hs.82226	glycoprotein (transmembrane) nmb	2.2	3.6
134374	N22687	Hs.8236	ESTs	1.9	3.6
134378	AL035766	Hs.82425	actin related protein 2/3 complex, subun	1.5	8.3
134382	BE512856	Hs.109051	SH3 domain binding glutamic acid-rich pr	1.1	3.6
134415	AI750762	Hs.82911	protein tyrosine phosphatase type IVA, m	1.9	4.6
134417	NM_006416	Hs.82921	solute carrier family 35 (CMP-sialic aci	1.2	7.5
134421	AU077196	Hs.82985	collagen, type V, alpha 2	6.6	8.7
134439	Z23024	Hs.138860	Rho GTPase activating protein 1	2	3.9
134454	NM_013230	Hs.286124	CD24 antigen (small cell lung carcinoma	3.5	1.1
134494	D86981	Hs.84084	amyloid beta precursor protein (cytoplas	1.5	4.4
134501	W84869	Hs.211568	eukaryotic translation initiation factor	1.2	5.7
134505	AW960673	Hs.177530	ATP synthase, H+ transporting, mitochond	1.3	3.9
134520	BE091005	Hs.74861	activated RNA polymerase II transcriptio	1.8	4.3
134528	M23161	Hs.84775	Human transposon-like element mRNA	0.8	5.6
134545	AI902899	Hs.85155	butyrate response factor 1 (EGF-response	1.4	5
134553	AI203545	Hs.296169	S-phase response (cyclin-related)	0.8	3.9
134573	NM_016142	Hs.279617	steroid dehydrogenase homolog	1.3	5.7
134576	AB033017	Hs.8594	KIAA1191 protein	0.9	3.7
134577	BE244323	Hs.85951	exportin, tRNA (nuclear export receptor	4	6.8
134579	AW936928	Hs.85963	DKFZP564M182 protein	2.2	4.3
134582	AA927177	Hs.86041	CGG triplet repeat binding protein 1	1.6	3.6
134600	AF078859	Hs.86347	hypothetical protein	2.1	3.5
134655	AF285208	Hs.123090	SWI/SNF related, matrix associated, acti	1.7	4.2
134700	AK000606	Hs.8868	golgi SNAP receptor complex member 1	4.4	0.9
134737	D17530	Hs.89434	drebrin 1	3.1	1.6
134762	T51986	Hs.283108	hemoglobin, gamma G	0.5	4.6
134843	AA428520	Hs.90061	progesterone binding protein	1.3	3.7
134854	J03464	Hs.179573	collagen, type I, alpha 2	8.7	17.3
134865	AA587775	Hs.66295	multi-PDZ-domain-containing protein	1.7	4
134868	AB020689	Hs.90419	KIAA0882 protein	3.4	0.9
134874	AI803761	Hs.90458	serine palmitoyltransferase, long chain	1.3	6.9
134885	AJ002030	Hs.9071	progesterone membrane binding protein	1.4	9.6
134891	R51083	Hs.90787	ESTs	1	10.1
134908	BE089782	Hs.9877	hypothetical protein	1.9	3.9
134934	AF005043	Hs.91390	poly (ADP-ribose) glycohydrolase	1	4.3
134970	BE560779	Hs.284233	NICE-5 protein	1.4	10.4
134982	AK002085	Hs.92308	Homo sapiens cDNA FLJ11223 fis, clone PL	1.6	4.1
135011	AB037835	Hs.92991	KIAA1414 protein	1.2	5.6
135032	AW301984	Hs.173585	hypothetical protein FLJ12619	1.7	7.6
135035	AL034344	Hs.284186	forkhead box C1	3.2	0.6
135051	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	4.2	4.1
135060	AK001887	Hs.259842	protein kinase, AMP-activated, gamma 2 n	1.3	4.8
135062	AK000967	Hs.93872	KIAA1682 protein	2	3.7
135077	AW503733	Hs.9414	KIAA1488 protein	2.8	3.7
135082	AB017363	Hs.94234	frizzled (Drosophila) homolog 1	2.4	4.8
135107	T97257	Hs.337531	ESTs, Moderately similar to I38022 hypot	1.4	5.8
135143	AA132813	Hs.69559	KIAA1096 protein	1.8	8.5
135156	BE563088	Hs.9552	binder of Arl Two	1.2	6.8
135172	AB028956	Hs.12144	KIAA1033 protein	3.1	1.4
135181	BE250865	Hs.279529	px19-like protein	1.3	7.5
135222	AA534009	Hs.183487	interferon stimulated gene (20kD)	1.3	3.8
135232	AL038812	Hs.96800	ESTs, Moderately similar to ALU7_HUMAN A	2.1	3.9
135289	AW372569	Hs.9788	hypothetical protein MGC10924 similar to	0.9	8.4
135290	AA331901	Hs.184736	hypothetical protein FLJ10097	1	3.8
135291	T83882	Hs.97927	ESTs	1.2	3.5
135349	AA114212	Hs.9930	serine (or cysteine) proteinase inhibito	2.6	6.9
135357	AI565004	Hs.79572	cathepsin D (lysosomal aspartyl protease	2.5	5.4
135398	M16029	Hs.287270	ret proto-oncogene (multiple endocrine n	0.4	7.9
135399	W79431	Hs.326249	ribosomal protein L22	1.5	4.5
135400	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	3.2	1.8

302665	R99693	Hs.224410	Homo sapiens cDNA FLJ12843 fis, clone NT	3.6	3.6
302892	AW176909	Hs.42346	calcineurin-binding protein calsarcin-1	3.3	1.8
302963	AW673106	Hs.151945	mitochondrial ribosomal protein L43	0.9	4.2
303131	AW081061	Hs.103180	DC2 protein	3	17.3
303150	AA887146	Hs.8217	stromal antigen 2	6.2	4
310125	AA147979	Hs.285005	mitochondrial import receptor Tom22	1.2	6.6
312662	AA233808	Hs.286241	protein kinase, cAMP-dependent, regulato	1	3.5
319429	BE616412	Hs.286218	junctional adhesion molecule 1	1.5	4.7
320591	AA054761	Hs.169149	karyopherin alpha 1 (importin alpha 5)	1.2	5.6
406779	AA412048	Hs.279574	CGI-39 protein; cell death-regulatory pr	1.3	3.5
410691	AW239226	Hs.65450	reticulon 4	1.2	13.9
410763	AF279145	Hs.8968	hypothetical protein FLJ21776	2	5.1
415738	BE539367	Hs.295953	ESTs, Weakly similar to AF220049 1 uncha	1.3	3.9
420186	NM_015925	Hs.95697	liver-specific bHLH-Zip transcription fa	1.5	6.2
422055	NM_014320	Hs.111029	putative heme-binding protein	2	11.3
425815	R94023	Hs.337531	ESTs, Moderately similar to I38022 hypot	1.7	3.6
426218	AF119043	Hs.168005	Homo sapiens cDNA FLJ13372 fis, clone PL	3.3	2.8
427397	AI929685	Hs.177656	calmodulin 1 (phosphorylase kinase, delt	1.3	4.7
427466	AA523543	Hs.7678	cellular retinoic acid-binding protein 1	1.1	3.7
427505	AA361562	Hs.178761	26S proteasome-associated pad1 homolog	3.2	2.5
427723	AI355260	Hs.279789	histone deacetylase 3	2.8	22
428673	AW601325	Hs.324278	Homo sapiens mRNA; cDNA DKFZp566M063 (fr	1.1	5.2
430219	X99209	Hs.235887	HMT1 (hnRNP methyltransferase, S. cerevi	1.8	8.8
430450	R23553	Hs.241489	hypothetical protein	1.1	5.6
432868	BE395875	Hs.279609	mitochondrial carrier homolog 2	1.5	6.1
433423	BE407127	Hs.8997	heat shock 70kD protein 1A	1.3	7.6
437562	AB001636	Hs.5683	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	1.6	6.5
437667	BE616412	Hs.286218	junctional adhesion molecule 1	1.3	3.5
437754	R60366	Hs.5822	Homo sapiens cDNA: FLJ22120 fis, clone H	2	5.7
440252	BE513940	Hs.6101	hypothetical protein MGC3178	1.1	6.2
441471	AL042988	Hs.7857	erythrocyte membrane protein band	0.5	3.7
448292	BE281316	Hs.47334	hypothetical protein FLJ14495	2.5	4.9
449404	H51068	Hs.23581	leptin receptor gene-related protein	1.1	3.6
449964	AW001741	Hs.273193	hypothetical protein FLJ10706	1.4	3.5
451389	N73222	Hs.279009	matrix Gla protein	4	11.2
452685	AI634651	Hs.30250	v-maf musculoaponeurotic fibrosarcoma (a	0.8	5.6
	RC_H15847_s		peptidylprolyl isomerase B (cyclophilin B)	1.8	4.8
	RC_W84712		calumenin	3.5	4.6
	X14008_ma1_f		lysozyme (renal amyloidosis)	0.9	4.5
	RC_H86543_f		ESTs	1.8	6.8
	H07011		ESTs; Weakly similar to SAS [H.sapiens]	1.8	3.9
	RC_AA164586_s			ESTs 6.2	0.8
	RC_AA070485		Homo sapiens clone 23987	3.4	2.6
	RC_H98714_s		ESTs	1.6	3.5
	RC_AA406145_f			ESTs 4.6	3
	AA458584		SRY (sex determining region Y)-box 4	3.4	0.4
	AA031548		cell division cycle 42 (GTP-binding protein; 25kD)	3.1	3.9
	X02761		fibronectin 1	3.6	15.2
	RC_AA487193		secreted frizzled-related protein 4	4.7	4
	R25326		Homo sapiens mRNA for putative vacuolar	0.9	5
	RC_AA393805		ESTs; Weakly similar to (define not	1.1	8.4
	RC_AA449333		ESTs	2.9	4.6
	RC_AA287681_s			ESTs 1.3	4
	RC_AA490664		ESTs; Highly similar to heat shock factor	1.4	5
	RC_C14243_f		ESTs; Highly similar to heat shock factor	1.7	5
	R21443		ESTs	1.6	3.7
	RC_AA251902		Homo sapiens lysophospholipase (LPL1)	2.2	3.8
	M21121_s		small inducible cytokine A5 (RANTES)	0.9	9.9
	C00038_s		ESTs	2.8	4.8
	Y00503		keratin 19	3.1	1.1
	RC_R27006_f		ESTs	1.6	3.7
	RC_AA416886		ESTs; Weakly similar to predicted using	3.1	3.1
	RC_AA460450		fibroblast growth factor receptor 2 (bacteria-	1.5	3.7
	RC_AA488433		ESTs; Weakly similar to deduced amino acid	1.1	4
	RC_AA278400_f		Homo sapiens HRIHFB2115 mRNA; partial cds	1.5	3.6
	U28831		Human protein immuno-reactive with anti-PTH	4.4	0.6
	RC_AA199588		Homo sapiens actin-related protein Arp3 (ARP3)	1.8	4.7

AF006082	Homo sapiens actin-related protein Arp2 (ARP2)	1.6	10.9	
RC_H90899	desmoplakin (DPI; DPII)	5.4	5.5	
RC_W95070	desmoplakin (DPI; DPII)	5	2.6	
RC_T90946_f	Human mRNA for KIAA263 gene; complete cds	1.1	3.9	
D87258	protease; serine; 11 (IGF binding)	2.4	3.5	
AA313414_s	ESTs; Weakly similar to cDNA EST EMBL:T1157	1.6	5.3	
RC_H73484_s	ESTs; Weakly similar to similar to Yeast	1.3	6.3	
AFFX-HUMISGF3A/M97935_3		2.3	13.5	
AFFX-HUMRGE/M10098_5		1.1	7.9	
AFFX-M27830_5		0.5	7.4	
AFFX-M27830_5		0.6	5.4	
RC_AA063431_f		ESTs	0.8	4.1
RC_T83769_f	ferritin; light polypeptide	1.1	3.7	

TABLE 8A

Table 8A shows the accession numbers for those pkeys lacking unigeneID's for Table 8. For each probeset, we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT number	Accessions
109469	116761_1	AA079487 AA128547 AA128291 AA079587 AA079600
125078	190299_1	AA973971 T88817 AA253263
114638	109698_1	AA075488 AA129081 AA074851 AA082852 AA074732 AA084908 AA084751 AA076042 AA131172 AA085374 AA079519 AA074510 AA113824 AA102437 AA070833 AA070143 AA084693 AA084389 AA076373 AA075492 AA062834 AA084335 AA078829 AA079344 AA069916 AA079275 AA070914 AA654069 AA081976 AA080957 AA083115 AA070942 AA085296
123526	genbank_AA608657	AA608657
123533	genbank_AA608751	AA608751
125090	genbank_T91518	T91518
125154	genbank_W38419	W38419
118475	genbank_N66845	N66845
118505	genbank_N67343	N67343
101046	entrez_K01160	K01160
129982	221_267	Z14221 AW381862 M97920 AW401444 Z66542 M29470 AW406502 X61011 M34024 AA327072 Z14166 Z14167 Z14165 AW403806 Z14200 AA383972 Z14205 Z14201 M18513 Z14202 AW403684 X14584 AF062221 U43760 X55892 X65883 X62107 Z80847 X65885 X65893 AF062142 X65891 X17675 Z47274 Z47277 Z47276 X65888 Z47275 X62109 AF062140 L01278 AF062134 AF062139 X81723 Z80840 X81733 X81743 X81744 X81732 Z80843 AW402942 AW403516 X65919 AF062190 AF062177 AF062222 AF062115 Z47240 AF062263 AF062261 AF062223 AF062211 Z47238 AW401714 AW404008 AW404991 AF062280 M99595 Z47214 Z47232 Z47218 M26995 AF062184 X65895 L38433 X81731 Z11946 Z47226 AF062205 AF174012 L01276 AF062168 AF062136 X81755 X81748 AF174019 AF062285 L06924 L11699 AW402665 L09070 L28049 L08090 AW407843 Z14171 AW402944 L08083 AW405627 L33035 L26907 M17750 L28052 M17751 AJ239360 U19885 L14821 X56526 AB014341 L12087 L12098 U68231 L12184 AF062242 AF022000 U64499 U00570 AI268604 Y15773 X64239 X62969 U00506 X73605 X99360 U00577 D83677 AB021539 AF035796 Z33899 U00588 AJ239353 AF174062 Z33901 X98899 AF174058 X63080 D83676 AB021529 Z18318 U00488 L01412 X81746 U21262 U21272 U00560 AF174060 U00547 U00561 Z18321 S73957 M26435 AF115130 AF115117 Z92896 U21254 Z92895 AF115112 AF062290 T28938 Y09386 AF174067 U27189 Y09384 U77373 AF174057 M17749 X69692 AF174038 U64478 U64486 AF174098 X99365 AF174077 AF174083 AF174089 AF015133 AF127792 AJ006171 U00510 U58144 AF004323 AF115109 AF004324 AF015130 AF090414 AF090418 AB021536 AB021519 Z96857 AF021986 Z92898 Z96956 L34164 AF062251 AF052524 U00549 U00541 D83687 AF052522 AF087420 AF052520 AF022011 L43085 U00536 L19915 L43083 AF090420 AB021530 AB021534 Z96955 Z96954 Z33903 X62964 AF103282 U00509 AF062298 AF062289 AF062307 AW408326 L33037 L04337 L04328 X81742 L04336 L03385 AF032360 S56184 AF062191 AF191092 AI906954 AF103184 L04343 AW364860 AF001424 AF103163 Z98717 AF103143 AJ008250 L04323 AF103321 AF103335 L04342 L03818 L03817 AW404978 AW403690 U86801 AF103150 AJ010334 AF035027 AJ007327 AF103115 AF017458 AJ008207 AJ008183 AJ008198 AJ008241 AJ008208 AF103210 AF068668 AF068670 AF068671 AF068664 AF068669 AF068668 AF068665 AF068672 AW371244 AW403670 AW408074 AW404575 AW362153 AW403803 AW406702 AW351514 D78345 T29140 J00231 NM_002179 AW405146 AA301091 X04646 H64660 AW402990 AW406534 T93007 AI857980 AW368899 AI905833 AW406586 AA482084 AI872299 AA715268 AW404328 AI831674 AI709348 AA603112 AW514864 AA485775 H64492 AW404789 AA487630 AA715498 AA295885 T27613 T98113
108470	genbank_AA079500	AA079500
101447	entrez_M21305	M21305
124447	genbank_N48000	N48000
101624	entrez_M55998	M55998
131791	221_260	X62111 S67984 AJ131056 Z47243 Z47235 AF062268 Z47237 AJ131058 AF062130 AF062282 X62108 AA385969 AA464794 X69861 AW402964 M90808 Z98735 Z98734 Z98736 AF035018 X79161 U00545 AF174046 AF174071 U00552 U96288 AF021989 AF062255 AF174061 S73953 AF062135 AF062155 X64147 U00555 AF174070 AF129754 U86789 Z98714 Z98738 S75886 AJ008175 AJ008188 AJ008188 Y08403 H15753 H22208 AA327241 AW405737 H42300 H39677 H26239 H26903 H45128 R86072 AA327565 AI660584 AW361537 AW383759 S71043 H15014 H45570 H42819 H45523 H45134 R72043 H24543 H27636 H27610 T28147 H25496 AW384071 AW384072 H45561 H45556 H42605 AI735017 T47421 R48719 H27570 H44599 AI459598 H42347 H41938 H24993 AA345888 H22339 AI538691 AJ012264 AA684201 AI880450 AA327310 AI991250 AI833028 AW001210 AI956075 H30467 AA326915 H41943 AI749266 AI744441 AA327377 AW512326 AI735170 H01834 AI587047 AI571623 AA327486 AA327103 AA327195 AA326973 T28143
124842	217726_1	R56485 R37248 R59992
103758	AA084874_f_at	AA084874_f
130064	221_264	X57815 L29157 AA367448 AW328098 AW404536 L29158 L29163 H27683 R83195 AA295096 AW327822 H25458 AW404592 X57819 X57823 AW405804 AW404447 Z34914 AW406542 AA427726 AA604389 AW405506 AW405918 AW405117 AW407182 L03632 AW405058 L03627 AW407470 R72738 L21959 AW375730 X87888 AF124166 AF034638 AJ241408 U09902 AW405284 M12025 AA360219 L03631 L03629 AW327727 AF194810 AF058078 AF194686 AF063774 AF063737 AF063755 AF063740 AF063739 AF063738 S73129 L43088 AF063775 L33026 AF060138 AF194813 AF194812 AF194811 AF194809 AF194814 AF194808 AF064505 AF064503 AF063765 AF063757 AF063752 AF063716 AF063736 AF194806 AF058077 AF063747 AF063772 AF063781 AF060137 AF194805 AF060134 AF060132 AF058074 AF063754 AF063704 U38589 Z18332 AF060122 AF194807 AF060135 AF064506 AF064504 AF063773 L26540 AF058072 AF060131 AF064500 AF060138 AF064513 AF194683 AF194711 AF058075 AF063717 Z19546 AF194581 X72748 U96393 U09890 X96897 AF194592 M80916 AJ241405 AF194632 AJ388659 AF194625 Z74694 AF194588 AF194601 U09901 U09911 U09892 AJ010338 AJ006162 AJ249377 AJ241414 AA327392 U97248 X72747 Z46850 X95739 AW406701 AJ243109 AF194609 S80758 AF194595 AF194596 L22483 Z70262 D84141 AW405758 AF001788 AF194580 D84143 U76684 AF194593 L03630 X87892 X91134 U21249 Z46345 AJ132426 AF103659 AJ233718 AF021038 AJ233727 H24657 U09882 S75827 AA573599 AF047231 AF047232 AF103616 AW404484 Z46848 S76132 AF103663 AF103713 Y17940 AF047216 AF103595 Y17956 AF052799 AF052797 AF052802 AF052798 AF052801 AF052794 AF052796 AF047218 AF052800 AF047217 AF052795 AF032351 AF103701 AF103708 AF103710 AF103706 S62232 AF103645 AF103632 AF103647 AF103644 AF103640 AF103692 AF093581 AF103620 AW405934 AI445389 AW363753 AA360256 AF099878 H21654 H39501 AI620828 H53689 W26785 AW384498 AW407708 AA541663 AA911602 AI821461 AA588300 AA327050 H42717 AI951280 AA421322 AI923193 AA884302 H25133 D87023 J03011 M61771 D87017 AA526865 AA253450
130232	18831_2	U29463 U06715 W24970 AA584303 T39581 AA155603 AA305043 AA429426 W05684 AA102382 AA482044 W24487 AA310060
T88946	F10106	AA232161 AA243117 AA158937 AA100864
109097	genbank_AA167512	AA167512

TABLE 9: Figure 9 from BRCA 001-2 US

Table 9 depicts a preferred group of genes upregulated in tumor tissue compared to normal breast tissue.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title

Pkey	ExAccn	UnigeneID	UnigeneTitle
100690	AA383256	Hs.1657	estrogen receptor 1
102211	BE314524	Hs.78776	putative transmembrane protein
103587	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein
104115	AF183810	Hs.26102	opposite strand to trichorhinophalangeal syndrome I
105038	AW503733	Hs.9414	KIAA1488 protein
105500	AW602166	Hs.222399	CEGP1 protein
105990	AI690586	Hs.29403	hypothetical protein FLJ22060
106155	AA425414	Hs.33287	nuclear factor I/B
106373	AW503807	Hs.21907	histone acetyltransferase
106414	BE568205	Hs.26827	mitogen-activated protein kinase kinase kinase 2
110009	BE075297	Hs.6614	ESTs, Weakly similar to A43932 mucin 2 precursor, intestinal
111900	AF131784	Hs.25318	Homo sapiens clone 25194 mRNA sequence
114540	AI904232	Hs.75323	prohibitin
116470	AI272141	Hs.83484	SRY (sex determining region Y)-box 4
117280	M18217	Hs.172129	Homo sapiens cDNA: FLJ21409 fis, clone COL03924
119771	AI905687	Hs.2533	EST
121723	AA243499	Hs.104800	hypothetical protein FLJ10134
124059	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypothetical protein YGL050w
131148	AW953575	Hs.303125	p53-induced protein PIGPC1
132371	AA235448	Hs.46577	PRO2000 protein
134169	AI690916	Hs.178137	transducer of ERBB2, 1
302235	AL049987	Hs.168361	Homo sapiens mRNA; cDNA DKFZp564F112
452410	AL133619	Hs.29383	Homo sapiens mRNA; cDNA DKFZp434

TABLE 10: Figure 10 from BRCA 001-3 PCT

Table 10 depicts a preferred group of genes upregulated in tumor tissue compared to normal breast tissue.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of tumor to normal body tissue
R2: Ratio of 90th percentile tumor to body
R3: Ratio of 75th percentile body to tumor
R4: Ratio of tumor to normal breast tissue

Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2	R3	R4
100082	AA130080	Hs.4295	proteasome (prosome, macropain) 26S subu	4.2	152	36	12.2
100103	AA380887	Hs.5085	dolichyl-phosphate mannosyltransferase p	9.8	123	13	5
100131	D12485	Hs.11951	ectonucleotide pyrophosphatase/phosphodi	13.2	244	19	9.9
100147	D13666	Hs.136348	osteoblast specific factor 2 (fasciclin .	15.7	1030	66	5
100154	H60720	Hs.81892	KIAA0101 gene product	4.1	320	78	10.6
100157	D14681	Hs.119	Wilms' tumour 1-associating protein	4.7	119	26	3
100169	AL037228	Hs.82043	D123 gene product	5.1	106	21	9.2
100203	BE242284	Hs.172199	adenylate cyclase 7	4.7	47	1	4.3
100210	D26361	Hs.3104	KIAA0042 gene product	4.7	47	4	0.7
100219	AW972300	Hs.118110	bone marrow stromal cell antigen 2	3.6	350	93	1.9
100234	D29677	Hs.3085	KIAA0054 gene product; Helicase	4.1	64	16	3
100248	NM_015156	Hs.78398	KIAA0071 protein	3.4	77	23	5.9
100252	NM_006207	Hs.170040	platelet-derived growth factor receptor-	4.5	45	4	4
100260	D38491	Hs.322478	KIAA0117 protein	5.9	59	1	2.6
100279	D42084	Hs.82007	KIAA0094 protein	3.5	96	28	1.3
100286	BE247550	Hs.86859	growth factor receptor-bound protein 7	3.1	306	98	1.5
100294	AA331881	Hs.75454	peroxiredoxin 3	12.8	128	1	11.7
100335	AW247529	Hs.6793	platelet-activating factor acetylhydrola	4.2	187	44	5.4
100365	AI878927	Hs.79284	mesoderm specific transcript (mouse) hom	4.5	129	29	3.1
100375	D80004	Hs.75909	KIAA0182 protein	3.5	78	23	4.8
100409	D86957	Hs.80712	KIAA0202 protein	10.2	102	1	4.8
100410	D86961	Hs.79269	lipoma HMGIC fusion partner-like 2	4	40	1	3.8
100414	NM_014735	Hs.82292	KIAA0215 gene product	3.2	32	2	2.9
100418	D86978	Hs.64790	KIAA0225 protein	3.6	36	7	3.2
100438	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	5.6	76	14	2
100439	AA347720	Hs.122669	KIAA0264 protein	3.5	35	9	3.1
100448	AF234887	Hs.57652	cadherin, EGF LAG seven-pass G-type rece	5.5	145	27	2.2
100449	D87470	Hs.75400	KIAA0280 protein	3.4	34	1	1.2
100522	X51501	Hs.99949	prolactin-induced protein	22.7	760	34	1.4
100552	AA019521	Hs.301946	lysosomal	14.4	144	9	4.7
100643	NM_005032	Hs.4114	plastin 3 (T isoform)	4.1	259	63	1.9
100661	BE623001	Hs.132748	Homo sapiens ribosomal protein L39 mRNA,	3.3	116	36	2.2
100666	L05424	Hs.169610	CD44 antigen (homing function and Indian	8.5	85	1	3.2
100667	L05424	Hs.169610	CD44 antigen (homing function and Indian	3	594	201	2.3
100745	BE207168	Hs.144630	nuclear receptor subfamily 2, group F, m	5	82	17	0.9
100774	J05581	Hs.89603	mucin 1, transmembrane	3.5	37	11	2.8
100783	AF078847	Hs.191358	general transcription factor IIH, polype	9.7	97	10	7.2
100821	M26460		gb:Homo sapiens (clone 104) retinoblasto	3.3	33	1	0.8
100864	BE563957	Hs.74861	activated RNA polymerase II transcriptio	3.7	477	130	3.1
100877	X80821	Hs.27973	KIAA0874 protein	6.3	63	4	5.7
100892	BE245294	Hs.160789	S164 protein	4.7	47	1	4.2
101038	BE297139	Hs.79411	replication protein A2 (32kD)	3.8	115	30	7.1
101046	K01160		NM_002122:Homo sapiens major histocompat	3.9	390	100	11.1
101079	BE264901	Hs.250502	carbonic anhydrase VIII	3.9	39	8	3.6

101084	AW409934	Hs.75528	nucleolar GTPase	4.1	53	13	4	
101104	AW862258	Hs.169266	neuropeptide Y receptor Y1	15.3	153	1	14.1	
101185	NM_001621	Hs.170087	aryl hydrocarbon receptor	11.3	113	8	3.9	
101188	L20320	Hs.184298	cyclin-dependent kinase 7 (homolog of Xe	3.1	118	38	2	
101201	L22524	Hs.2256	matrix metalloproteinase 7 (MMP7; uterin	8.2	396	48	0.9	
101232	AU077288	Hs.242894	ADP-ribosylation factor-like 1	4	110	28	10.7	
101275	BE545277	Hs.3273	Ts translation elongation factor, mitoch	4.2	50	12	4.4	
101300	BE535511	Hs.74137	transmembrane trafficking protein	6.6	135	21	13.1	
101396	BE267931	Hs.78996	proliferating cell nuclear antigen	6.4	249	39	22.4	
101447	M21305		gb:Human alpha satellite and satellite 3	6.5	878	135	0.8	
101448	NM_000424	Hs.195850	keratin 5 (epidermolysis bullosa simplex	4.8	622	130	0.7	
101470	NM_000546	Hs.1846	tumor protein p53 (Li-Fraumeni syndrome)	5.1	97	19	9.3	
101478	NM_002890	Hs.758	RAS p21 protein activator (GTPase activa	9.6	96	1	8.5	
101484	AA053486	Hs.20315	interferon-induced protein with tetratri	11.2	112	8	5.9	
101507	X16898	Hs.82112	interleukin 1 receptor, type I	3.9	39	2	3.5	
101821	BE391804	Hs.62661	guanylate binding protein 1, interferon-	3.6	36	1	2.6	
101824	M55998		gb:Human alpha-1 collagen type I gene, 3	3.1	2898	923	2.2	
101864	AA436989	Hs.121017	H2A histone family, member A	6.9	103	15	8.4	
101884	M63256	Hs.75124	cerebellar degeneration-related protein	6.4	64	2	4.9	
101724	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	9.4	94	1	0.3	
101754	S70114	Hs.239489	TIA1 cytotoxic granule-associated RNA-bi	8.9	89	5	8	
101767	M81057	Hs.180884	carboxypeptidase B1 (tissue)	3.6	824	227	1.4	
101791	M83822	Hs.62354	cell division cycle 4-like	9	144	16	13	
101794	M84605	Hs.857	putative opioid receptor, neuromedin K (	3.3	38	11	2.4	
101803	AW024390	Hs.155691	pre-B-cell leukemia transcription factor	5.4	180	34	15.9	
101809	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	12	120	8	9	
101839	AA446644	Hs.692	GA733-2 antigen; epithelial glycoprotein	3.1	353	116	2.8	
101888	AL049610	Hs.95243	transcription elongation factor A (SII)-	7.3	73	1	5.3	
101950	AL036287	Hs.194662	calponin 3, acidic	3.8	399	105	3.3	
102009	BE245149	Hs.82643	protein tyrosine kinase 9	4.6	148	32	11.3	
102095	U11313	Hs.75760	sterol carrier protein 2	9.5	95	4	8.8	
102123	NM_001809	Hs.1594	centromere protein A (17kD)	4.2	42	7	3.4	
102125	NM_006456	Hs.288215	sialyltransferase	9.3	93	4	3	
102139	NM_004419	Hs.2128	dual specificity phosphatase 5	5.4	137	26	2.5	
102162	AA450274	Hs.1592	CDC16 (cell division cycle 16, S. cerevi	4.8	151	33	2	
102165	BE313280	Hs.169627	death associated protein 3	9.3	93	5	8	
102193	AL035335	Hs.313	secreted phosphoprotein 1 (osteopontin,	45.7	457	1	39.7	
102211	BE314524	Hs.78776	putative transmembrane protein	3.9	442	114	1.3	
102221	NM_006769	Hs.3844	LIM domain only 4	4.9	49	1	3.6	
102242	U27185	Hs.82547	retinoic acid receptor responder (tazaro	3.1	31	1	1.3	
102258	NM_001546	Hs.34853	inhibitor of DNA binding 4, dominant neg	3.8	163	43	0.5	
102302	AA306342	Hs.69171	protein kinase C-like 2	4.5	45	1	3.6	
102304	AF015224	Hs.46452	mammaglobin 1	8.5	2058	243	1.4	
102348	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	6.4	428	67	2.3	
102369	U39840	Hs.299857	hepatocyte nuclear factor 3, alpha	6.7	67	9	6.3	
102407	AW602154	Hs.82143	E74-like factor 2 (ets domain transcript	5.3	53	1	4.8	
102409	BE300330	Hs.118725	selenophosphate synthetase 2	3.3	111	34	7.5	
102457	NM_001394	Hs.2359	dual specificity phosphatase 4	20.2	202	5	1.3	
102544	NM_003937	Hs.169139	kynureninase (L-kynurenine hydrolase)	3.8	38	1	1.5	
102567	U63830	Hs.146847	TRAF family member-associated NFKB activ	8.2	82	1	6.8	
102580	U60808	Hs.152981	CDP-diacylglycerol synthase (phosphatida	4.1	41	1	3.3	
102618	AL037672	Hs.81071	extracellular matrix protein 1	10.2	628	62	17.2	
102638	U67319	Hs.9216	caspase 7, apoptosis-related cysteine pr	5	66	13	5.3	
102683	NM_002270	Hs.168075	karyopherin (importin) beta 2	6.1	126	21	2.4	
102669	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	4.5	45	1	2.8	
102742	U79293	Hs.159264	Human clone 23948 mRNA sequence	4.1	41	1	2.4	
102784	U85658	Hs.61796	transcription factor AP-2 gamma (activat	4.4	255	58	1.6	
102805	U90304	Hs.25351	troponin homeobox protein 5	3.6	142	39	1.6	
102813	BE242035	Hs.151461	embryonic ectoderm development	3.5	35	1	2.7	
102823	D85390	Hs.5057	carboxypeptidase D	5.6	56	1	5.3	
102825	BE262386	Hs.7137	clones 23667 and 23775 zinc finger prote	4.2	42	7	3.7	
102899	AI815559	Hs.75730	signal recognition particle receptor ('d	3.2	58	18	5	
102913	NM_002275	Hs.80342	keratin 15	5.8	753	131	0.4	
102927	BE512730	Hs.65114	keratin 18	3.1	815	266	1.7	
102961	AL119505	Hs.198166	activating transcription factor 2	3.2	32	4	2.6	
102968	AU076611	Hs.154672	methylene tetrahydrofolate dehydrogenase	5.7	251	44	6.6	
103003	AI910275	Hs.1406	trefoil factor 1 (pS2)	5.6	1346	239	5.4	

103023	AW500470	Hs.117950	multifunctional polypeptide similar to S	5.8	218	38	13	
103024	NM_002343	Hs.105938	lactotransferrin	3.7	1421	388	1.9	
103036	M13509	Hs.83169	matrix metalloproteinase 1 (MMP1; inters	3.1	94	30	5.8	
103038	AA926960	Hs.334883	CDC28 protein kinase 1	3.5	332	94	3.1	
103119	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	4.8	312	65	30.9	
103134	X65724	Hs.2839	Norrie disease (pseudoglioma)	5.2	331	64	1.5	
103134	X65724	Hs.2839	Norrie disease (pseudoglioma)	4.9	49	5	3.8	
103171	AW583058	Hs.234726	serine (or cysteine) proteinase inhibito	3.3	1497	456	2.1	
103206	X72755	Hs.77367	monokine induced by gamma interferon	3.5	796	228	3.2	
103208	AW411340	Hs.31314	retinoblastoma-binding protein 7	5.6	191	34	3.5	
103226	X75042	Hs.44313	v-rel avian reticuloendotheliosis viral	4.1	53	13	4.9	
103333	AA206186	Hs.79889	monocyte to macrophage differentiation-a	3.4	34	8	2.3	
103346	X87613	Hs.5464	thyroid hormone receptor coactivating pr	3.9	43	11	1	
103352	H09366	Hs.78853	uracil-DNA glycosylase	9.3	93	8	8.2	
103375	NM_005982	Hs.84416	sine oculis homeobox (Drosophila) homolo	9.7	97	1	9.3	
103376	AL038166	Hs.323378	coated vesicle membrane protein	6.3	98	16	9.1	
103391	X94453	Hs.114368	pyrroline-5-carboxylate synthetase (glut	4.3	77	18	7.2	
103438	AW175781	Hs.152720	M-phase phosphoprotein 6	4.9	153	31	2.4	
103453	AI878922	Hs.180139	SMT3 (suppressor of mif two 3, yeast) ho	4.9	261	53	3.7	
103471	Y00815	Hs.75216	protein tyrosine phosphatase, receptor t	3.5	564	162	1.7	
103500	AW408009	Hs.22580	alkylglycerone phosphate synthase	3.9	49	13	2.5	
103557	AL133415	Hs.297753	vimentin	7.5	138	18	3.4	
103587	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	7.9	79	2	6.9	
103605	BE409838	Hs.194657	cadherin 1, type 1, E-cadherin (epitheli	3.3	745	229	1.8	
103606	AW403814	Hs.41714	BCL2-associated athanogene	3.2	41	13	2.6	
103613	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (ca	7.3	73	1	5.2	
103658	NM_000088	Hs.172928	collagen, type I, alpha 1	3.8	1612	429	3.1	
103666	NM_003528	Hs.2178	H2B histone family, member Q	3.2	32	5	2.8	
103988	AA314389	Hs.42500	ADP-ribosylation factor-like 5	3.2	32	9	2.7	
103990	AB033112	Hs.42178	bromodomain and PHD finger containing, 3	4.9	49	1	4.2	
104052	NM_002407	Hs.97644	mammaglobin 2	7.2	498	69	9.3	
104115	AF183810	Hs.26102	opposite strand to trichorhinophalangeal	29	290	1	26.8	
104129	H63349	Hs.98806	hypothetical protein	3.7	37	7	2.1	
104146	AW880614	Hs.146381	RNA binding motif protein, X chromosome	5.2	52	1	4.3	
104147	BE081342	Hs.283037	HSPC039 protein	8	84	11	6.3	
104209	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	5.8	58	1	3.2	
104239	AB002367	Hs.21355	doublecortin and CaM kinase-like 1	6.4	64	8	3	
104278	AW583693	Hs.109253	N-terminal acetyltransferase complex ard	4.7	229	49	7.9	
104309	AI337300	Hs.284123	hypothetical protein MGC4604	3.2	32	7	2.4	
104394	AA129551	Hs.172129	Homo sapiens cDNA: FLJ21409 fis, clone C	5.3	144	27	13.1	
104432	X51501	Hs.99949	prolactin-induced protein	6.9	1494	218	1.3	
104558	R56878	Hs.88959	hypothetical protein MGC4816	7.7	77	8	6.9	
104567	AA040620	Hs.5672	hypothetical protein AF140225	3.7	37	5	2.5	
104590	AW373082	Hs.83623	nuclear receptor subfamily 1, group I, m	6.1	493	81	0.7	
104602	H47610		gb:yp75f03.s1 Soares fetal liver spleen	3.8	38	4	1.2	
104613	AF123303	Hs.24713	hypothetical protein	4.8	231	49	7.3	
104633	H00820	Hs.30977	ESTs, Weakly similar to B34087 hypotheti	3.4	154	46	3	
104636	R82252	Hs.106106	protein kinase (cAMP-dependent, catalyti	5	468	94	4.7	
104660	BE298685	Hs.14846	Homo sapiens mRNA; cDNA DKFZp564D016 (fr	3.8	82	22	3.1	
104667	AI239923	Hs.30098	ESTs	14.9	149	1	6.4	
104766	BE244072	Hs.20815	macrophage erythroblast attacher	6.3	165	26	3.2	
104787	AA027317		gb:ze97d11.s1 Soares_fetal_heart_NbHH19W	3.8	40	11	3.8	
104804	AI858702	Hs.31803	ESTs, Weakly similar to N-WASP [H.sapien	7.7	77	1	5.1	
104807	AI139058	Hs.125790	leucine-rich repeat-containing 2	7	70	1	6.5	
104846	AI250789	Hs.32478	ESTs	4.7	201	43	4.5	
104896	AW015318	Hs.23165	ESTs	7.4	74	1	6	
104919	AA026880	Hs.25252	prolactin receptor	3.9	280	72	3.3	
104926	BE298808	Hs.33363	DKFZP434N093 protein	4.2	135	32	4	
104943	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	16.2	162	1	4.2	
104968	AI249502	Hs.29669	ESTs	3.8	38	1	2.4	
104977	AI392640	Hs.18272	amino acid transporter system A1	3.2	522	165	1.9	
104997	AA121686	Hs.10592	ESTs	3.2	32	4	2.9	
105029	AI122691	Hs.13268	ESTs	3.7	157	43	3.6	
105038	AW503733	Hs.9414	KIAA1488 protein	5.5	55	1	5.2	
105041	AB037716	Hs.26204	KIAA1295 protein	10.3	103	1	3.9	
105086	AA148710	Hs.79914	lumican	6.6	66	1	5.4	
105088	H58589	Hs.35156	Homo sapiens cDNA FLJ11027 fis, clone PL	3.1	31	1	2.5	

105091	AA148859	Hs.179909	hypothetical protein FLJ22995	3.2	32	1	3	
105143	AI368836	Hs.24808	ESTs, Weakly similar to I38022 hypotheti	7.3	73	1	3.6	
105154	AA307279	Hs.35947	methyl-CpG binding domain protein 4	4.2	90	22	2.8	
105162	AL133033	Hs.4084	KIAA1025 protein	6	60	6	4.6	
105167	AW612147	Hs.32058	Homo sapiens C1orf19 mRNA, partial cds	3.8	38	2	3.2	
105178	AA313825	Hs.21941	AD036 protein	9.3	436	47	5.8	
105195	AA975096	Hs.19522	hypothetical protein PRO2849	5.7	57	8	5.3	
105200	AA328102	Hs.24641	cytoskeleton associated protein 2	4.5	45	1	3.6	
105248	AW952479	Hs.22826	tropomodulin 3 (ubiquitous)	4.3	43	1	3.9	
105252	AB039670	Hs.9728	ALEX1 protein	8	80	6	7.3	
105253	AW997484	Hs.5003	KIAA0456 protein	3.9	39	6	3.2	
105280	AA894638	Hs.14600	ESTs	3.5	35	7	2.7	
105288	N99673	Hs.3585	ESTs, Weakly similar to AF126743 1 DNAJ	4.5	45	10	0.5	
105309	AK000796	Hs.4104	hypothetical protein	3.8	93	25	7.5	
105329	AA234581	Hs.22862	ESTs	2.8	131	47	3.9	
105344	AF151073	Hs.8645	hypothetical protein	3.9	79	20	6.5	
105376	AW994032	Hs.8768	hypothetical protein FLJ10849	5.1	181	36	15.8	
105386	AW500718	Hs.8115	Homo sapiens, clone MGC:16169, mRNA, com	4.1	41	2	3.3	
105400	AF198620	Hs.65648	RNA binding motif protein 8A	6.2	62	6	5.6	
105426	W20027	Hs.23439	ESTs	3.3	208	63	2.2	
105483	AL137257	Hs.23458	Homo sapiens cDNA: FLJ23015 fis, clone L	3.2	466	146	8.4	
105496	AL117441	Hs.301997	hypothetical protein FLJ13033	16.6	166	8	12.7	
105500	AW602166	Hs.222399	CEGP1 protein	25.4	508	20	3	
105508	AA173942	Hs.326416	Homo sapiens mRNA; cDNA DKFZp564H1916 (f	9	117	13	10.6	
105511	AB037829	Hs.3862	regulator of nonsense transcripts 2; DKF	3.2	32	6	1.5	
105516	AK001269	Hs.30738	hypothetical protein FLJ10407	8.3	83	3	1.8	
105539	AB040884	Hs.109694	KIAA1451 protein	3.5	73	21	1.6	
105564	BE616694	Hs.288042	hypothetical protein FLJ14299	5.8	336	58	2	
105610	AA280072	Hs.99872	fetal Alzheimer antigen	3.2	32	1	1	
105618	R35343	Hs.24968	Human DNA sequence from clone RP1-233G16	4.8	79	17	5.2	
105627	AA281279	Hs.23317	hypothetical protein FLJ14681	4	75	19	1.7	
105640	AA001021	Hs.6685	thyroid hormone receptor interactor 8	4.5	45	1	3.7	
105645	AW294631	Hs.11325	ESTs	3.8	38	1	0.1	
105674	AI609530	Hs.279789	histone deacetylase 3	6.4	64	8	6	
105687	NM_014517	Hs.28423	upstream binding protein 1 (LBP-1a)	4.7	152	33	5.3	
105691	AI680737	Hs.289068	Homo sapiens cDNA FLJ11918 fis, clone HE	5.7	57	8	4.1	
105730	AW377314	Hs.5364	DKFZP564I052 protein	6.9	69	1	4.4	
105731	AA834684	Hs.29131	nuclear receptor coactivator 2	3.4	34	1	3.1	
105743	BE246502	Hs.9598	sema domain, immunoglobulin domain (Ig),	3	30	10	0.9	
105759	AI123118	Hs.15159	chemokine-like factor, alternatively spl	5.4	54	1	4.4	
105772	H57111	Hs.221132	ESTs	5.3	67	13	5.3	
105774	AW369278	Hs.23412	hypothetical protein FLJ20160	4.9	49	1	4.5	
105784	W84446	Hs.226434	hypothetical protein MGC4643	3.3	98	30	4.7	
105795	AA878183	Hs.17448	Homo sapiens cDNA FLJ13618 fis, clone PL	3.2	143	46	3.6	
105806	AF206019	Hs.110347	REV1 (yeast homolog)- like	4	40	3	3.2	
105807	AA788946	Hs.16869	ESTs, Moderately similar to CA1C RAT COL	4.7	747	158	5.7	
105823	AI559444	Hs.293960	ESTs	3.9	371	94	4.6	
105832	AW802282	Hs.22265	pyruvate dehydrogenase phosphatase	3.6	68	19	6	
105840	AA501518	Hs.22209	secreted modular calcium-binding protein	4.8	134	28	3.2	
105851	AI827976	Hs.24391	hypothetical protein FLJ13612	4.3	772	179	1.7	
105864	AI640775	Hs.28332	Homo sapiens cDNA: FLJ21560 fis, clone C	4.3	43	1	3.7	
105870	AW021691	Hs.101067	GCN5 (general control of amino-acid synt	3.6	36	7	3.1	
105875	AK001708	Hs.32271	hypothetical protein FLJ10846	3.4	34	8	2.9	
105888	AK001735	Hs.22983	UDP-glucose:glycoprotein glucosyltransfe	3.8	45	13	1.3	
105906	N25986	Hs.22380	ESTs	3.4	34	1	1.5	
106012	AI240665	Hs.8895	ESTs	21.2	212	6	17.4	
106020	AA043039	Hs.7870	hypothetical protein	3.9	47	12	4.4	
106024	AL122072	Hs.103804	heterogeneous nuclear ribonucleoprotein	4.4	174	40	1.6	
106034	AW952005	Hs.14928	hypothetical protein FLJ12903	4.7	47	1	4	
106038	AA382267	Hs.10653	ESTs	3.4	49	15	4.4	
106055	AA417034		gb:zu04f10.s1 Soares_testis_NHT Homo sap	3.5	53	15	1.2	
106057	BE614474	Hs.289074	F-box only protein 22	3.4	116	35	2.2	
106060	NM_001329	Hs.171391	C-terminal binding protein 2	3.6	444	125	4.6	
106070	T74445	Hs.5957	Homo sapiens clone 24416 mRNA sequence	3.6	365	103	6.9	
106095	AF115402	Hs.11713	E74-like factor 5 (ets domain transcript	26.3	356	14	1	
106098	AW379378	Hs.170121	protein tyrosine phosphatase, receptor t	3.2	267	83	2.3	
108126	AA576953	Hs.22972	hypothetical protein FLJ13352	3.8	38	1	3.3	

106155	AA425414	Hs.33287	nuclear factor I/B	9.9	483	49	1.8	
106157	W37943	Hs.34892	KIAA1323 protein	6.7	94	14	8	
106198	AI244563	Hs.325531	Homo sapiens clone 015h12 My015 protein	3.3	95	20	4.4	
106236	AB040896	Hs.21104	KIAA1463 protein	3.8	83	22	7.5	
106286	AI765107	Hs.274422	hypothetical protein FLJ20550	3.3	97	30	6.4	
106290	AW981393	Hs.16384	hypothetical protein FLJ10955	4.5	116	26	4.5	
106310	R98185	Hs.17240	ESTs	7	70	3	1.3	
106323	AB007866	Hs.158249	KIAA0406 gene product	3.2	37	12	2.6	
106330	AW977397	Hs.35580	ESTs	3.8	38	1	1.9	
106383	AA447453	Hs.27860	Homo sapiens mRNA; cDNA DKFZp586M0723 (f	16	255	16	6.6	
106389	AW748420	Hs.6238	Homo sapiens cDNA: FLJ21487 fis, clone C	4.9	337	70	2.7	
106394	Z42993	Hs.25320	Homo sapiens clone 25142 mRNA sequence	3.1	72	23	5	
106432	AK000310	Hs.17138	hypothetical protein FLJ20303	3.1	165	54	1.6	
106459	AA789081	Hs.4029	glioma-amplified sequence-41	3.1	31	1	2.6	
106503	AB033042	Hs.29879	cofactor required for Sp1 transcriptiona	5.5	147	27	4.4	
106508	AI205785	Hs.30348	ESTs	4.4	222	51	1.8	
106565	NM_014892	Hs.227602	KIAA1116 protein	7.4	74	3	1.7	
106586	AA243837	Hs.57787	ESTs	15.2	152	1	12.6	
106589	AK000933	Hs.28661	Homo sapiens cDNA FLJ10071 fis, clone HE	3.8	263	69	3.9	
106596	AA452379	Hs.293552	ESTs, Moderately similar to ALU7_HUMAN A	4.9	49	1	4.1	
106611	R49131	Hs.26267	ATP-dependant interferon response protei	5.8	58	5	3.1	
106628	AW188205	Hs.12311	Homo sapiens clone 23570 mRNA sequence	5.3	168	32	14.9	
106650	AL049951	Hs.22370	Homo sapiens mRNA; cDNA DKFZp564O0122 (f	5.4	75	14	0.8	
106683	BE298396	Hs.14512	DIP8 protein	3.6	210	58	4.7	
106698	N28524	Hs.29403	hypothetical protein FLJ22060	5.7	57	10	4.8	
106710	N38902	Hs.334437	hypothetical protein MGC4248	4.4	371	84	3.2	
106717	AA600357	Hs.239489	TIA1 cytotoxic granule-associated RNA-bi	4.3	101	24	1.6	
106747	NM_007118	Hs.171957	triple functional domain (PTPRF interact	4.6	46	1	4	
106834	AL044182	Hs.28070	KIAA0753 gene product	3.5	58	17	1.6	
106846	AB037744	Hs.34892	KIAA1323 protein	5.4	192	36	4.4	
106868	BE185536	Hs.301183	molecule possessing ankyrin repeats indu	3.3	696	214	1.6	
106882	AA149537	Hs.26994	hypothetical protein FLJ20477	3.8	38	1	1.6	
106893	AA835868	Hs.25253	mannosidase, alpha, class 1A, member 1	4.3	43	10	2.2	
106895	AK001826	Hs.25245	hypothetical protein FLJ11289	3.6	36	1	1.2	
106897	AF039023	Hs.167496	RAN binding protein 6	4.5	45	1	3.8	
106916	AA134329	Hs.24170	Homo sapiens, clone IMAGE:3685398, mRNA,	5.7	94	17	7.3	
106962	AI868848	Hs.22315	ESTs	3.5	180	52	2.3	
106968	AF216751	Hs.26813	CDA14	5.5	130	24	12.5	
106990	AA280722	Hs.24758	ESTs, Weakly similar to I38022 hypotheti	3.2	266	83	1.6	
107008	AL157479	Hs.23740	KIAA1598 protein	5.1	298	59	4.4	
107014	AA598820		gb:ae36h12.s1 Gessler Wilms tumor Homo s	3.3	228	69	2.8	
107032	AV650537	Hs.247309	succinate-CoA ligase, GDP-forming, beta	3.1	55	18	3.8	
107056	AW401864	Hs.18720	programmed cell death 8 (apoptosis-induc	3.1	75	24	2.2	
107071	AW385224	Hs.35198	ectonucleotide pyrophosphatase/phosphodi	3.1	367	119	2.3	
107080	AL122043	Hs.19221	hypothetical protein DKFZp586G1424	3.9	98	25	6.6	
107102	AB037765	Hs.30652	KIAA1344 protein	6.3	63	1	5.4	
107109	AA249096	Hs.32793	ESTs	4.6	71	16	3.6	
107136	AV661958	Hs.8207	GK001 protein	2.5	392	155	4.3	
107151	AW378065	Hs.8687	ESTs	15.6	156	7	10.8	
107217	AL080235	Hs.35861	DKFZP586E1621 protein	4.8	48	8	3.1	
107222	BE172058	Hs.82689	tumor rejection antigen (gp96) 1	3.4	251	74	23.7	
107240	AI290284	Hs.159872	ESTs	3.8	38	6	0.5	
107248	AW263124	Hs.315111	nuclear receptor co-repressor/HDAC3 comp	5.4	483	90	4	
107295	AA186629	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp	4.6	199	44	19.2	
107299	BE277457	Hs.30661	hypothetical protein MGC4606	12.5	156	13	2.9	
107316	T63174	Hs.193700	Homo sapiens mRNA; cDNA DKFZp586I0324 (f	3.2	110	35	9.6	
107318	T74445	Hs.5957	Homo sapiens clone 24416 mRNA sequence	3.5	35	1	2.6	
107485	AL042613	Hs.262476	S-adenosylmethionine decarboxylase 1	5.8	151	28	11.4	
107612	AI498988	Hs.60090	Homo sapiens cDNA FLJ13595 fis, clone PL	3.2	32	5	2.1	
107638	AI580492	Hs.42743	hypothetical protein	4.4	73	17	6.2	
107727	AA149707	Hs.173091	ubiquitin-like 3	3.6	262	80	3.7	
107859	AW732573	Hs.47584	potassium voltage-gated channel, delayed	5.7	85	15	7.8	
107876	AW372451	Hs.61184	CGI-79 protein	3.5	35	1	1	
107884	AA054949	Hs.61307	ESTs	4.3	43	10	2.7	
107886	AA025782	Hs.61284	ESTs	3.1	31	9	2.2	
107908	AF087999	Hs.42826	ESTs	4.7	47	4	4.3	
107922	BE153855	Hs.61460	Ig superfamily receptor LNIR	9	90	1	5.5	

107994	AA036811	Hs.48469	LIM domains containing 1	4.5	45	1	3.8
108040	AL121031	Hs.159971	SWI/SNF related, matrix associated, acti	6.5	65	2	6
108055	AJ404672	Hs.334483	hypothetical protein FLJ23571	7.4	74	8	6
108063	BE548479	Hs.14838	hypothetical protein FLJ10773	3.4	34	1	2.3
108339	AW151340	Hs.51615	ESTs, Weakly similar to ALU7_HUMAN ALU S	18.7	187	1	17
108467	AI478658	Hs.94631	brefeldin A-inhibited guanine nucleotide	3.8	38	1	3.2
108539	AA084677	Hs.54558	hypothetical protein FLJ22222	5.7	57	1	4.9
108634	AW022410	Hs.68507	ESTs	3.2	32	5	1.7
108647	BE546947	Hs.44276	homeo box C10	8.7	247	29	5.7
108695	AB029000	Hs.70823	KIAA1077 protein	3.7	625	168	3.8
108778	AF133123	Hs.90847	general transcription factor IIIC, polyp	3.7	37	1	3.2
108806	AF070578	Hs.71168	Homo sapiens clone 24674 mRNA sequence	3.4	34	1	2.8
108807	AI652236	Hs.48376	hypothetical protein FLJ20644	3.5	35	1	3.2
108810	AW295647	Hs.71331	hypothetical protein MGC5350	5.3	53	1	2.8
108846	AL117452	Hs.44155	DKFZP586G1517 protein	4.8	96	20	6.5
108857	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	5.4	54	1	4
108893	BE276891	Hs.194691	retinoic acid induced 3	3.1	529	170	4.1
108917	AI380268	Hs.173648	ESTs, Weakly similar to Zinc-finger prot	3.3	33	5	1.7
109010	NM_007240	Hs.44229	dual specificity phosphatase 12	3.4	34	1	2.6
109060	BE062109	Hs.241551	chloride channel, calcium activated, fam	3.1	31	8	2
109101	AW608930	Hs.52184	hypothetical protein FLJ20618	3.4	71	21	2.4
109112	AW419196	Hs.257924	hypothetical protein FLJ13782	4.1	334	82	3.4
109124	AK000684	Hs.183887	hypothetical protein FLJ22104	3.3	33	1	2.9
109128	H89083	Hs.181915	ESTs	4	40	7	1.1
109160	BE220601	Hs.301997	hypothetical protein FLJ13033	3.8	233	62	3.8
109166	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	8.8	199	23	16.1
109173	AA179962	Hs.73643	EST	3.2	32	1	2.2
109178	AW976516	Hs.283707	Homo sapiens cDNA: FLJ21354 fis, clone C	3.2	32	10	2.9
109235	AI381800	Hs.300684	calcitonin gene-related peptide-receptor	4.9	121	25	10.4
109273	AA375752	Hs.82719	Homo sapiens mRNA; cDNA DKFZp586F1822 (f	2.9	114	39	9.9
109292	AW975746	Hs.188662	KIAA1702 protein	7.1	71	1	6.5
109391	AL096858	Hs.184245	KIAA0929 protein Msx2 interacting nuclea	6.9	69	5	6.2
109411	R98881	Hs.109655	sex comb on midleg (Drosophila)-like 1	3.3	39	12	1.5
109412	BE543313	Hs.209473	hypothetical protein FLJ10520	4.2	56	14	2.2
109415	U80736	Hs.110826	trinucleotide repeat containing 9	12.3	123	1	11.3
109481	AA878923	Hs.289069	hypothetical protein FLJ21016	3.2	286	91	5.7
109517	AI631874	Hs.155140	casein kinase 2, alpha 1 polypeptide	8.3	83	8	1.9
109597	AA989362	Hs.293780	ESTs	5.9	59	10	4.2
109729	F10024	Hs.268740	ESTs	3.2	41	13	3.3
109795	AA173942	Hs.326416	Homo sapiens mRNA; cDNA DKFZp564H1916 (f	15.9	208	36	1.8
109799	AW965076	Hs.180378	hypothetical protein 669	5	50	5	4.1
109883	R68827	Hs.95011	syntrophin, beta 1 (dystrophin-associate	3.7	37	4	2
109912	AW390822	Hs.301528	L-kynurenine/alpha-aminoadipate aminotra	14.2	142	1	9.5
109937	AI084066	Hs.20072	myosin regulatory light chain interactin	4.1	41	7	1.7
109958	AA001266	Hs.133521	ESTs	4.2	58	14	0.8
109984	AI796320	Hs.10299	Homo sapiens cDNA FLJ13545 fis, clone PL	3.2	138	43	3.6
110009	BE075297	Hs.6614	ESTs, Weakly similar to A43932 mucin 2 p	6.3	693	110	7.2
110240	AI668594	Hs.176588	ESTs, Weakly similar to CP4Y_HUMAN CYTOC	4.6	913	199	2.9
110369	AK000768	Hs.107872	hypothetical protein FLJ20761	3.8	38	7	2.8
110426	AI610702	Hs.28212	ESTs, Weakly similar to TRHY_HUMAN TRICH	6.7	78	12	3
110478	H11236	Hs.31034	peroxisomal biogenesis factor 11A	3.7	37	1	2.1
110481	AF075089	Hs.36823	ESTs	3.6	36	10	2.5
110581	H61560		gb:yr22g03.s1 Soares fetal liver spleen	3.3	33	1	1.8
110674	AA071276	Hs.19469	KIAA0859 protein	3.5	35	8	1.9
110705	AB007902	Hs.32168	KIAA0442 protein	3.6	282	79	1.7
110721	H97678	Hs.31319	ESTs	4.4	103	24	3.8
110731	NM_014899	Hs.188006	KIAA0878 protein	3.3	138	42	3.6
110769	BE000831	Hs.23837	Homo sapiens cDNA FLJ11812 fis, clone HE	13.5	135	1	5.1
110775	N22414		gb:yw39a07.s1 Weizmann Olfactory Epithel	5.4	54	1	3.7
110787	AA831267	Hs.12244	hypothetical protein FLJ20097	4.7	47	4	4.2
110799	AI089660	Hs.323401	dpy-30-like protein	5	50	1	4.3
110818	AL157503	Hs.27552	Homo sapiens mRNA; cDNA DKFZp586N2424 (I	3.1	31	1	2.7
110839	AF153330	Hs.30246	solute carrier family 19 (thiamine trans	8.4	84	1	5.3
110844	AI740792	Hs.167531	methylcrotonoyl-Coenzyme A carboxylase 2	10.5	105	4	7.1
110854	BE612992	Hs.27931	hypothetical protein FLJ10607 similar to	7.9	79	1	6.2
110882	AW963705	Hs.301183	molecule possessing ankyrin repeats indu	3.9	353	90	1.2
110908	AI433165	Hs.9856	ESTs	3.1	31	1	1.3

110915	BE092285	Hs.29724	hypothetical protein FLJ13187	20.9	209	1	19.5
110930	BE242691	Hs.14947	ESTs	3.4	115	34	2.4
110970	Y19062	Hs.96870	staufen (Drosophila, RNA-binding protein	3.5	35	9	3.2
111084	H44186	Hs.15456	PDZ domain containing 1	4.3	43	1	2
111125	N63823	Hs.269115	ESTs, Moderately similar to Z195_HUMAN Z	5.4	54	1	4.3
111132	AB037807	Hs.83293	hypothetical protein	7.2	72	10	6.1
111164	N45180	Hs.122489	Homo sapiens cDNA FLJ13289 fis, clone OV	7.7	77	1	5
111179	AK000136	Hs.10760	asporin (LRR class 1)	25.1	288	12	6.7
111184	AI815486	Hs.243901	Homo sapiens cDNA FLJ20738 fis, clone HE	3.9	146	37	9.6
111190	AK002055	Hs.151046	hypothetical protein FLJ11193	6.3	63	1	5.8
111221	AB037782	Hs.15119	KIAA1361 protein	3.7	119	33	6.7
111223	AA852773	Hs.334838	KIAA1866 protein	3.8	402	112	4.9
111229	AW389845	Hs.110855	ESTs	4.3	43	1	1
111234	AA902656	Hs.21943	NIF3 (Ngg1 interacting factor 3, S.pombe	3.3	33	1	1.1
111241	AA345644	Hs.288880	PAN2 protein	4.8	61	13	5.6
111345	AW263155	Hs.14559	hypothetical protein FLJ10540	4.3	43	5	2.2
111353	W20090	Hs.6516	ESTs	4.1	41	1	2.6
111357	BE314949	Hs.87128	hypothetical protein FLJ23309	3.8	425	111	4
111378	AW160993	Hs.326292	hypothetical gene DKFZp434A1114	4.3	65	15	5.7
111389	AK000987	Hs.169111	oxidation resistance 1	3.4	314	91	2.4
111540	U82670	Hs.9786	zinc finger protein 275	3.5	35	1	2.1
111806	BE071382	Hs.279008	hypothetical protein FLJ20170	3.5	105	30	9.6
111884	AW502285	Hs.127236	hypothetical protein FLJ12879	3.2	37	12	3.5
111923	BE383234	Hs.25925	Homo sapiens, clone MGC:15393, mRNA, com	6.2	62	2	5.9
111929	AF027208	Hs.112360	prominin (mouse)-like 1	8.1	328	41	1.7
111942	R40576	Hs.21590	hypothetical protein DKFZp564O0523	4.2	125	30	7.4
111987	NM_015310	Hs.6763	KIAA0942 protein	6.5	65	10	1.5
112092	R44538		gb:yg29c02.s1 Soares infant brain 1NIB H	3.3	33	10	2.3
112134	R41823	Hs.7413	ESTs; calsyntenin-2	6.1	185	31	6.6
112197	NM_003655	Hs.5637	ESTs	3.5	507	145	3.3
112198	AI432872	Hs.288539	hypothetical protein FLJ22191	3.5	40	12	2.5
112244	AB029000	Hs.70823	KIAA1077 protein	5.7	567	100	6.7
112253	R51818		gb:yg77h12.s1 Soares infant brain 1NIB H	4	70	18	6.8
112269	R53734	Hs.25978	ESTs, Weakly similar to 2109260A B cell	3.7	37	1	3
112275	AW972635	Hs.301904	hypothetical protein FLJ12671	4.3	45	11	4.4
112280	AA863360	Hs.26040	ESTs, Weakly similar to fatty acid omega	2.8	751	270	1.3
112305	AK000914	Hs.26244	hypothetical protein FLJ10052	3.5	41	12	3.7
112483	AW969785	Hs.285885	Homo sapiens cDNA FLJ11321 fis, clone PL	4.2	42	6	3.6
112513	R68425	Hs.13809	hypothetical protein FLJ10648	4.7	54	12	4.5
112571	AA412205	Hs.140996	ESTs	4.8	48	2	3.4
112971	Z42387	Hs.83883	transmembrane, prostate androgen induced	4.5	390	87	5.3
113023	AL134324	Hs.7312	ESTs	3.2	99	31	3.1
113047	AI571940	Hs.7549	ESTs	9.6	124	13	9
113073	N39342	Hs.103042	microtubule-associated protein 1B	9.1	91	6	8.3
113083	AA283057	Hs.266957	hypothetical protein FLJ14281	6.5	65	6	4.6
113287	T56847	Hs.194040	ESTs, Weakly similar to I38022 hypothet	3.5	35	1	1.4
113296	AW449560	Hs.89576	inner mitochondrial membrane peptidase 2	3.5	35	4	3.3
113523	AI791905	Hs.95549	hypothetical protein	7.6	76	1	4.2
113604	AI075407	Hs.296083	ESTs, Moderately similar to I54374 gene	3.1	453	148	7
113617	AI869372	Hs.17207	Homo sapiens cDNA FLJ11922 fis, clone HE	3.6	36	4	2.6
113702	T97307		gb:ye53h05.s1 Soares fetal liver spleen	12.3	129	11	11.7
113783	AL359588	Hs.7041	hypothetical protein DKFZp762B228	4.6	46	4	4.3
113791	AI269096	Hs.135578	chitobiase, di-N-acetyl-	3.6	36	1	1.2
113794	T62849	Hs.11090	membrane-spanning 4-domains, subfamily A	3.3	744	227	2.5
113804	BE247683	Hs.14611	dual specificity phosphatase 11 (RNA/RNP	3.3	180	54	2.1
113808	W44735	Hs.9286	Homo sapiens cDNA: FLJ21278 fis, clone C	5.1	51	5	4.5
113847	NM_005032	Hs.4114	plastin 3 (T isoform)	3.2	236	75	2.1
113849	AA457211	Hs.8858	bromodomain adjacent to zinc finger doma	4.3	43	8	3.6
113867	AW002834	Hs.24095	ESTs	6.1	110	18	10.2
113886	W76027	Hs.23920.	hypothetical protein FLJ11105	4	48	12	4
113923	AW953484	Hs.3849	hypothetical protein FLJ22041 similar to	3.7	239	65	3.6
113936	W17056	Hs.83623	nuclear receptor subfamily 1, group I, m	4.3	819	191	1.2
113950	AI267652	Hs.30504	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	10.7	123	12	7
114030	AI825388	Hs.184476	hypothetical protein FLJ21939 similar to	4.4	44	6	2.3
114051	AB026438	Hs.177534	dual specificity phosphatase 10	4.5	45	4	2.6
114057	AF116653	Hs.34192	Homo sapiens PRO0823 mRNA, complete cds	3.5	35	6	3.2
114082	AK001612	Hs.26962	Homo sapiens cDNA FLJ10750 fis, clone NT	3.1	31	8	1.5

114124	W57654	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	24.2	242	10	5.6
114138	AW384793	Hs.15740	Homo sapiens mRNA; cDNA DKFZp434E033 (fr	8.7	67	1	6.3
114162	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase	3.8	73	19	1.8
114196	AF017445	Hs.150926	fucose-1-phosphate guanylyltransferase	4.4	104	24	5.1
114208	AL049468	Hs.7859	ESTs	5.7	57	1	4.9
114239	AL137687	Hs.267445	Homo sapiens mRNA; cDNA DKFZp434B231 (fr	3.3	33	1	2.4
114251	H15261	Hs.21948	ESTs	4.2	46	11	1.4
114306	AF100143	Hs.6540	fibroblast growth factor 13	4.5	45	2	3
114460	AF183810	Hs.26102	trichorhinophalangeal syndrome I	4.4	44	1	3
114542	AW970128	Hs.91011	anterior gradient 2 (Xenopus laevis) hom	4.7	770	168	5.8
114652	AI521936	Hs.107149	novel protein similar to archaeal, yeast	5.2	52	3	2.3
114767	AI859865	Hs.154443	minichromosome maintenance deficient (S.	4.6	196	43	10
114768	AF212848	Hs.182339	ets homologous factor	13.7	137	1	8.9
114774	AV656017	Hs.184325	CGI-76 protein	3.3	168	51	7.3
114798	AA159181	Hs.54900	serologically defined colon cancer antig	7.4	137	19	1.8
114821	AI648602	Hs.55468	ESTs	4.7	57	12	4.7
114860	AL157545	Hs.42179	bromodomain and PHD finger containing, 3	9.1	91	1	7.6
114918	BE165762	Hs.23518	hypothetical protein from BCRA2 region	10.1	111	11	10.2
114940	BE092696	Hs.75928	ESTs	6.4	67	11	5
114965	AI733881	Hs.72472	BMP-R1B	35.9	359	10	29.7
114969	AW162998	Hs.24684	KIAA1376 protein	9.4	94	8	7.3
114988	AA251089		gb:zs04f05.s1 NCI_CGAP_GCB1 Homo sapiens	11.5	115	1	6.9
115004	AA329340	Hs.4867	mannosyl (alpha-1,3-)-glycoprotein beta-	4.2	42	9	1.1
115054	AW265668	Hs.87729	hypothetical protein FLJ12428	5.1	51	1	4.2
115061	AI751438	Hs.41271	Homo sapiens mRNA full length insert cDN	4.5	290	65	3.7
115140	NM_014158	Hs.279938	HSPC067 protein	4.8	48	1	4.4
115142	AI623693	Hs.191533	ESTs	3.2	49	16	4.2
115188	AK000219	Hs.88367	hypothetical protein FLJ20212	3.3	33	1	3
115206	AW183695	Hs.186572	ESTs	5.8	58	1	5
115221	AW365434	Hs.79741	hypothetical protein FLJ10116	5.6	343	62	2.5
115262	AI422867	Hs.88594	ESTs	11.2	112	1	10.3
115291	BE545072	Hs.122579	hypothetical protein FLJ10461	4.5	98	21	7.8
115536	AK001468	Hs.62180	anillin (Drosophila Scrapa homolog), act	5.9	59	1	4.2
115583	NM_012317	Hs.45231	leucine zipper, down-regulated in cancer	9.8	98	1	8.8
115600	AA081395	Hs.42173	Homo sapiens cDNA FLJ10366 fis, clone NT	4.8	48	2	1.8
115622	AI088691	Hs.208414	Homo sapiens mRNA; cDNA DKFZp564D0472 (f	4.4	44	7	1.1
115646	N36110	Hs.305971	solute carrier family 2 (facilitated glu	3.2	372	115	2.1
115674	AW992356	Hs.8364	Homo sapiens pyruvate dehydrogenase kina	10.2	506	50	2.8
115675	W87707	Hs.82065	interleukin 6 signal transducer (gp130,	5.2	405	78	10.1
115719	AW992405	Hs.59622	Homo sapiens, clone IMAGE:3507281, mRNA,	7.6	144	19	13.9
115725	AW899053	Hs.76917	F-box only protein 8	3.1	58	19	2.5
115764	AW582256	Hs.91011	anterior gradient 2 (Xenopus laevis) hom	5.7	368	65	26.5
115821	AW338063	Hs.130965	zinc-finger protein ZBRK1	3.9	39	8	2.2
115825	R50956	Hs.159993	glycosyltransferase	4.2	79	19	1.9
115839	BE300266	Hs.28935	transducin-like enhancer of split 1, hom	5.8	58	1	4.4
115844	AI373062	Hs.332938	hypothetical protein MGC5370	6.2	62	1	5.4
115892	AA281377	Hs.50831	ESTs	3.2	40	13	0.7
115967	AI745379	Hs.42911	ESTs	8.4	101	12	8.7
116093	AW673312	Hs.50848	hypothetical protein FLJ20331	3.6	36	1	2
116097	AI198719	Hs.178378	ESTs	5.1	51	1	2
116107	AL133916	Hs.172572	hypothetical protein FLJ20093	3.4	34	8	1
116127	AF126743	Hs.279884	DNAJ domain-containing	3.5	35	8	3.3
116129	AF189011	Hs.49163	putative ribonuclease 10	4.5	45	9	3.4
116204	AW881622	Hs.108646	Homo sapiens cDNA FLJ14934 fis, clone PL	5.2	52	4	3.9
116226	AW976438	Hs.17428	RBP1-like protein	3.8	38	7	2.1
116238	AV660717	Hs.47144	DKFZP586N0819 protein	5.1	198	39	17.9
116250	N76712	Hs.44829	ESTs, Weakly similar to I38022 hypothet	13.3	133	8	3.2
116256	AA328153	Hs.88201	ESTs, Weakly similar to A Chain A, Cryst	3.3	108	33	9.8
116298	AI955411	Hs.94109	Homo sapiens cDNA FLJ13634 fis, clone PL	4.8	179	38	2.8
116336	AL133033	Hs.4084	KIAA1025 protein	3.2	173	55	3
116351	AL133623	Hs.82501	similar to mouse Xm1 / Dhm2 protein	3.7	37	1	1.8
116365	N50174	Hs.46765	ESTs	3.9	39	10	0.6
116379	AA448588	Hs.71252	hypothetical protein DKFZp761C169	5.6	106	19	9
116429	AF191018	Hs.279923	putative nucleotide binding protein, est	3.6	256	72	3.7
116450	AI654450	Hs.47274	Homo sapiens mRNA; cDNA DKFZp564B176 (fr	3.1	119	39	2
116481	AA313607	Hs.58633	Homo sapiens cDNA: FLJ22145 fis, clone H	5.5	315	58	3.1
116470	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	3.4	496	144	1.6

116507	AI418368	Hs.68501	ESTs	3.1	31	4	1.9
116579	AW888411	Hs.81915	leukemia-associated phosphoprotein p18 (	3.3	931	279	5.8
116625	F01601	Hs.241567	RNA binding motif, single stranded inter	3.6	36	1	1.9
116674	AI768015	Hs.92127	ESTs	4.5	98	22	6.9
116680	AW902848	Hs.273829	ESTs	4.2	42	1	2.7
116710	F10577	Hs.306068	v-crk avian sarcoma virus CT10 oncogene	7.1	71	9	6.9
116724	AA741307	Hs.65641	hypothetical protein FLJ20073	4.3	190	44	5.4
116788	H25836	Hs.301527	ESTs, Moderately similar to unknown [H.s	22.8	228	9	12.4
116787	AW382955	Hs.15641	Homo sapiens cDNA FLJ14415 fis, clone HE	4.9	108	22	9
116790	AW161357	Hs.101174	microtubule-associated protein tau	4.6	163	35	7.3
116844	H64938	Hs.337434	ESTs, Weakly similar to A46010 X-linked	6.9	69	10	2.4
117027	AW085208	Hs.130093	ESTs	4.8	48	1	2.5
117067	H91184	Hs.335797	ESTs	3.3	33	1	2.3
117129	H95785	Hs.167652	ESTs, Highly similar to 1619485A CENP-E	3.1	38	13	1.7
117147	AW901347	Hs.38592	hypothetical protein FLJ23342	4.8	48	1	0.9
117170	N25929	Hs.42500	ADP-ribosylation factor-like 5	3.1	295	96	27.9
117209	W03011	Hs.306881	MSTP043 protein	3.6	41	12	2.8
117280	M18217	Hs.172129	Homo sapiens cDNA: FLJ21409 fis, clone C	3.9	322	83	4.4
117367	AI041793	Hs.42502	ESTs	3.5	72	21	1.3
117412	N32536	Hs.42845	solute carrier family 16 (monocarboxylic	17.4	174	9	6.9
117475	N30205	Hs.93740	ESTs, Weakly similar to I38022 hypothet	3.2	35	11	0.7
117634	AW341639	Hs.13323	hypothetical protein FLJ22059	5	50	1	4.7
117667	U59305	Hs.44708	Ser-Thr protein kinase related to the my	4.5	211	47	5
117852	AW877787	Hs.136102	KIAA0853 protein	4.6	46	1	3.8
117873	N49987	Hs.46624	HSPC043 protein	3.1	31	1	2.7
117924	AI521436	Hs.38891	ESTs	4.9	49	1	4.4
118138	AA374756	Hs.93560	Homo sapiens mRNA for KIAA1771 protein,	5	50	2	3.1
118449	AI813865	Hs.164478	hypothetical protein FLJ21939 similar to	3.8	89	25	0.9
118467	AF091434	Hs.43080	platelet derived growth factor C	3.2	378	117	2.8
118472	AL157545	Hs.42179	bromodomain and PHD finger containing, 3	14.5	145	1	2.4
118475	N68845		gb:za46c11.s1 Soares fetal liver spleen	3.1	199	64	1
118509	N22617	Hs.43228	Homo sapiens cDNA FLJ11835 fis, clone HE	6	60	5	3.7
118528	AI949952	Hs.49397	ESTs	3.3	81	25	1.5
118828	N78496	Hs.50824	EST, Moderately similar to I54374 gene N	3.4	740	217	2.8
118838	AW134482	Hs.173001	hypothetical protein FLJ13964	4.3	162	38	12.1
118854	T58283	Hs.10450	Homo sapiens cDNA: FLJ22063 fis, clone H	3.4	118	35	2.3
118873	AI824009	Hs.44577	ESTs	3.5	35	1	2.9
118888	AI191811	Hs.54629	ESTs	8.4	84	10	0.8
118901	AW292577	Hs.94445	ESTs	7.3	73	3	5.4
118981	N29309	Hs.39288	ESTs	5	50	5	4.7
118991	NM_016857	Hs.250696	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic	3.7	37	6	0.5
119023	N98488		gb:zb82h01.s1 Soares_senescent_fibroblas	3.3	36	11	0.6
119088	R39281	Hs.90790	Homo sapiens cDNA: FLJ22930 fis, clone K	3.3	167	51	2.6
119126	R45175	Hs.117183	ESTs	5.3	53	6	2.3
119128	H09334	Hs.92482	ESTs	3.7	37	4	3
119271	AI061118	Hs.65328	Fanconi anemia, complementation group F	8.2	82	1	6.4
119298	NM_001241	Hs.155478	cyclin T2	4	40	4	1.2
119307	BE048061	Hs.37054	ephrin-A3	3.3	571	171	2
119367	T78324	Hs.250695	ribosomal protein L34	3.4	34	3	2.4
119427	AW474547	Hs.53565	Homo sapiens PIG-M mRNA for mannosyltran	4.8	60	13	4.8
119560	AL079310	Hs.92260	high-mobility group protein 2-like 1	8.1	94	12	6.5
119586	AF088033	Hs.159225	ESTs	3.3	33	8	0.9
119638	NM_016122	Hs.56148	NY-REN-58 antigen	3.3	33	10	0.5
119676	AA243837	Hs.57787	ESTs	5.4	54	1	4.1
119717	AA918317	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	4.6	46	7	0.8
119771	AI905687	Hs.2533	EST	3.5	2073	595	2.1
119780	NM_016825	Hs.191381	hypothetical protein	4.4	44	1	3.1
119786	AL133396	Hs.121281	prion protein 2 (dublet)	3.4	34	1	2.6
119805	AJ223810	Hs.43213	ESTs, Weakly similar to IEF8_HUMAN TRANS	3.6	36	1	2.9
119859	AW245741	Hs.58461	ESTs, Weakly similar to A35659 trueppel-	5.2	52	6	1.8
119899	AI057404	Hs.58698	ESTs	3.7	37	4	1.9
119940	AL050097	Hs.272531	DKFZP586B0319 protein	6.9	162	24	2.6
119943	BE565849	Hs.14158	copine III	3.7	590	159	3.6
120132	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	6.9	319	47	2.1
120150	BE005771	Hs.153746	hypothetical protein FLJ22490	5.3	53	5	0.9
120215	AF109219	Hs.108787	phosphatidylinositol glycan, class N	3.2	106	34	3.3
120260	AK000081	Hs.101590	hypothetical protein	3.4	34	1	1.7

120298	AW995911	Hs.299883	hypothetical protein FLJ23399	4.2	124	30	1.8
120352	R06859	Hs.193172	ESTs, Weakly similar to I38022 hypothet	7.5	112	15	2.5
120378	AA223249	Hs.285728	abl-interactor 12 (SH3-containing protei	3.3	33	10	2.8
120418	AW966893	Hs.26613	Homo sapiens mRNA; cDNA DKFZp586F1323 (f	4.6	46	1	0.5
120473	AA251973	Hs.269988	ESTs	3.4	34	4	0.1
120493	AW958080	Hs.152939	Homo sapiens clone 24630 mRNA sequence	3.9	161	42	2
120524	AA281852	Hs.192905	ESTs	6.8	66	1	0.2
120554	AA284447	Hs.271887	ESTs	3.2	32	5	0.6
120562	BE244580	Hs.302267	hypothetical protein FLJ10330	8.5	127	15	1.6
120571	AB037744	Hs.34892	KIAA1323 protein	3.7	37	1	0.5
120572	H39599	Hs.294008	ESTs	3.6	36	8	0.2
120588	AA703226	Hs.16193	Homo sapiens mRNA; cDNA DKFZp586B211 (fr	5.6	101	18	1.6
120649	AA687322	Hs.192843	leucine zipper protein FKSG14	5.4	54	10	2.5
120658	AI952639	Hs.98267	ESTs	3.2	32	8	3
120713	AW449855	Hs.96557	Homo sapiens cDNA FLJ12727 fis, clone NT	5.3	58	11	3.3
120821	Y19062	Hs.96870	staufen (Drosophila, RNA-binding protein	3.3	33	3	0.2
120822	AA347422	Hs.238040	EST, Weakly similar to B34087 hypothetic	3.8	38	7	0.2
120915	AL135556	Hs.97104	ESTs	3.5	37	11	0.1
120922	AA481003	Hs.97128	ESTs	3.1	31	1	0.4
120977	AA398155	Hs.97600	ESTs	7.9	79	1	2.7
120999	AI972375	Hs.29628	hypothetical brain protein my038	5.1	51	1	2.4
121125	AL042981	Hs.251278	KIAA1201 protein	3.7	37	10	1
121176	AL121523	Hs.97774	ESTs	7	70	1	0.9
121202	AA970946	Hs.97794	ESTs	3.9	39	1	0.2
121429	AA406293	Hs.41167	ESTs	3.4	34	1	0.8
121448	AF044197	Hs.100431	B-cell attracting chemokine 1 (CXCL13;	3.5	35	1	2.6
121463	AK000282	Hs.239681	hypothetical protein FLJ20275	10.3	103	1	9.3
121517	AI002968	Hs.235402	ESTs, Weakly similar to T26525 hypothet	3.5	143	41	2.6
121553	AA412488	Hs.48820	TATA box binding protein (TBP)-associate	4.6	46	3	0.8
121556	AA412494	Hs.98152	EST	4.2	77	19	1.4
121581	AA416568		gb:zu05c10.s1 Soares_testis_NHT Homo sap	3.2	32	1	0.8
121709	AI338247	Hs.98314	Homo sapiens mRNA; cDNA DKFZp586L0120 (f	3.4	34	10	0.7
121723	AA243499	Hs.104800	hypothetical protein FLJ10134	2.9	214	74	3.7
121831	AA449644	Hs.193063	Homo sapiens cDNA FLJ14201 fis, clone NT	3.9	39	1	0.2
121853	AA425887	Hs.98502	hypothetical protein FLJ14303	4.4	48	11	0.9
121873	AV650929	Hs.145696	splicing factor (CC1.3)	3.8	150	42	3.2
121913	AI249368	Hs.98558	ESTs; protease inhibitor 15 (PI15)	2.7	864	321	0.6
121916	AW117207	Hs.98523	ESTs	3.5	35	3	2.3
122004	AI810721	Hs.95424	ESTs	4.9	49	7	3.7
122063	AW794215	Hs.301226	KIAA1085 protein	3.2	88	28	1.2
122223	AF169797	Hs.27413	adaptor protein containing pH domain, PT	12.6	126	7	7.5
122235	AA436475	Hs.112227	membrane-associated nucleic acid binding	4.1	43	11	1.6
122273	AI298368	Hs.150926	fucose-1-phosphate guanylyltransferase	3.1	31	1	1
122383	AA446189	Hs.99051	ESTs	3.3	53	16	4
122507	BE567620	Hs.99210	ESTs	3.2	291	91	4
122524	AA449453	Hs.192915	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.1	31	6	0.8
122636	AW551706	Hs.99519	hypothetical protein FLJ14007	3.5	35	1	3
122637	AA454149	Hs.99357	EST	3.2	32	10	3.1
122798	AW366286	Hs.145696	splicing factor (CC1.3)	3.2	36	11	2.5
122861	AA335721	Hs.119394	ESTs	5.6	108	20	1.8
122873	AA749382	Hs.118797	ubiquitin-conjugating enzyme E2D 3 (homo	3.6	36	1	3.4
122946	AI718702	Hs.308026	major histocompatibility complex, class	3.7	162	44	12.4
122963	AA478446	Hs.69559	KIAA1096 protein	7.2	72	1	5.7
122974	AA447871	Hs.194215	ESTs, Weakly similar to I38022 hypothet	4.7	59	13	4.7
123016	AW338067	Hs.323231	Homo sapiens cDNA FLJ11946 fis, clone HE	3.3	207	63	3.5
123090	AL135185	Hs.48778	niban protein	3.8	207	55	5.5
123137	AI073913	Hs.100688	ESTs, Weakly similar to JE0350 Anterior	9.9	351	36	13.9
123255	AA630335	Hs.105273	ESTs	4.1	72	18	1.5
123284	AA488988	Hs.293796	ESTs	3.7	41	11	1.6
123442	AA299652	Hs.111498	Homo sapiens cDNA FLJ11643 fis, clone HE	6.7	67	2	2.1
123449	AL049325	Hs.112493	Homo sapiens mRNA; cDNA DKFZp564D036 (fr	3.4	34	1	2.6
123475	BE439553	Hs.250528	Homo sapiens, clone IMAGE:4098694, mRNA,	9.7	102	11	6
123494	AW179019	Hs.112110	mitochondrial ribosomal protein L42	4.2	42	7	2.9
123503	AW975051	Hs.293156	ESTs, Weakly similar to I78885 serine/th	3.9	39	1	3.2
123516	AB037860	Hs.173933	nuclear factor I/A	4.3	43	1	3.5
123518	AL035414	Hs.21068	hypothetical protein	5.8	58	1	4.9
123523	AA608588		gb:ae54e06.s1 Stratagene lung carcinoma	3.1	927	295	2.1

123527	AF150208	Hs.108327	damage-specific DNA binding protein 1 (1	5	121	25	5.9
123570	AA608956	Hs.109653	ESTs	6.8	68	10	6.1
123619	AA602964		gb:no97c02.s1 NCI_CGAP_Pr2 Homo sapiens	8.5	85	1	4.3
123673	BE550112	Hs.158549	ESTs, Weakly similar to T2D3_HUMAN TRANS	3.9	39	5	3.7
123709	AA706910	Hs.112742	ESTs	3.9	60	16	4.8
123926	AA425769	Hs.227933	Alg5, S. cerevisiae, homolog of	3.4	80	24	3.8
123960	AW082852	Hs.287733	hypothetical protein FLJ23189	4.5	45	2	3.6
124006	AI147155	Hs.270016	ESTs	5.8	321	55	17
124059	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypothet	10.4	880	85	5.3
124287	H88296	Hs.5123	inorganic pyrophosphatase	3.1	41	14	2.7
124292	H11341	Hs.13368	Homo sapiens cDNA: FLJ23567 fis, clone L	3.2	32	1	1.5
124308	AA249027	Hs.241507	ribosomal protein S6	10.5	105	1	9.9
124315	NM_005402	Hs.288757	v-rel simian leukemia viral oncogene hom	12.8	141	11	12.2
124461	AF283778	Hs.80285	Homo sapiens mRNA; cDNA DKFZp586C1723 (f	3.1	31	1	1.8
124483	AI821780	Hs.179864	ESTs	3.3	33	1	1.7
124677	R01073		gb:ye84c03.s1 Soares fetal liver spleen	4.2	42	7	3
124777	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.4	210	63	3.3
124940	AF068846	Hs.103804	heterogeneous nuclear ribonucleoprotein	6.5	182	25	14.7
125079	T90298	Hs.271396	ESTs	3.1	31	6	2.4
125091	T91518		gb:ye20f05.s1 Stratagene lung (937210) H	3.4	985	286	2.8
125103	AA570056	Hs.122730	ESTs, Moderately similar to KIAA1215 pro	3.6	224	63	4
125144	AB037742	Hs.24338	KIAA1321 protein	6.3	63	6	5
125150	W38240		Empirically selected from AFFX single pr	3.6	38	11	2.6
125156	W93048	Hs.250723	hypothetical protein MGC2747	3.1	31	1	2.8
125226	AA782536	Hs.122647	N-myristoyltransferase 2	3.2	37	12	3.6
125279	AW401809	Hs.4779	KIAA1150 protein	13.1	131	1	5.1
125299	T32982	Hs.102720	ESTs	7.7	81	11	7.6
125303	AA173319	Hs.288193	hypothetical protein MGC12217	14.3	143	9	13.1
125377	W72949	Hs.77495	UBX domain-containing 1	3.3	34	11	3.2
125390	AL038165	Hs.75187	translocase of outer mitochondrial membr	8.2	124	15	11.5
125471	AA421691	Hs.152601	UDP-glucose ceramide glucosyltransferase	3.7	224	61	21
125617	AA287921	Hs.164950	ESTs	6.7	67	1	6
125621	T82841	Hs.278544	acetyl-Coenzyme A acetyltransferase 2 (a	5.5	55	10	4.2
125628	AA418069	Hs.241493	natural killer-tumor recognition sequenc	5.5	63	12	1
125660	AW292171	Hs.23978	scaffold attachment factor B	4.3	68	16	2.6
125698	AF078847	Hs.191356	general transcription factor IIH, polype	4.8	48	5	4.1
125745	AI858032	Hs.75722	ribophorin II	6.8	223	33	2.8
125770	AA143045	Hs.81665	v-kit Hardy-Zuckerman 4 feline sarcoma v	6.3	87	11	0.4
125827	NM_003403	Hs.97496	YY1 transcription factor	11.3	124	11	9.7
125852	AW630088	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (f	30.6	306	4	26.5
126349	T30968	Hs.13531	hypothetical protein FLJ10971	4.9	68	14	1.4
126384	AW090198	Hs.4779	KIAA1150 protein	6.4	74	12	6.6
126590	W78968	Hs.181307	H3 histone, family 3A	5	264	53	3.4
126645	AA316181	Hs.61635	sbx transmembrane epithelial antigen of	3.8	38	1	2.7
126663	AW518478	Hs.181297	ESTs	3.6	36	6	2.9
126695	AA643322	Hs.172028	a disintegrin and metalloproteinase doma	3.1	31	1	2.5
126764	AA036755	Hs.102178	syntaxin 16	4.4	76	18	1
126801	AW663887	Hs.7337	hypothetical protein FLJ10936	3.8	38	1	3
126813	AW163483	Hs.48320	double ring-finger protein, Dorfin	6.7	155	23	1.4
126838	AL043489	Hs.279609	mitochondrial carrier homolog 2	8.8	110	13	10.5
126855	AA129640	Hs.128065	ESTs	3.6	36	10	1.9
126971	T26989	Hs.283664	aspartate beta-hydroxylase	5.5	79	15	4.4
127167	AA625690	Hs.190272	ESTs	3.1	33	11	2.3
127251	AA936428	Hs.128638	ESTs	3.5	35	1	3.1
127349	AA412108	Hs.269350	ESTs	4.8	106	22	1
127439	D60237	Hs.14368	SH3 domain binding glutamic acid-rich pr	7.5	75	1	6.5
127537	AI926047	Hs.182859	ESTs	3.8	38	7	3.4
127542	AA703584	Hs.245474	ESTs, Moderately similar to ALU5_HUMAN A	3.3	33	9	0.9
127677	AF175265	Hs.284190	vacuolar protein sorting 35 (yeast homol	4.3	152	35	12.5
127774	AA313639	Hs.119488	cystein-rich hydrophobic domain 2	5.4	73	14	6.6
127999	AW976827	Hs.69851	nucleolar protein family A, member 1 (H/	5.2	81	16	1.1
128218	AA186733	Hs.292154	stromal cell protein	3.9	220	57	2.5
128305	AI954968	Hs.279009	matrix Gla protein	9.4	94	3	5.3
128470	AL049974	Hs.100261	Homo sapiens mRNA; cDNA DKFZp564B222 (fr	4.6	46	8	3.9
128482	AI694143	Hs.296251	programmed cell death 4	7.2	72	1	6.8
128501	AL133572	Hs.199009	protein containing CXXC domain 2	3.8	38	1	0.9
128517	AW994403	Hs.100861	hypothetical protein FLJ14600	5.6	73	13	6.1

128530	AI932995	Hs.183475	Homo sapiens clone 25061 mRNA sequence	4.2	104	25	7.8
128579	N25956	Hs.101810	Homo sapiens cDNA FLJ14232 fis, clone NT	3.1	172	55	3.1
128595	U31875	Hs.272499	short-chain alcohol dehydrogenase family	3.3	105	32	3
128810	N48373	Hs.10247	activated leucocyte cell adhesion molecu	7.3	106	15	5
128653	D87432	Hs.10315	solute carrier family 7 (cationic amino	3.1	31	1	2.2
128742	AA307211	Hs.251531	proteasome (prosome, macropain) subunit,	3.6	130	36	3.6
128773	NM_004131	Hs.1051	granzyme B (granzyme 2, cytotoxic T-lymp	3.9	43	11	1.8
128790	AF026692	Hs.105700	secreted frizzled-related protein 4	17.4	409	24	7.8
128783	AB011125	Hs.105749	KIAA0553 protein	3.1	34	11	2.7
128794	NM_014720	Hs.105751	Ste20-related serine/threonine kinase	3.6	36	5	1.5
128835	AK001731	Hs.106390	Homo sapiens mRNA; cDNA DKFZp586H0924 (f	13.3	288	87	7.9
128906	R57988	Hs.10708	epithelial protein lost in neoplasm beta	11.3	113	8	2.5
128925	R67419	Hs.21851	Homo sapiens cDNA FLJ12900 fis, clone NT	7.1	382	56	3.6
128949	AA009647	Hs.8850	a disintegrin and metalloproteinase dome	4.6	132	29	9.7
129017	AA115333	Hs.107988	ESTs	8.2	82	1	7.4
129075	BE250162	Hs.83765	dihydrofolate reductase	5	50	1	3.3
129095	L12350	Hs.108623	thrombospondin 2	3.2	814	257	2.4
129151	N23018	Hs.171391	C-terminal binding protein 2	4.4	44	1	3.8
129168	AI132988	Hs.109052	chromosome 14 open reading frame 2	14.2	142	6	9.4
129229	AF013758	Hs.109643	polyadenylate binding protein-interactin	7.1	71	1	6.2
129243	BE169531	Hs.109727	TAK1-binding protein 2; KIAA0733 protein	5	64	13	6.3
129259	AF220050	Hs.181385	uncharacterized hematopoietic stem/proge	5.2	75	15	6.4
129278	NM_015344	Hs.11000	leptin receptor overlapping transcript-l	3.7	39	11	3.2
129337	NM_014918	Hs.110488	KIAA0990 protein	9.5	95	1	8.5
129351	AL049538	Hs.62349	ras association (RalGDS/AF-6) domain con	7.6	92	12	1.4
129366	BE220806	Hs.184697	Homo sapiens clone 23785 mRNA sequence	7.1	150	21	14.5
129393	BE219987	Hs.166982	phosphatidylinositol glycan, class F	3.9	54	14	5.1
129457	X61959	Hs.207776	aspartylglucosaminidase	3.6	36	1	2.7
129486	NM_005754	Hs.220689	Ras-GTPase-activating protein SH3-domain	4	40	4	3.2
129568	AW964541	Hs.11500	hypothetical protein FLJ21127	4.6	199	44	2.3
129598	N30436	Hs.11556	Homo sapiens cDNA FLJ12566 fis, clone NT	4.2	42	1	3.6
129691	M26939	Hs.119571	collagen, type III, alpha 1 (Ehlers-Danl	6.4	1111	175	5
129698	BE242144	Hs.12013	ATP-binding cassette, sub-family E (OABP	4.8	48	8	3.8
129721	NM_001415	Hs.211539	eukaryotic translation initiation factor	5.8	171	30	2.9
129740	BE165866	Hs.83623	nuclear receptor subfamily 1, group I, m	4.5	45	1	2.4
129755	R42218	Hs.12342	Homo sapiens clone 24538 mRNA sequence	5.3	53	9	3.6
129801	R39248	Hs.239666	Homo sapiens cDNA FLJ13495 fis, clone PL	3.1	31	2	2.5
129821	AB028945	Hs.12696	cortactin SH3 domain-binding protein	11.4	114	1	10
129869	AI222069	Hs.13015	hypothetical protein similar to mouse Dn	4.7	558	119	4.5
129965	T71333	Hs.13854	ESTs	3.1	31	3	3
129977	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	3.2	32	1	0.2
130038	BE061916	Hs.125849	chromosome 8 open reading frame 2	6.7	67	1	5.7
130057	AF027153	Hs.324787	solute carrier family 5 (inositol transp	1	1	1	1
130095	AK001835	Hs.14838	hypothetical protein FLJ10773	14.6	219	15	7.6
130115	T47294	Hs.149923	X-box binding protein 1	3.1	1336	434	1.4
130170	AW977534	Hs.151469	calcium/calmodulin-dependent serine prot	5.3	53	9	3.2
130173	U38847	Hs.151518	TAR (HIV) RNA-binding protein 1	4.2	46	11	1.1
130343	AB040914	Hs.278628	KIAA1481 protein	13.2	331	25	12.4
130358	AF127577	Hs.155017	nuclear receptor interacting protein 1	3.3	354	108	4
130367	AL135301	Hs.8768	hypothetical protein FLJ10849	8.1	81	9	5.5
130385	AW067800	Hs.155223	stanniocalcin 2	72.2	722	1	1.9
130407	BE385099	Hs.334727	hypothetical protein MGC3017	6.5	65	4	5.3
130417	AW163518	Hs.153485	huntingtin interacting protein 2	3.5	79	23	2.5
130441	U63630	Hs.155837	protein kinase, DNA-activated, catalytic	6.1	61	1	5.7
130455	D90041	Hs.155956	N-acetyltransferase 1 (arylamine N-acety	10.6	706	66	9.2
130468	W19744	Hs.180059	Homo sapiens cDNA FLJ20653 fis, clone KA	3.9	39	1	1.9
130526	AW876523	Hs.15929	hypothetical protein FLJ12910	3.9	39	1	2.6
130567	AA383092	Hs.1608	replication protein A3 (14kD)	4.4	44	1	4.1
130604	AA383256	Hs.1657	estrogen receptor 1	32.2	322	1	4.7
130614	AI354355	Hs.16697	down-regulator of transcription 1, TBP-b	5.2	251	48	21
130617	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	10	100	1	7.6
130619	AI963376	Hs.12532	chromosome 1 open reading frame 21	3.9	39	1	3.4
130625	AF176012	Hs.260720	J domain containing protein 1	10.5	105	1	9
130677	AL161961	Hs.17767	KIAA1554 protein	6.8	129	19	12.1
130681	R62676	Hs.17820	Rho-associated, coiled-coil containing p	4.1	41	1	3.8
130693	R68537	Hs.17962	ESTs	9.2	234	26	16.8
130712	AJ271881	Hs.279762	bromodomain-containing 7	17.5	175	2	12.8

130723	BE247676	Hs.18442	E-1 enzyme	8.1	81	3	2.8
130731	AF052105	Hs.18879	chromosome 12 open reading frame	4.9	49	1	4.3
130780	AA197226	Hs.19347	hypothetical protein MGC11321	3.6	100	28	6.6
130863	Y10805	Hs.20521	HMT1 (hnRNP methyltransferase, S. cerevi	3.4	525	154	5.3
130871	AF080158	Hs.226573	inhibitor of kappa light polypeptide gen	10.5	121	12	1.8
130888	AL044315	Hs.173094	Homo sapiens mRNA for KIAA1750 protein,	6	202	34	3.7
130974	NM_003528	Hs.2178	H2B histone family, member Q	7.1	100	14	7.5
130979	NM_012446	Hs.169833	single-stranded-DNA-binding protein	3.2	87	27	1.7
130987	BE613269	Hs.21893	hypothetical protein DKFZp761N0624	3.5	124	35	6.5
130993	T97401	Hs.21929	ESTs	4.5	45	1	2.5
131076	AA749230	Hs.26433	dolichyl-phosphate (UDP-N-acetylglucosam	3.2	210	66	3.8
131085	BE207357	Hs.3454	KIAA1821 protein	3.8	42	11	0.6
131126	NM_016156	Hs.181326	KIAA1073 protein	8.7	87	6	1.9
131129	BE541042	Hs.23240	Homo sapiens cDNA: FLJ21848 fis, clone H	5.8	115	20	2.5
131148	AW953575	Hs.303125	p53-induced protein PIGPC1	3.8	585	153	3.7
131154	AW013807	Hs.182265	keratin 19	5.2	1320	256	3.2
131176	AA465113	Hs.23853	ESTs, Weakly similar to A34815 profilagg	3.8	38	1	3.3
131200	BE540516	Hs.293732	hypothetical protein MGC3195	4.8	48	1	4.1
131216	AI815486	Hs.243901	Homo sapiens cDNA FLJ20738 fis, clone HE	6.1	343	56	16.4
131245	AL080080	Hs.24766	thioredoxin domain-containing	8	100	13	2.9
131248	AI038989	Hs.332633	Bardet-Biedl syndrome 2	4	95	24	1.1
131273	AW205008	Hs.283378	Homo sapiens cDNA: FLJ21778 fis, clone H	4.6	239	53	3.5
131319	NM_003155	Hs.25590	stanniocalcin 1	3.5	402	114	2.1
131367	AI750575	Hs.173933	nuclear factor I/A	3.3	775	233	2.4
131375	AW293165	Hs.143134	ESTs	3.8	38	1	3
131379	AK001123	Hs.26176	hypothetical protein FLJ10261	3.9	116	30	0.5
131388	NM_014810	Hs.92200	KIAA0480 gene product	7.6	76	1	5
131475	AA992841	Hs.27263	KIAA1458 protein	5.1	113	22	6.1
131492	AI452601	Hs.288869	nuclear receptor subfamily 2, group F, m	8.4	169	20	4.6
131501	AV661958	Hs.8207	GK001 protein	3.1	197	63	18.7
131535	N22120	Hs.75277	hypothetical protein FLJ13910	5.9	59	1	4.4
131544	AL355715	Hs.28555	programmed cell death 9 (PDCD9)	5.1	51	1	3.9
131546	AA093668	Hs.28578	muscleblind (Drosophila)-like	3.8	79	21	6.9
131562	NM_003512	Hs.28777	H2A histone family, member L	4	350	88	3
131564	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	4.7	381	81	6.4
131604	AA306477	Hs.29379	hypothetical protein FLJ10687	4.6	46	7	3.8
131684	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	3.2	82	26	6.6
131687	BE297635	Hs.3069	heat shock 70kD protein 9B (mortalin-2)	6.7	93	14	8.4
131689	AB012124	Hs.30696	transcription factor-like 5 (basic helix	3.8	51	14	1.7
131693	AW963776	Hs.110796	SAR1 protein	7.2	72	4	5.7
131739	AF017986	Hs.31386	secreted frizzled-related protein 2	2.1	1561	757	1.7
131742	AA961420	Hs.31433	ESTs	11.7	117	1	10.1
131775	AB014548	Hs.31921	KIAA0648 protein	4.8	48	1	4.6
131787	D87077	Hs.196275	KIAA0240 protein	3.2	207	64	5.5
131798	X86098	Hs.301449	adenovirus 5 E1A binding protein	3.4	115	34	9.1
131836	W00712	Hs.32990	DKFZP566F084 protein	5.8	91	16	1.4
131853	AI681917	Hs.3321	ESTs, Highly similar to IRX1_HUMAN IROQU	4.9	632	129	1.7
131877	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	6.8	68	1	5.6
131881	AW361018	Hs.3383	upstream regulatory element binding prot	4	140	35	1.8
131885	BE502341	Hs.3402	ESTs	5.7	57	1	4.5
131904	AF078866	Hs.284296	Homo sapiens cDNA: FLJ22993 fis, clone K	5.5	90	17	2.9
131919	T15803	Hs.272458	protein phosphatase 3 (formerly 2B), cat	5.6	95	17	9.1
131941	BE252983	Hs.35088	ubiquitin specific protease 1	7.4	103	14	6.5
131945	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	3.7	37	1	3.4
131949	AK000010	Hs.258798	hypothetical protein FLJ20003	3.5	35	1	2.5
131965	W79283	Hs.35962	ESTs	5.5	168	31	4.4
131977	U90441	Hs.3622	procollagen-proline, 2-oxoglutarate 4-dl	3.7	37	9	2.8
131985	AA503020	Hs.36563	hypothetical protein FLJ22418	40.2	402	1	4
131993	AI878910	Hs.3688	cisplatin resistance-associated overexpr	7.3	73	1	1.2
132064	AA121098	Hs.3838	serum-inducible kinase	22.6	226	10	0.9
132094	NM_016045	Hs.3945	CGI-107 protein	3.1	227	73	16.8
132109	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	3.5	73	21	6.3
132116	AW960474	Hs.40289	ESTs	3.6	141	39	12.8
132143	D52059	Hs.7972	KIAA0871 protein	4.9	49	1	4.1
132160	W26408	Hs.295923	seven in absentia (Drosophila) homolog 1	4.4	53	12	2.1
132164	AI752235	Hs.41270	procollagen-lysine, 2-oxoglutarate 5-dio	5	225	45	9.1
132180	NM_004460	Hs.418	fibroblast activation protein, alpha	10.7	433	41	7.2

132197	AI699482	Hs.42151	ESTs	3.4	58	17	4
132256	AI078845	Hs.431	murine leukemia viral (bml-1) oncogene h	4.2	42	1	2.2
132298	NM_015986	Hs.7120	cytokine receptor-like molecule 9	3.4	34	2	3
132316	U28831	Hs.44566	KIAA1841 protein	18.6	186	10	1.5
132325	N37065	Hs.44856	hypothetical protein FLJ12116	5.5	323	59	10.5
132358	NM_003542	Hs.46423	H4 histone family, member G	3.3	979	298	2.2
132384	AA312135	Hs.46967	HSPCO34 protein	3.6	36	1	3.1
132388	W32624	Hs.278626	Arg/Abl-interacting protein ArgBP2	5.9	186	32	3.7
132393	AL135094	Hs.47334	hypothetical protein FLJ14495	4.2	159	38	7.1
132407	BE513126	Hs.47783	B aggressive lymphoma gene	4.6	46	1	4.3
132425	N87549	Hs.125287	zinc finger protein ZNF140-like protein	3.6	146	41	1.1
132440	AB020699	Hs.112751	KIAA0892 protein	3.3	33	4	2.9
132465	AW169847	Hs.49169	KIAA1634 protein	8.3	145	18	3.7
132522	AB023164	Hs.5070	KIAA0947 protein	4.6	46	1	4.4
132528	T78738	Hs.50758	SMC4 (structural maintenance of chromoso	9.3	93	1	8.4
132530	AA308105	Hs.50785	SEC22, vesicle trafficking protein (S. c	4.9	49	1	4.4
132543	BE568452	Hs.5101	protein regulator of cytokinesis 1	11.8	201	17	19.1
132572	AI929659	Hs.237825	signal recognition particle 72kD	3.8	38	1	3
132592	AW803564	Hs.288850	Homo sapiens cDNA: FLJ22528 fis, clone H	4.8	93	20	3.1
132602	AW606927	Hs.5306	hypothetical protein DKFZp586F1122 simil	6.1	61	2	5.9
132616	BE262677	Hs.283558	hypothetical protein PRO1855	3.4	193	58	12.3
132617	AF037335	Hs.5338	carbonic anhydrase XII	14.2	390	28	22.5
132618	AL050025	Hs.279916	hypothetical protein FLJ20151	3.3	909	274	3.2
132632	AU076916	Hs.5398	guanine monphosphate synthetase	5	50	1	4.1
132668	AB018319	Hs.5460	KIAA0776 protein	4.2	171	41	12.6
132742	AA025480	Hs.292812	ESTs, Weakly similar to T33468 hypothetl	6.5	65	1	5.6
132790	AW242243	Hs.168870	peroxisomal farnesylated protein	3.7	37	1	2.2
132811	U25435	Hs.57419	CCCTC-binding factor (zinc finger protei	7	115	17	5.4
132852	AL120050	Hs.58220	Homo sapiens cDNA: FLJ23005 fis, clone L	3.3	61	19	5.1
132856	NM_001448	Hs.58367	glypican 4	4.8	48	1	3.6
132880	BE077155	Hs.177537	hypothetical protein DKFZp761B1514	12.6	126	8	9.9
132902	AI936442	Hs.59838	hypothetical protein FLJ10808	11	187	17	10.4
132906	BE613337	Hs.234896	geminin	3.3	106	33	2.6
132914	AL047045	Hs.60293	Homo sapiens clone 122482 unknown mRNA	3.5	110	32	2.1
132968	AF234532	Hs.61638	myosin X	4.1	62	15	4.9
132977	AA093322	Hs.301404	RNA binding motif protein 3	22.1	221	9	17.8
132990	X77343	Hs.334334	transcription factor AP-2 alpha (activat	12.7	311	25	2.4
132994	AA112748	Hs.279905	clone HQ0310 PRO0310p1	3	380	127	5.5
133011	NM_006379	Hs.171921	sema domain, immunoglobulin domain (Ig),	7.3	271	37	2.3
133015	AJ002744	Hs.246315	UDP-N-acetyl-alpha-D-galactosamine:polyp	4.6	427	93	10.4
133070	U92649	Hs.64311	a disintegrin and metalloproteinase doma	3.6	36	1	3.1
133091	AK001628	Hs.64691	KIAA0483 protein	5.2	117	23	5
133192	AA218564	Hs.67052	vacuolar protein sorting 26 (yeast homol	3.1	359	118	2.5
133197	AI275243	Hs.180201	hypothetical protein FLJ20671	5.1	58	12	5.7
133199	AF231981	Hs.250175	homolog of yeast long chain polyunsatura	3	816	275	3.9
133221	W32474	Hs.301746	RAP2A, member of RAS oncogene family	3.1	234	76	8.8
133240	AK001489	Hs.242894	ADP-ribosylation factor-like 1	8.1	81	1	4.6
133271	Z48633	Hs.283742	H.sapiens mRNA for retrotransposon	12.4	124	6	10.8
133291	BE297855	Hs.69855	NRAS-related gene	3.3	33	1	2.9
133294	AJ001388	Hs.69997	zinc finger protein 238	7.9	234	30	18.9
133350	AI499220	Hs.71573	hypothetical protein FLJ10074	4.6	46	5	3.5
133362	AK001519	Hs.7194	CGI-74 protein	5	110	22	9.7
133370	AF245505	Hs.72157	DKFZP564I1922 protein	3.2	725	227	3.2
133407	AF017987	Hs.7308	secreted frizzled-related protein 1	4.1	374	91	1.1
133422	AB033061	Hs.73287	KIAA1235 protein	4.3	43	1	3.9
133435	AI929357	Hs.323966	Homo sapiens clone H63 unknown mRNA	5.5	186	34	16.5
133479	W01556	Hs.238797	ESTs, Moderately similar to I38022 hypot	3.5	35	7	2.1
133493	AW998046	Hs.194369	arginine-glutamic acid dipeptide (RE) re	3.6	39	11	0.4
133504	NM_004415	Hs.74316	desmoplakin (DPI, DPII)	4.1	640	158	3
133517	NM_000165	Hs.74471	gap junction protein, alpha 1, 43kD (con	3.2	351	111	5.2
133536	W25797	Hs.177486	amyloid beta (A4) precursor protein (pro	3.2	226	71	2.8
133578	AU077050	Hs.75066	transtin	3.4	178	53	8.8
133633	D21262	Hs.75337	nucleolar and coiled-body phosphoprotein	4.7	47	1	4
133640	AW248428	Hs.75355	ubiquitin-conjugating enzyme E2N (homolo	8.5	85	1	7.2
133669	NM_006925	Hs.166975	splicing factor, arginine/serine-rich 5	3.6	36	1	0.4
133681	AI352558	Hs.75544	tyrosine 3-monooxygenase/tryptophan 5-mo	3.4	234	68	10.7
133748	AW410035	Hs.75682	MAD (mothers against decapentaplegic, Dr	9.3	93	1	7.8

133765	M62194	Hs.75929	cadherin 11, type 2, OB-cadherin (osteob	3.2	560	174	2.6
133780	AA557660	Hs.76152	decorin	5.4	144	27	13.3
133784	BE622743	Hs.301064	arfaptin 1	4.7	47	1	4.1
133814	NM_002462	Hs.76391	myxovirus (influenza) resistance 1, homo	3.3	380	114	4.9
133829	AW830088	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (f	6.7	304	46	7.8
133845	AA147026	Hs.76704	ESTs	6.2	600	97	4.1
133913	AU076964	Hs.7753	calumenin	3.3	889	267	5
133968	AA355986	Hs.232068	transcription factor 8 (represses interl	3.7	91	25	2.6
133990	R48318	Hs.7822	Homo sapiens mRNA; cDNA DKFZp564C1216 (f	3.4	91	27	8.5
133999	AA535244	Hs.78305	RAB2, member RAS oncogene family	7.8	78	1	5.6
134032	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibito	5.9	59	1	3.3
134064	AF091822	Hs.78893	KIAA0244 protein	5.8	58	1	4.9
134087	U51166	Hs.173824	thymine-DNA glycosylase	8.4	100	16	4.4
134089	R51273	Hs.79029	ESTs	5.1	51	9	3.8
134095	NM_004354	Hs.79069	cyclin G2	5	50	1	3.2
134098	BE513171	Hs.79088	mitochondrial ribosomal protein L3	4.8	246	51	3.9
134110	U41060	Hs.79136	LIV-1 protein, estrogen regulated	4.5	1472	330	2.1
134125	NM_014781	Hs.50421	KIAA0203 gene product	4.8	69	15	5.8
134246	D28459	Hs.80612	ubiquitin-conjugating enzyme E2A (RAD6 h	7	97	14	7.5
134257	C05768	Hs.8078	Homo sapiens clone FBD3 Cri-du-chat crit	3.4	34	5	2.6
134272	X76040	Hs.278614	protease, serine, 15	3.6	36	1	2.8
134282	R45621	Hs.81057	hypothetical protein MGC2718	6.7	67	9	5.7
134288	AI022650	Hs.8117	erbb2-interacting protein ERBIN	4.5	137	31	12
134321	BE538082	Hs.8172	ESTs, Moderately similar to A46010 X-lin	5.2	52	1	4.9
134326	AW903838	Hs.81800	chondroitin sulfate proteoglycan 2 (vers	8.6	568	68	22.4
134328	AW959281	Hs.8184	ESTs	4.8	53	11	3.7
134348	AW291948	Hs.82065	interleukin 6 signal transducer (gp130,	7.1	71	4	6.4
134359	NM_001982	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	3	68	23	2.8
134367	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	4.4	44	1	4.1
134374	N22687	Hs.8236	ESTs	13.3	445	34	6
134380	AU077143	Hs.179565	minichromosome maintenance deficient (S.	4.5	45	2	3.4
134395	AA456539	Hs.8262	lysosomal	6	60	5	5.9
134401	AI916662	Hs.211577	kinectin 1 (kinesin receptor)	4.1	301	73	6.1
134405	AW067903	Hs.82772	collagen, type XI, alpha 1	4.6	1216	267	4.4
134415	AI750762	Hs.82911	protein tyrosine phosphatase type IVA, m	4.9	163	34	15.1
134417	NM_006416	Hs.82921	solute carrier family 35 (CMP-sialic aci	4.9	49	3	3.8
134419	W95642	Hs.82961	trefoil factor 3 (intestinal)	3.2	1872	592	3.3
134421	AU077198	Hs.82985	collagen, type V, alpha 2	6.3	1075	171	3.8
134436	U29344	Hs.83190	fatty acid synthase	3.3	710	217	2
134485	X82153	Hs.83942	cathepsin K (pycnodysostosis)	34.3	411	12	5.1
134487	AF051739	Hs.83954	protein associated with PRK1	4.8	153	32	4.3
134495	D63477	Hs.84087	KIAA0143 protein	3.1	147	46	12.7
134520	BE091005	Hs.74861	activated RNA polymerase II transcriptio	3.3	33	1	2
134542	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi	4.2	42	5	2.6
134570	U66615	Hs.172280	SWI/SNF related, matrix associated, acti	3.9	39	1	2.5
134590	AW903849	Hs.173840	HUEL (C4orf1)-interacting protein	3.7	41	11	0.6
134604	NM_002884	Hs.865	RAP1A, member of RAS oncogene family	5.2	52	1	3
134612	AW068223	Hs.171581	ubiquitin C-terminal hydrolase UCH37	4.9	49	1	3.7
134643	AW299723	Hs.87223	bone morphogenetic protein receptor, typ	5.2	52	5	3.5
134654	AK001741	Hs.8739	hypothetical protein FLJ10879	6.4	64	1	5.1
134656	AI750878	Hs.87409	thrombospondin 1	12.6	126	1	10.8
134672	AF271212	Hs.322901	disrupter of silencing 10	5.4	81	15	2.6
134700	AK000606	Hs.8868	golgi SNAP receptor complex member 1	3.4	179	52	1.5
134711	X04011	Hs.88974	cytochrome b-245, beta polypeptide (chro	3.2	143	45	13.9
134722	AF129536	Hs.284226	F-box only protein 6	7	70	6	6
134856	BE281128	Hs.9030	TONDU	3.1	31	1	2.3
134880	AI879195	Hs.90606	15 kDa selenoprotein	5.7	57	1	5
134917	X87241	Hs.166994	FAT tumor suppressor (Drosophila) homolo	3.2	153	48	4.7
134921	AL137491	Hs.125511	Homo sapiens mRNA; cDNA DKFZp434P1530 (f	4	452	114	2
134982	AK002085	Hs.92308	Homo sapiens cDNA FLJ11223 fis, clone PL	5.1	150	30	7.2
134989	AW968058	Hs.92381	nudix (nucleoside diphosphate linked mol	8.2	114	14	9.9
135029	H58818	Hs.187579	hydroxysteroid (17-beta) dehydrogenase 7	11.5	115	1	10
135035	AL034344	Hs.284186	forkhead box C1	5.4	259	48	1.4
135051	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	3.3	1298	394	2.2
135082	AK000987	Hs.93872	KIAA1682 protein	3.8	240	64	3.2
135073	W55956	Hs.94030	Homo sapiens mRNA; cDNA DKFZp586E1624 (f	8.1	101	13	7.9
135098	AW274526	Hs.277721	ovarian carcinoma antigen CA125	3.3	33	1	2.6

135117	W52493	Hs.94694	Homo sapiens cDNA FLJ10561 fis, clone NT	5.3	53	1	4.1	
135144	NM_016255	Hs.95260	Autosomal Highly Conserved Protein	7.4	74	5	2.4	
135154	AK001835	Hs.267812	sorting nexin 4	6.6	69	11	6.3	
135155	AI207958	Hs.166556	Homo sapiens, Similar to TEA domain fami	6.1	61	1	5.1	
135172	AB028956	Hs.12144	KIAA1033 protein	3.4	88	26	1.4	
135242	AI583187	Hs.9700	cyclin E1	3.1	31	1	2.3	
135243	BE463721	Hs.97101	putative G protein-coupled receptor	3.4	169	50	9.1	
135269	NM_003403	Hs.97496	YY1 transcription factor	3.4	475	142	2.5	
135356	BE312948	Hs.18104	hypothetical protein FLJ11274	3.1	31	10	1.7	
135357	AI565004	Hs.79572	cathepsin D (lysosomal aspartyl protease	4.7	710	151	2.5	
135389	U05237	Hs.99872	fetal Alzheimer antigen	20.6	206	4	19.1	
135397	L14922	Hs.166563	replication factor C (activator 1) 1 (14	3.2	32	1	2.4	
135400	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	3.2	117	37	9.4	
	AI471525	Hs.247486	ESTs	3.8	58	16	5.5	
	X70683	Hs.93668	ESTs	1.8	1047	596	1.6	
	L14922	Hs.82128	5T4 oncofetal trophoblast glycoprotein	5	285	58	1.2	
	M23263	Hs.904	amylo-1;6-glucosidase; 4-alpha-glucanotransferas		3.1	31	1	2.6
	AI267886	Hs.148027	polymerase (RNA) II (DNA directed) polypeptide B		7.8	137	18	11.9
	AA044840	Hs.241676	stromal cell-derived factor 1	4.7	114	25	0.9	
	N90960	Hs.227459	ESTs; Moderately similar to !!!! ALU SUBFAMILY		4.7	151	32	9.3
	AA873285	Hs.137947	ESTs	4.7	47	3	4.4	
	T56679	Hs.865	RAP1A; member of RAS oncogene family	4	40	1	3.4	
	AA305536		*EST176522 Colon carcinoma (Caco-2) cell line II		3.6	121	34	11.8
	AI393384		arylsulfatase D	3.5	113	33	1.7	
	AA219081	Hs.242396	ESTs; Moderately similar to !!!! ALU SUBFAMILY		3.4	107	32	9.9

TABLE 10A

Table 10 A shows the accession numbers for those pkeys lacking unigeneID's for Table 10. For each probeset, we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT number	Accession	
123619	371681_1	AA602964 AA609200	
104602	524482_2	H47610 R86920	
121581	283769_1	AA418568 AA442689 AA417233 AA442223	
123523	genbank_AA608588	AA608588	
100821	tigr_HT4306	M26460 U09116	
125091	genbank_T91516	T91516	
125150	NOT_FOUND_entrez_W38240	W38240	
116475	genbank_N66845	N66845	
104787	genbank_AA027317	AA027317	
106055	genbank_AA417034	AA417034	
113702	genbank_T97307	T97307	
101046	entrez_K01160	K01160	
101447	entrez_M21305	M21305	
101624	entrez_M55998	M55998	
124677	genbank_R01073	R01073	
110581	genbank_H61560	H61560	
119023	genbank_N98488	N98488	
110775	genbank_N22414	N22414	
112092	genbank_R44538	R44538	
112253	genbank_R51818	R51818	
107014	genbank_AA598820	AA598820	
114988	genbank_AA251089	AA251089	

TABLE 11: Figure 11 from BRCA 001-3 PCT

Table 11 depicts a preferred group of genes upregulated in tumor tissue compared to normal breast tissue.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of tumor to normal body tissue
R2: Ratio of 90th percentile tumor to normal body
R3: Ratio of 75th percentile normal body to tumor
R4: Ratio of tumor to normal breast tissue

Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2	R3	R4
100131	D12485	Hs.11951	ectonucleotide pyrophosphatase/phosphodi	13.2	244	19	9.9
100147	D13666	Hs.136348	osteoblast specific factor 2 (fasciclin	15.7	1030	68	5
100522	X51501	Hs.89949	prolactin-induced protein	22.7	760	34	1.4
100668	L05424	Hs.169610	CD44 antigen (homing function and Indian	8.5	85	1	3.2
101104	AW862258	Hs.169266	neuropeptide Y receptor Y1	15.3	153	1	14.1
101478	NM_002890	Hs.758	RAS p21 protein activator (GTPase activa	9.6	96	1	8.5
101724	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	9.4	94	1	0.3
101754	S70114	Hs.239489	TIA1 cytotoxic granule-associated RNA-bi	8.9	89	5	8
101888	AL049610	Hs.95243	transcription elongation factor A (SII)-	7.3	73	1	5.3
102165	BE313280	Hs.159627	death associated protein 3	9.3	93	5	8
102304	AF015224	Hs.46452	mammaglobin 1	8.5	2058	243	1.4
102348	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	6.4	428	67	2.3
102457	NM_001394	Hs.2359	dual specificity phosphatase 4	20.2	202	5	1.3
102567	U63830	Hs.146847	TRAF family member-associated NFKB activ	8.2	82	1	6.8
102823	D85390	Hs.5057	carboxypeptidase D	5.6	56	1	5.3
103557	AL133415	Hs.297753	vimentin	7.5	136	16	3.4
103613	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (ca	7.3	73	1	5.2
104115	AF183810	Hs.26102	opposite strand to trichorhinophalangeal	29	290	1	26.8
104667	AI239923	Hs.30098	ESTs	14.9	149	1	6.4
104804	AI858702	Hs.31803	ESTs, Weakly similar to N-WASP [H.sapien	7.7	77	1	5.1
104807	AI139058	Hs.125790	leucine-rich repeat-containing 2	7	70	1	6.5
104896	AW015318	Hs.23165	ESTs	7.4	74	1	6
104943	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	16.2	162	1	4.2
105038	AW503733	Hs.9414	KIAA1488 protein	5.5	55	1	5.2
105329	AA234561	Hs.22862	ESTs	2.8	131	47	3.9
105500	AW602166	Hs.222399	CEGP1 protein	25.4	508	20	3
105516	AK001269	Hs.30738	hypothetical protein FLJ10407	8.3	83	3	1.8
105730	AW377314	Hs.5364	DKFZP564I052 protein	6.9	69	1	4.4
106012	AI240665	Hs.8895	ESTs	21.2	212	6	17.4
106095	AF115402	Hs.11713	E74-like factor 5 (ets domain transcript	26.3	358	14	1
106155	AA425414	Hs.33287	nuclear factor I/B	9.9	483	49	1.8
107102	AB037755	Hs.30652	KIAA1344 protein	6.3	63	1	5.4
107136	AV661858	Hs.8207	GK001 protein	2.5	392	155	4.3
107151	AW378065	Hs.8687	ESTs	15.6	156	7	10.8
107922	BE153855	Hs.61460	Ig superfamily receptor LNIR	9	90	1	5.5
108339	AW151340	Hs.51615	ESTs, Weakly similar to ALU7_HUMAN ALU S	18.7	187	1	17
109112	AW419196	Hs.257924	hypothetical protein FLJ13782	4.1	334	82	3.4
109292	AW975746	Hs.188662	KIAA1702 protein	7.1	71	1	6.5
109415	U80736	Hs.110826	trinucleotide repeat containing 9	12.3	123	1	11.3
109912	AW390822	Hs.301528	L-kynurenine/alpha-aminoadipate aminotra	14.2	142	1	9.5
110009	BE075297	Hs.6614	ESTs, Weakly similar to A43932 mucin 2 p	6.3	693	110	7.2
110915	BE092285	Hs.29724	hypothetical protein FLJ13187	20.9	209	1	19.5
111164	N46160	Hs.122469	Homo sapiens cDNA FLJ13289 fis, clone OV	7.7	77	1	5

111179	AK000136	Hs.10780	asporin (LRR class 1)	25.1	288	12	8.7
111190	AK002055	Hs.151046	hypothetical protein FLJ11193	6.3	63	1	5.8
111223	AA852773	Hs.334838	KIAA1868 protein	3.6	402	112	4.9
111357	BE314949	Hs.87128	hypothetical protein FLJ23309	3.8	425	111	4
112244	AB029000	Hs.70823	KIAA1077 protein	5.7	567	100	6.7
113047	AI571940	Hs.7549	ESTs	9.6	124	13	9
113702	T97307		gb:ye53h05.s1 Soares fetal liver spleen	12.3	129	11	11.7
114124	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	24.2	242	10	5.6
114138	AW384793	Hs.15740	Homo sapiens mRNA; cDNA DKFZp434E033 (fr	6.7	67	1	6.3
114768	AF212848	Hs.182339	ets homologous factor	13.7	137	1	6.9
114860	AL157545	Hs.42179	bromodomain and PHD finger containing, 3	9.1	91	1	7.6
114965	AI733881	Hs.72472	BMP-R1B	35.9	359	10	29.7
114968	AA251089		gb:zs04l05.s1 NCI_CGAP_GCB1 Homo sapiens	11.5	115	1	6.9
115206	AW183695	Hs.186572	ESTs	5.8	58	1	5
115719	AW992405	Hs.59622	Homo sapiens, clone IMAGE:3507281, mRNA,	7.6	144	19	13.9
115844	AI373082	Hs.332938	hypothetical protein MGC5370	6.2	62	1	5.4
116470	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	1.8	1047	596	1.6
116786	H25836	Hs.301527	ESTs, Moderately similar to unknown (H.s	22.8	228	9	12.4
117280	M18217	Hs.172129	Homo sapiens cDNA: FLJ21409 fis, clone C	3.9	322	83	4.4
117412	N32536	Hs.42645	solute carrier family 16 (monocarboxylic	17.4	174	9	6.9
118472	AL157545	Hs.42179	bromodomain and PHD finger containing, 3	14.5	145	1	2.4
119271	AI061118	Hs.65326	Fanconi anemia, complementation group F	8.2	82	1	6.4
119771	AI905687	Hs.2533	EST	3.5	2073	595	2.1
120562	BE244580	Hs.302267	hypothetical protein FLJ10330	8.5	127	15	1.6
121463	AK000282	Hs.239881	hypothetical protein FLJ20275	10.3	103	1	9.3
121723	AA243499	Hs.104800	hypothetical protein FLJ10134	2.8	214	74	3.7
122963	AA478448	Hs.69559	KIAA1098 protein	7.2	72	1	5.7
123137	AI073913	Hs.100686	ESTs, Weakly similar to JE0350 Anterior	9.9	351	36	13.9
123619	AA602964		gb:no97c02.s1 NCI_CGAP_Pr2 Homo sapiens	8.5	85	1	4.3
123709	AA706910	Hs.112742	ESTs	3.9	60	18	4.8
124006	AI147155	Hs.270016	ESTs	5.8	321	55	17
124059	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	10.4	880	85	5.3
124308	AA249027	Hs.241507	ribosomal protein S6	10.5	105	1	9.9
125279	AW401809	Hs.4779	KIAA1150 protein	13.1	131	1	5.1
125617	AA287921	Hs.164950	ESTs	6.7	67	1	6
127439	D60237	Hs.14368	SH3 domain binding glutamic acid-rich pr	30.6	306	4	26.5
128305	AI954968	Hs.279009	matrix Gla protein	7.5	75	1	6.5
128482	AI694143	Hs.296251	programmed cell death 4	7.2	72	1	5.6
128790	AF026692	Hs.105700	secreted frizzled-related protein 4	17.4	409	24	7.8
128925	R67419	Hs.21851	Homo sapiens cDNA FLJ12900 fis, clone NT	7.1	392	56	3.6
129017	AA115333	Hs.107968	ESTs	8.2	82	1	7.4
129229	AF013758	Hs.109643	polyadenylate binding protein-interactin	7.1	71	1	6.2
129337	NM_014918	Hs.110488	KIAA0990 protein	9.5	95	1	6.5
129366	BE220806	Hs.184697	Homo sapiens clone 23785 mRNA sequence	7.1	150	21	14.5
129621	AB028945	Hs.12696	cortactin SH3 domain-binding protein	11.4	114	1	10
130038	BE061916	Hs.125849	chromosome 8 open reading frame 2	6.7	67	1	5.7
130057	AF027153	Hs.324787	solute carrier family 5 (inositol transp	1	1	1	1
130095	AK001635	Hs.14838	hypothetical protein FLJ10773	14.6	219	15	7.6
130343	AB040914	Hs.278828	KIAA1481 protein	13.2	331	25	12.4
130385	AW087800	Hs.155223	stanniocalcin 2	72.2	722	1	1.9
130407	BE385099	Hs.334727	hypothetical protein MGC3017	6.5	65	4	5.3
130441	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	6.1	61	1	5.7
130455	D90041	Hs.155956	N-acetyltransferase 1 (arylamine N-acety	10.8	706	68	9.2
130604	AA383258	Hs.1657	estrogen receptor 1	32.2	322	1	4.7
130617	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	10	100	1	7.6
130712	AJ271881	Hs.279762	bromodomain-containing 7	17.5	175	2	12.8
131148	AW953575	Hs.303125	p53-induced protein PIGPC1	3.9	585	153	3.7
131388	NM_014810	Hs.92200	KIAA0480 gene product	7.6	76	1	5
131564	T83500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	4.7	381	61	6.4
131742	AA961420	Hs.31433	ESTs	11.7	117	1	10.1
131877	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	6.8	68	1	5.6
131985	AA503020	Hs.36563	hypothetical protein FLJ22418	40.2	402	1	4
132316	U28831	Hs.44566	KIAA1641 protein	18.6	186	10	1.5
132528	T78736	Hs.50758	SMC4 (structural maintenance of chromoso	9.3	93	1	8.4
132742	AA025480	Hs.292812	ESTs, Weakly similar to T33468 hypothet	6.5	65	1	5.6
132990	X77343	Hs.334334	transcription factor AP-2 alpha (activat	12.7	311	25	2.4
133015	AJ002744	Hs.246315	UDP-N-acetyl-alpha-D-galactosamine:polyp	4.6	427	93	10.4

133199	AF231981	Hs.250175	homolog of yeast long chain polyunsatura	3	816	275	3.9
133240	AK001489	Hs.242894	ADP-ribosylation factor-like 1	8.1	81	1	4.6
133271	Z48633	Hs.283742	H.sapiens mRNA for retrotransposon	12.4	124	6	10.8
133640	AW246428	Hs.75355	ubiquitin-conjugating enzyme E2N (homolo	8.5	85	1	7.2
133746	AW410035	Hs.75862	MAD (mothers against decapentaplegic, Dr	9.3	93	1	7.8
133999	AA535244	Hs.78305	RAB2, member RAS oncogene family	7.8	78	1	5.6
134110	U41060	Hs.79136	LIV-1 protein, estrogen regulated	4.5	1472	330	2.1
134485	X82153	Hs.83942	cathepsin K (pycnodysostosis)	34.3	411	12	5.1
134654	AK001741	Hs.8739	hypothetical protein FLJ10879	6.4	64	1	5.1
134880	AI879195	Hs.90606	15 kDa selenoprotein	5.7	57	1	5
135029	H58818	Hs.187579	hydroxysteroid (17-beta) dehydrogenase 7	11.5	115	1	10
135389	U05237	Hs.99872	fetal Alzheimer antigen	20.8	208	4	19.1
128305	AI954968	Hs.279009	matrix Gla protein	9.4	94	3	5.3

TABLE 11A

Table 11A shows the accession numbers for those pkeys lacking unigeneID's for Table 11. For each probeset, we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT number	Accession
123619	371681_1	AA602964 AA609200
113702	genbank_T97307	T97307
114988	genbank_AA251089	AA251089

TABLE 12: Figure 12 from BRCA 001-3 PCT

Table 12 depicts a preferred group of genes upregulated in tumor tissue compared to normal breast tissue.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of tumor to normal body tissue
R2: Ratio of 90th percentile tumor to body
R3: Ratio of 75th percentile body to tumor
R4: Ratio of tumor to normal breast tissue

Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2	R3	R4
100131	D12485	Hs.11951	phosphodiesterase I (PC-1)	13.2	244	19	9.9
105500	AW602166	Hs.222399	ESTs	25.4	508	20	3
112244	AB029000	Hs.70823	KIAA1077 protein	5.7	567	100	6.7
114124	W57554	Hs.125019	ESTs	24.2	242	10	5.6
119771	AI905687	Hs.2533	ESTs	3.5	2073	595	2.1
121723	AA243499	Hs.104800	ESTs	2.9	214	74	3.7
128790	AF026692	Hs.105700	secreted frizzled-related protein 4	17.4	409	24	7.8
131148	AW853575	Hs.303125	ESTs	3.8	585	153	3.7
131985	AA503020	Hs.36563	ESTs	40.2	402	1	4
133199	AF231981	Hs.250175	Homo sapiens clone 23904 mRNA sequence	3	616	275	3.9

TABLE 13: Table 1 from BRCA 001-5 US

Table 13 depicts a preferred group of genes upregulated in breast cancer cells.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of tumor to normal body tissue

Pkey	ExAccn	UniGene ID	Unigene Title	R1
100038	M97935		control	16.7
100039	M97935		control	6.3
100040	M97935		control	6.3
100041	M97935		control	14.8
100082	AB003103	Hs.4295	proteasome (prosome; macropain) 26S sub	7.5
100091	AF000177	Hs.111783	Lsm1 protein	4.9
100100	AF006084	Hs.11538	actin related protein 2/3 complex; subunit	4.7
100103	AF007875	Hs.5085	dolichyl-phosphate mannosyltransferase p	13.4
100114	D00596	Hs.82962	thymidylate synthetase	15.9
100121	D10495	Hs.155342	protein kinase C; delta	4.6
100123	D10523	Hs.166669	oxoglutarate dehydrogenase (lipoamide)	7.5
100128	D11094	Hs.81153	proteasome (prosome; macropain) 26S sub	4.4
100131	D12485	Hs.11951	phosphodiesterase I/nucleotide pyrophosp	8.7
100137	D13627	Hs.15071	chaperonin containing TCP1; subunit 8 (t	9.5
100144	D13643	Hs.75816	Human mRNA for KIAA0018 gene; comp	6
100147	D13666	Hs.136348	osteoblast specific factor 2 (fasciclin I-like	8.5
100154	D14657	Hs.81892	KIAA0101 gene product	10.5
100164	D14812	Hs.173714	MORF-related gene X	4.6
100169	D14878	Hs.82043	D123 gene product	7.9
100190	D21090	Hs.178658	RAD23 (S. cerevisiae) homolog B	5.8
100203	D25538	Hs.172189	adenylate cyclase 7	9.9
100209	D26308	Hs.76289	biliverdin reductase B (flavin reductase (N	4.9
100215	D26598	Hs.82793	proteasome (prosome; macropain) subunit	14.2
100216	D26599	Hs.1390	proteasome (prosome; macropain) subunit	11.3
100219	D28137	Hs.118110	bone marrow stromal cell antigen 2	5.7
100227	D28915	Hs.82316	interferon-induced; hepatitis C-associated	5.7
100248	D31888	Hs.78398	KIAA0071 protein	7.4
100287	D43950	Hs.1600	chaperonin containing TCP1; subunit 5 (e	5.8
100294	D49396	Hs.75454	antioxidant protein 1	12.9
100307	D50525	Hs.699	hypothetical protein	8.4
100335	D63391	Hs.6793	platelet-activating factor acetylhydrolase;	6.8
100340	D63487	Hs.82563	KIAA0153 protein	4.4
100355	D78129	Hs.71465	Homo sapiens mRNA for squalene epoxid	12.6
100363	D78514	Hs.78563	ubiquitin-conjugating enzyme E2G 1 (hom	4.6
100368	D79987	Hs.153479	extra spindle poles; S. cerevisiae; homolo	6.5
100372	D79997	Hs.184339	KIAA0175 gene product	8.4
100375	D80004	Hs.75909	KIAA0182 protein	4.5
100379	D82060	Hs.278721	Ke4 gene; mouse; human homolog of	8.1
100387	D83777	Hs.75137	KIAA0193 gene product	10.7
100393	D84145	Hs.39913	novel RGD-containing protein	7.2
100398	D84557	Hs.155462	minichromosome maintenance deficient (m	7.2
100405	D86425	Hs.82733	nidogen 2	5.4
100406	D86479	Hs.118397	AE-binding protein 1	4.3
100409	D86957	Hs.80712	KIAA0202 protein	11.9
100421	D86985	Hs.79276	Human mRNA for KIAA0232 gene; comp	9.7
100446	D87464	Hs.10037	KIAA0274 gene product	6.4
100447	D87465	Hs.74583	KIAA0275 gene product	10
100448	D87469	Hs.57852	EGF-like-domain; multiple 2	6.2

100467	D89052	Hs.7476	ATPase; H+ transporting; lysosomal (vacu	7.5
100468	D89289	Hs.118722	fucosyltransferase 8 (alpha (1;6) fucosyltr	5
100486	HT1112	Hs.10842	Ras-Like Protein Tc4	16.9
100497	HT1400	Hs.79137	Carboxyl Methyltransferase, Aspartate, A	5.6
100618	HT2710	Hs.114599	Collagen, Type VII, Alpha 1	7.5
100661	HT3018	Hs.132748	Ribosomal Protein L39 Homolog	4.4
100667	HT3127	Hs.169610	Epican, Alt. Splice 11	4.6
100668	HT3938	Hs.169610	Epican, Alt. Splice 12	4.4
100676	HT3742	Hs.287820	Fibronectin, Alt. Splice 1	9
100775	HT26388	Hs.89603	Mucin 1, Epithelial, Alt. Splice 9	4.7
100783	HT4018	Hs.191356	Basic Transcription Factor, 44 Kda Subun	13.7
100829	HT4343	Hs.278544	Cytosolic Acetoacetyl-Coenzyme A Thio	10.6
100830	HT4344	Hs.4756	Rad2	5.5
100840	HT4392	Hs.183418	Protein Kinase Pilstre, Alpha, Alt. Splice	4.1
100850	HT417	Hs.297939	Cathepsin B	4
100866	HT4582	Hs.75113	Transcription Factor IIa	4.9
100906	HT5158	Hs.6398	Guanosine 5'-Monophosphate Synthase	8.7
100914	HT511	Hs.324178	Ras Inhibitor Inf	7.2
100918	HT544	Hs.73946	Endothelial Cell Growth Factor 1	5.9
100945	HT884	Hs.180686	Oncogene E6-Ap, Papillomavirus	4.6
100975	J02923	Hs.76506	lymphocyte cytosolic protein 1 (L-plastin	30.1
100988	J03589	Hs.76480	ubiquitin-like 4	8.3
100996	J03909	Hs.14623	interferon; gamma-inducible protein 30	6.9
100999	J03934	Hs.80706	diaphorase (NADH/NADPH) (cytochrom	4.3
101011	J04430	Hs.1211	acid phosphatase 5; tartrate resistant	5.9
101017	J04599	Hs.821	biglycan	5.1
101031	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B;	37.2
101038	J05249	Hs.79411	replication protein A2 (32kD)	6.1
101054	K02405	Hs.73931	Human MHC class II HLA-DQ-beta mRN	4.3
101061	K03515	Hs.180532	glucose phosphate isomerase	4.3
101091	L08132	Hs.149155	voltage-dependent anion channel 1	7.4
101097	L06797	Hs.89414	chemokine (C-X-C motif); receptor 4 (fus	4.6
101104	L07615	Hs.169266	Human neuropeptide Y receptor Y1 (NPY	18.3
101143	L12723	Hs.90093	heat shock 70kD protein 4	17.4
101152	L13800	Hs.9884	Homo sapiens liver expressed protein gen	7.6
101183	L19779	Hs.795	H2A histone family; member O	10.9
101216	L25876	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	7.4
101233	L29008	Hs.878	sorbitol dehydrogenase	14.6
101247	L33801	Hs.78802	glycogen synthase kinase 3 beta	7.5
101282	L38810	Hs.79387	proteasome (prosome; macropain) 26S sub	4.4
101326	L42572	Hs.78504	inner membrane protein; mitochondrial (m	5.8
101332	L47276	Hs.156346	Homo sapiens (cell line HL-6) alpha topo	18.9
101348	L77213	Hs.30954	phosphomevalonate kinase	7.5
101352	L77701	Hs.18297	COX17 (yeast) homolog; cytochrome c ox	9.3
101378	M13755	Hs.833	interferon-stimulated protein; 15 kDa	18.1
101396	M15796	Hs.78996	proliferating cell nuclear antigen	8.6
101404	M18342	Hs.182447	heterogeneous nuclear ribonucleoprotein C	4.5
101439	M20902	Hs.268571	apolipoprotein C-I	6.1
101464	M22538	Hs.51299	NADH dehydrogenase (ubiquinone) flavo	8.7
101469	M22877	Hs.169248	Human somatic cytochrome c (HCS) gene	4.2
101472	M22960	Hs.118126	protective protein for beta-galactosidase (	6.5
101478	M23379	Hs.758	RAS p21 protein activator (GTPase activa	14
101484	M24594	Hs.20315	interferon-induced protein 56	9.2
101539	M30818	Hs.926	myxovirus (influenza) resistance 2; homol	5.1
101540	M30938	Hs.84981	X-ray repair complementing defective rep	4.7
101544	M31169		Human propionyl-CoA carboxylase beta-s	5.5
101552	M31642	Hs.82314	hypoxanthine phosphoribosyltransferase 1	8.5
101580	M34677	Hs.83363	DNA segment on chromosome X (unique)	4.5
101600	M37583	Hs.119192	H2A histone family; member Z	5.7
101663	M60750	Hs.2178	H2B histone family; member A	5.8
101664	M60752	Hs.121017	H2A histone family; member A	13.5
101667	M60858	Hs.79110	nucleolin	4
101684	M63256	Hs.75124	cerebellar degeneration-related protein (62	7.6
101702	M64929	Hs.179574	protein phosphatase 2 (formerly 2A); regu	4.2
101754	M77142	Hs.239489	TIA1 cytotoxic granule-associated RNA-b	4.5
101758	M77836	Hs.79217	pyrroline-5-carboxylate reductase 1	5.7
101767	M81057	Hs.180884	carboxypeptidase B1 (tissue)	21.7

101770	M81601	Hs.78869	transcription elongation factor A (SII); 1	4.6
101791	M83822	Hs.62354	cell division cycle 4-like	9.7
101803	M88546	Hs.155691	pre-B-cell leukemia transcription factor 1	5.5
101809	M88849	Hs.323733	Homo sapiens connexin 26 (GJB2) mRNA	22.5
101839	M93036	Hs.692	membrane component; chromosomal 4; su	4
101851	M94250	Hs.82045	midkine (neurite growth-promoting factor	7.6
101888	M99701	Hs.95243	transcription elongation factor A (SII)-like	11.4
101973	S82597	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:po	4.6
101991	U00968	Hs.166	Human SREBP-1 mRNA; complete cds	4.1
102009	U02680	Hs.82643	protein tyrosine kinase 9	4.4
102025	U03911	Hs.78934	mutS (E. coli) homolog 2 (colon cancer; n	4
102047	U07158	Hs.83734	syntaxin 4A (placental)	6.1
102051	U07550	Hs.1197	heat shock 10kD protein 1 (chaperonin 10	4.4
102083	U10323	Hs.75117	interleukin enhancer binding factor 2; 45k	10.4
102095	U11313	Hs.75760	sterol carrier protein 2	9.5
102130	U15009	Hs.1575	small nuclear ribonucleoprotein D3 polyp	6.6
102133	U15173	Hs.155596	BCL2/adenovirus E1B 19kD-interacting p	4.3
102148	U16954	Hs.75823	ALL1-fused gene from chromosome 1q	6.9
102179	U19713	Hs.76364	allograft inflammatory factor 1	4.8
102180	U19718	Hs.83551	microfibrillar-associated protein 2	7.2
102193	U20758	Hs.313	secreted phosphoprotein 1 (osteopontin; b	7.2
102198	U21090	Hs.74598	polymerase (DNA directed); delta 2; regu	4.3
102202	U21931	Hs.574	fructose-bisphosphatase 1	4.5
102209	U22970	Hs.265827	interferon; alpha-inducible protein (clone	9.9
102211	U23070	Hs.78776	putative transmembrane protein	4.9
102220	U24389	Hs.65436	lysyl oxidase-like 1	8.5
102224	U24704	Hs.148495	proteasome (prosome; macropain) 26S sub	5.4
102234	U26312	Hs.278554	chromobox homolog 3 (Drosophila HP1 g	7.7
102250	U28014	Hs.74122	caspase 4; apoptosis-related cysteine prot	5.4
102260	U28386	Hs.159557	karyopherin alpha 2 (RAG cohort 1; impo	6.3
102261	U28488	Hs.155935	complement component 3a receptor 1	5.7
102273	U30888	Hs.75981	ubiquitin specific protease 14 (tRNA-guan	6.1
102298	U32849	Hs.54483	N-myc (and STAT) interactor	4.1
102302	U33052	Hs.89171	protein kinase C-like 2	4.3
102305	U33286	Hs.90073	chromosome segregation 1 (yeast homolo	5.4
102320	U34683	Hs.82327	glutathione synthetase	4.1
102330	U35451	Hs.77254	chromobox homolog 1 (Drosophila HP1 b	4
102348	U37519	Hs.87539	aldehyde dehydrogenase 8	9.4
102361	U39400	Hs.75859	chromosome 11 open reading frame 4	5.2
102362	U39412	Hs.75932	N-ethylmaleimide-sensitive factor attachm	9.3
102369	U39840	Hs.299867	hepatocyte nuclear factor 3; alpha	7.7
102395	U41767	Hs.92208	a disintegrin and metalloproteinase domai	10.4
102409	U43286	Hs.118725	selenophosphate synthetase 2	6.2
102418	U43923	Hs.79058	suppressor of Ty (S.cerevisiae) 4 homolog	4.1
102425	U44772	Hs.3873	palmitoyl-protein thioesterase (ceroid-lipo	4.8
102457	U48807	Hs.2359	dual specificity phosphatase 4	6.3
102465	U49352	Hs.81548	2;4-dienoyl CoA reductase 1; mitochondri	9.4
102495	U51240	Hs.79356	Lysosomal-associated multispanning mem	6.5
102534	U56833	Hs.198307	von Hippel-Lindau binding protein 1	8.6
102546	U57877	Hs.3577	succinate dehydrogenase complex; subunI	4.3
102549	U58046	Hs.198899	eukaryotic translation initiation factor 3; s	6.3
102557	U58766	Hs.264428	tissue specific transplantation antigen P35	5
102562	U59309	Hs.75653	fumarate hydratase	6
102568	U59877	Hs.223025	RAB31; member RAS oncogene family	9.1
102580	U60808	Hs.152981	CDP-diacylglycerol synthase (phosphatid	7.9
102581	U61145	Hs.77256	enhancer of zeste (Drosophila) homolog 2	7.6
102590	U62136	Hs.79300	Homo sapiens enterocyte differentiation a	7
102591	U62325	Hs.324125	amyloid beta (A4) precursor protein-bindi	4
102592	U62389	Hs.11223	Human putative cytosolic NADP-depende	5
102617	U65928	Hs.198767	Jun activation domain binding protein	6.1
102618	U65932	Hs.81071	extracellular matrix protein 1	23.2
102638	U67319	Hs.9216	caspase 7; apoptosis-related cysteine prot	8.9
102663	U70322	Hs.168075	karyopherin (importin) beta 2	7.1
102668	U70660	Hs.279910	ATX1 (antioxidant protein 1; yeast) homo	4.7
102679	U72681	Hs.11342	ninjurin 1; nerve injury-induced protein-1	4.7
102687	U73379	Hs.93002	ubiquitin carrier protein E2-C	7.7
102704	U76638	Hs.54089	BRCA1 associated RING domain 1	5.6

102705	U77180	Hs.50002	small inducible cytokine subfamily A (Cy	11.8
102721	U79241	Hs.118666	Human clone 23759 mRNA; partial cds	15
102729	U79254	Hs.181311	asparaginyl-tRNA synthetase	5
102739	U79282	Hs.155572	Human clone 23801 mRNA sequence	6
102742	U79293	Hs.159264	Human clone 23948 mRNA sequence	13.1
102761	U82130	Hs.118910	tumor susceptibility gene 101	7
102788	U86602	Hs.74407	nucleolar protein p40	4.1
102790	U87269	Hs.154196	E4F transcription factor 1	7.1
102801	U89605	Hs.38041	pyridoxal (pyridoxine; vitamin B6) kinase	4.7
102808	U90426	Hs.179608	nuclear RNA helicase; DECD variant of D	7.5
102817	U90904	Hs.83724	Human clone 23773 mRNA sequence	15.2
102823	U90914	Hs.5057	carboxypeptidase D	6.6
102827	U91327	Hs.6456	chaperonin containing TCP1; subunit 2 (b	6
102838	U94592	Hs.80658	Human uncoupling protein homolog (UCP	6.1
102841	U95006	Hs.37616	Human D9 splice variant B mRNA; comp	4.2
102844	U96113	Hs.324275	Homo sapiens Nedd-4-like ubiquitin-prot	6.8
102868	X02419	Hs.77274	plasminogen activator; urokinase	4
102907	X06985	Hs.202833	heme oxygenase (decycling) 1	22.7
102919	X12447		aldolase A; fructose-bisphosphate	9.9
102929	X13238	Hs.74649	cytochrome c oxidase subunit VIc	5.4
102973	X16663	Hs.14601	hematopoietic cell-specific Lyn substrate	4.8
102983	X17620	Hs.118638	non-metastatic cells 1; protein (NM23A)	4.6
102985	X17644	Hs.2707	G1 to S phase transition 1	20.6
103003	X52003	Hs.1406	trefoil factor 1 (breast cancer; estrogen-ind	10.7
103018	X53296	Hs.81134	interleukin 1 receptor antagonist	5.8
103023	X53793	Hs.117950	multifunctional polypeptide similar to SA	4
103038	X54925	Hs.83169	matrix metalloproteinase 1 (interstitial col	7.3
103060	X57766	Hs.155324	matrix metalloproteinase 11 (stromelysin	17.8
103073	X59417	Hs.74077	proteasome (prosome; macropain) subunit	5.6
103075	X59543	Hs.2934	ribonucleotide reductase M1 polypeptide	4.2
103080	X59798	Hs.82932	cyclin D1 (PRAD1: parathyroid adenomat	6.7
103094	X60787	Hs.296281	interleukin enhancer binding factor 1	5.7
103105	X61970	Hs.76913	proteasome (prosome; macropain) subunit	5.8
103121	X63879	Hs.4147	translocating chain-associating membrane	4.2
103149	X66363	Hs.171634	PCTAIRE protein kinase 1	12
103180	X69433	Hs.5337	isocitrate dehydrogenase 2 (NADP+); mit	18.9
103182	X69819	Hs.99995	intercellular adhesion molecule 3	10.7
103188	X70040	Hs.2942	macrophage stimulating 1 receptor (c-met	4.1
103191	X70218	Hs.2903	protein phosphatase 4 (formerly X); cataly	10.7
103193	X70476	Hs.75724	coatomer protein complex; subunit beta 2	8.2
103194	X70649	Hs.78580	DEAD/H (Asp-Glu-Ala-Asp/His) box pol	13.7
103195	X70940	Hs.2642	eukaryotic translation elongation factor 1	13.4
103206	X72755	Hs.77367	monokine induced by gamma interferon	15.1
103207	X72790		Human endogenous retrovirus mRNA for	5.3
103208	X72841	Hs.31314	retinoblastoma-binding protein 7	12.3
103216	X74262	Hs.16003	retinoblastoma-binding protein 4	4.1
103226	X75042	Hs.44313	v-rel avian reticuloendotheliosis viral onco	6.9
103230	X75861	Hs.74837	testis enhanced gene transcript	7.9
103262	X78565	Hs.289114	hexabrachion (tenascin C; cytotactin)	5
103278	X79882	Hs.80680	lung resistance-related protein	5.7
103297	X81788	Hs.9078	immature colon carcinoma transcript 1	4.6
103302	X82103	Hs.3059	coatomer protein complex; subunit beta	4.5
103316	X83301	Hs.324728	SMA5	7.1
103330	X85373	Hs.77496	small nuclear ribonucleoprotein polypepti	4
103349	X89059		serine/threonine kinase 9	4.7
103352	X89398	Hs.76853	uracil-DNA glycosylase	5.3
103364	X90872	Hs.279929	SULT1C sulfotransferase	4
103374	X91788	Hs.84974	chloride channel; nucleotide-sensitive; 1A	4.2
103380	X92396	Hs.24167	synaptobrevin-like 1	13.6
103395	X94754	Hs.278946	methionine-tRNA synthetase	14.2
103402	X95404	Hs.180370	cofilin 1 (non-muscle)	4.6
103410	X96506	Hs.285362	DR1-associated protein 1 (negative cofact	8.3
103420	X97065	Hs.173497	Sec23 (S. cerevisiae) homolog B	4.9
103421	X97074	Hs.119591	adaptor-related protein complex 2; sigma	5
103427	X97303	Hs.250655	H.sapiens mRNA for Ptg-12 protein	7
103430	X97544	Hs.20716	translocase of inner mitochondrial membr	4.5
103438	X98263	Hs.152720	M-phase phosphoprotein 6	4.5

103464	Y00285	Hs.76473	insulin-like growth factor 2 receptor	4.2
103470	Y00796	Hs.174103	integrin; alpha L (antigen CD11A (p180);	4.5
103494	Y08991	Hs.83050	phosphatidylinositol 3-kinase-associated p	4.1
103505	Y09912	Hs.33102	transcription factor AP-2 beta (activating	4.5
103547	Z14982	Hs.180062	proteasome (prosome; macropain) subunit	4.3
103551	Z15115	Hs.75248	topoisomerase (DNA) II beta (180kD)	4
103565	Z22548	Hs.148354	thioredoxin-dependent peroxide reductase	7.6
103587	Z29083	Hs.82128	5T4 oncofetal trophoblast glycoprotein	14.6
103621	Z47727	Hs.150675	polymerase (RNA) II (DNA directed) pol	6.3
103622	Z48042	Hs.278672	membrane component; chromosome 11; s	4.4
103658	Z74615	Hs.172928	collagen; type I; alpha 1	5.9
103680	Z93784		Homo sapiens DNA sequence from PAC	4.4
103772	AA092473	Hs.278554	chromobox homolog 3 (Drosophila HP1 g	4.9
103774	AA092898	Hs.92918	ESTs; Weakly similar to R07G3.8 [C.eleg	6.1
103821	AA157623	Hs.198793	KIAA0750 gene product	23.3
103835	AA172215	Hs.93748	ESTs; Moderately similar to TRANSCRIP	4
103886	AA236384	Hs.105737	ESTs; Weakly similar to gene 9305 protei	4.9
103890	AA238843	Hs.72085	ESTs; Weakly similar to unknown [S.cere	7.8
103892	AA243523	Hs.239189	ESTs	4.8
104054	AA393432	Hs.7100	hypothetical protein	5.3
104115	AA428090	Hs.26102	ESTs	28.7
104136	AA442669	Hs.268371	zv68f6.r1 Soares_total_fetus_Nb2HF8_9w	5.7
104147	AA451992	Hs.283037	ESTs; Highly similar to HSPC039 protein	6.9
104173	AA476564	Hs.76561	ESTs; Weakly similar to finger protein HZ	5.2
104181	AA479521	Hs.283740	ESTs	7.6
104183	AA480838	Hs.114309	ESTs	5.1
104192	AA486946	Hs.21321	Homo sapiens mRNA; cDNA DKFZp564	4.3
104209	AB000221	Hs.16530	small inducible cytokine subfamily A (Cy	12.3
104234	AB002357	Hs.168212	kinesin family member 3B	6.2
104271	C01687	Hs.7381	ATP synthase; H+ transporting; mitochon	4.2
104276	C02582	Hs.109253	ESTs; Highly similar to N-terminal acetyl	4.5
104307	D52818	Hs.111680	endosulfine alpha	4.7
104309	D55869	Hs.284123	Homo sapiens mRNA full length insert cD	4.2
104370	H19378	Hs.21851	Homo sapiens mRNA; cDNA DKFZp586	6.4
104446	L44497	Hs.7351	ESTs	4.9
104453	M19169	Hs.123114	cystatin SN	11.6
104476	N33807	Hs.324275	protease; serine; 15	5.6
104558	R56678	Hs.88959	Human DNA sequence from clone 967N2	6.3
104592	R81003	Hs.325820	serine protease; umbilical endothelium	13.6
104634	AA004274	Hs.19151	ESTs	6.3
104636	AA004415	Hs.106106	ESTs	10.1
104658	AA007145	Hs.27268	Homo sapiens mRNA; cDNA DKFZp564	4.3
104667	AA007234	Hs.30098	ESTs	16.6
104675	AA009596	Hs.301553	ESTs; Moderately similar to !!!! ALU SU	4.8
104767	AA025534	Hs.8652	ESTs	4.8
104785	AA027163	Hs.7942	ESTs	8.1
104791	AA029046	Hs.301871	ESTs; Moderately similar to cAMP induc	10.9
104804	AA031357	Hs.31803	ESTs; Weakly similar to N-WASP [H.sap	5.5
104807	AA032147	Hs.23296	ESTs	10.4
104837	AA039469	Hs.21128	ESTs; Weakly similar to KIAA0299 [H.s	4.6
104849	AA040270	Hs.241507	Homo sapiens mRNA; cDNA DKFZp564	4.3
104867	AA045481	Hs.225979	Human gene from PACs 37M17 and 305B	4.5
104884	AA053021	Hs.14511	SCO (cytochrome oxidase deficient; yeast	4.7
104906	AA055809	Hs.26802	ESTs; Weakly similar to phosphoprotein [	8.8
104919	AA057193	Hs.25252	ESTs	5.5
104921	AA057839	Hs.1508	ESTs	4.2
104926	AA058846	Hs.33363	DKFZP434N093 protein	7
104938	AA064627	Hs.318725	ESTs; Highly similar to CGI-72 protein [H	7.1
104943	AA065217	Hs.114218	ESTs	5.7
104957	AA074919	Hs.10026	ESTs; Weakly similar to ORF YJL063c [S	4.7
104961	AA076872	Hs.33905	ESTs	5.6
104968	AA084602	Hs.29669	ESTs	4.3
104975	AA086071	Hs.50758	chromosome-associated polypeptide C	8.3
104977	AA088228	Hs.18272	ESTs	6.2
104978	AA088458	Hs.19322	ESTs	6.7
104987	AA101723	Hs.11861	ESTs	9.2
105002	AA113266	Hs.182704	ESTs; Moderately similar to alternatively	6.9

105012	AA116036	Hs.9329	chromosome 20 open reading frame 1	10.7
105019	AA121879	Hs.9280	proteasome (prosome; macropain) subunit	5.7
105029	AA126855	Hs.13268	ESTs	4.4
105033	AA127984	Hs.274329	TP53 target gene 1	6.3
105035	AA128486	Hs.8859	ESTs	6.5
105039	AA130349	Hs.36475	ESTs	4
105062	AA134968	Hs.36529	ESTs	4.3
105076	AA142858	Hs.37810	ESTs	6.4
105087	AA147884	Hs.9812	ESTs	9.2
105091	AA148859	Hs.179909	ESTs; Weakly similar to IIII ALU SUBFA	5.7
105093	AA149051	Hs.32405	ESTs	6.3
105107	AA152302	Hs.25035	DKFZP566G223 protein	6.2
105127	AA158132	Hs.301957	ESTs; Weakly similar to contains similari	5.7
105132	AA159501	Hs.247280	HBV associated factor	4.2
105143	AA165333	Hs.24808	ESTs	4.7
105154	AA171736	Hs.35947	methyl-CpG binding domain protein 4	9
105162	AA176690	Hs.4084	KIAA1025 protein	9.1
105188	AA191512	Hs.28005	Homo sapiens mRNA; cDNA DKFZp564	19.3
105209	AA205072	Hs.227743	KIAA0980 protein	7.4
105223	AA211388	Hs.7750	ESTs	5.1
105252	AA227428	Hs.9728	ESTs; Weakly similar to KIAA0512 prote	11.1
105253	AA227448	Hs.5003	KIAA0456 protein	6.4
105261	AA227871	Hs.6361	MEK partner 1	9.1
105263	AA227926	Hs.6682	ESTs	6.7
105274	AA228122	Hs.281866	ATPase; H+ transporting; lysosomal (vacu	5.3
105297	AA233451	Hs.183858	transcriptional intermediary factor 1	8.7
105309	AA233790	Hs.4104	ESTs; Weakly similar to cDNA EST yk38	7.4
105312	AA233854	Hs.23348	S-phase kinase-associated protein 2 (p45)	5.8
105342	AA235286	Hs.157078	ESTs	4.5
105376	AA236559	Hs.8768	ESTs; Weakly similar to IIII ALU SUBFA	5.8
105386	AA236950	Hs.8115	ESTs	5.5
105397	AA242868	Hs.7395	ESTs; Weakly similar to house-keeping p	7.7
105399	AA243007	Hs.16420	ESTs; Highly similar to SH3 domain-bind	5.6
105400	AA243052	Hs.65648	RNA binding motif protein 8	5.8
105404	AA243303	Hs.21187	ESTs	9.1
105409	AA243562	Hs.301855	ESTs	4.4
105436	AA252172	Hs.237856	ESTs; Moderately similar to cAMP induc	5.1
105483	AA255874	Hs.23458	ESTs	4.9
105493	AA256268	Hs.10283	ESTs	6
105495	AA256317	Hs.28785	Homo sapiens mRNA; cDNA DKFZp586	5.2
105496	AA256323	Hs.301997	DKFZP434N126 protein	8.7
105500	AA256485	Hs.222399	CGI-96 protein	9.5
105507	AA256678	Hs.226318	ESTs; Moderately similar to CCR4-associ	4.1
105538	AA256860	Hs.32597	ring finger protein (C3H2C3 type) 6	4.1
105544	AA261954	Hs.24678	ESTs	8
105546	AA262032	Hs.268281	ESTs; Weakly similar to 62D9.a [D.melan	8.1
105549	AA262417	Hs.5415	ESTs	4.6
105551	AA262477	Hs.25292	ribonuclease HI; large subunit	9.1
105560	AA262783	Hs.306915	ESTs	4.5
105565	AA278302	Hs.18349	ESTs; Weakly similar to partial CDS [C.e	4.2
105566	AA278323	Hs.17481	Homo sapiens clone 24606 mRNA sequen	11.9
105575	AA278717	Hs.12772	ESTs	5.9
105584	AA279012	Hs.3454	ESTs; Weakly similar to KIAA0685 prote	4.4
105596	AA279418	Hs.18490	ESTs	4
105604	AA279787	Hs.15467	ESTs; Moderately similar to putative pho	5.6
105610	AA279991	Hs.99872	ESTs; Weakly similar to trithorax homolo	5.3
105621	AA280885	Hs.6375	Homo sapiens mRNA; cDNA DKFZp564	4.6
105627	AA281245	Hs.23317	ESTs	7.5
105638	AA281599	Hs.247817	Homo sapiens mRNA for for histone H2B	5.9
105645	AA282138	Hs.11325	ESTs	6.4
105650	AA282347	Hs.25635	ESTs; Highly similar to HSPC003 [H.sap	11.3
105666	AA283930	Hs.34906	ESTs	4.7
105674	AA284755	Hs.279789	CDW52 antigen (CAMPATH-1 antigen)	8
105687	AA286809	Hs.28423	ESTs	7.1
105700	AA287643	Hs.35254	ESTs; Weakly similar to hypothetical pro	4.9
105705	AA290767	Hs.101282	Homo sapiens mRNA; cDNA DKFZp434	8
105709	AA291258	Hs.26761	DKFZP586L0724 protein	6.8

105731	AA292711	Hs.29131	ESTs	6.4
105753	AA299789	Hs.110857	ESTs	7
105774	AA348014	Hs.23412	ESTs	7.1
105784	AA350771	Hs.17850	ESTs	13.4
105791	AA358038	Hs.14368	SH3-binding domain glutamic acid-rich p	4.3
105807	AA393803	Hs.16869	ESTs; Moderately similar to COLLAGEN	5.3
105808	AA393808	Hs.286131	KIAA0438 gene product	4.1
105812	AA394128	Hs.20814	ESTs; Highly similar to CGI-27 protein [H	14.6
105813	AA394140	Hs.18585	ESTs	4.9
105819	AA397920	Hs.28783	Homo sapiens mRNA; cDNA DKFZp564	4.9
105870	AA399623	Hs.101067	ESTs	4.6
105874	AA400074	Hs.171118	ESTs	4
105896	AA400999	Hs.7838	Human ring zinc-finger protein (ZNF127-	4.6
105934	AA404248	Hs.16577	ESTs	5.2
105935	AA404277	Hs.263727	ESTs; Weakly similar to bisphosphate 3'-	4
105966	AA406105	Hs.5344	adaptor-related protein complex 1; gamma	6.3
105974	AA406321	Hs.6224	KIAA0895 protein	4.6
105990	AA410336	Hs.29403	ESTs; Weakly similar to PROBABLE AT	4.5
105995	AA410510	Hs.5345	ESTs	4.9
106000	AA410972	Hs.20726	ESTs	5.8
106007	AA411462	Hs.11042	ESTs; Weakly similar to veli 1 [H.sapiens	6.9
106016	AA411819	Hs.8164	KIAA0898 protein	5
106034	AA412473	Hs.14928	ESTs	6.6
106042	AA412700	Hs.169895	ubiquitin-conjugating enzyme E2L 6	4.6
106057	AA417067	Hs.289074	ESTs	4.5
106065	AA417558	Hs.25206	ESTs	12.3
106070	AA417761	Hs.5957	Homo sapiens clone 24416 mRNA sequen	5
106103	AA421104	Hs.12094	ESTs	15.4
106126	AA424006	Hs.22972	ESTs; Moderately similar to H5AR [M.m	6.4
106154	AA425304	Hs.6994	ESTs	5.1
106157	AA425367	Hs.34892	ESTs	11.1
106166	AA425872	Hs.19561	NADH dehydrogenase (ubiquinone) 1 alp	19.3
106204	AA428024	Hs.21479	ESTs	4.7
106210	AA428239	Hs.10338	ESTs	5.7
106220	AA428582	Hs.32196	ESTs; Moderately similar to metargidin p	7.7
106236	AA429951	Hs.21104	ESTs	8
106240	AA430074	Hs.18552	ESTs; Weakly similar to Ylr218cp [S.cere	4.4
106263	AA431462	Hs.28329	ESTs	4.9
106288	AA435536	Hs.24338	ESTs	8.8
106293	AA435591	Hs.301444	signal sequence receptor; gamma (transloc	8.7
106310	AA436244	Hs.17240	ESTs	4.5
106317	AA436568	Hs.108124	ESTs	4
106328	AA436705	Hs.28020	KIAA0766 gene product	4.4
106341	AA441788	Hs.5243	ESTs; Moderately similar to pIL2 hypoth	23.7
106348	AA442253	Hs.10702	ESTs	4.7
106350	AA442783	Hs.194698	cyclin B2	8.1
106371	AA443923	Hs.170310	ESTs	6.6
106389	AA446949	Hs.6236	ESTs	4.7
106394	AA447223	Hs.25320	Homo sapiens clone 25142 mRNA sequen	4.4
106426	AA448282	Hs.16206	ESTs; Weakly similar to F55C12.5 [C.ele	4.5
106459	AA449741	Hs.4029	glioma-amplified sequence-41	4.8
106462	AA449912	Hs.30532	ESTs; Highly similar to CGI-77 protein [H	5.2
106468	AA450047	Hs.14770	ESTs	6.8
106479	AA450351	Hs.75251	ESTs	12.4
106494	AA452108	Hs.18387	transcription factor AP-2 alpha (activating	4.5
106503	AA452411	Hs.29679	ESTs; Highly similar to mediator [H.saple	5.1
106507	AA452584	Hs.287819	protein phosphatase 1; regulatory (inhibito	4.9
106533	AA453786	Hs.145998	ESTs	8.3
106568	AA455970	Hs.28285	patched related protein translocated in ren	7.6
106586	AA456598	Hs.57787	ESTs	8.2
106589	AA456846	Hs.28681	ESTs	4.8
106606	AA457730	Hs.283437	Homo sapiens clone 23851 mRNA sequen	4.4
106611	AA458904	Hs.26267	ESTs; Weakly similar to torsinA [H.saple	7
106614	AA458934	Hs.256150	ESTs	4.8
106628	AA459857	Hs.12311	Homo sapiens clone 23570 mRNA sequen	6.5
106637	AA459961	Hs.250824	ESTs	5.5
106644	AA460239	Hs.12680	ESTs	4.4

106684	AA460969	Hs.7510	mitogen-activated protein kinase kinase ki	8.4
106698	AA463745	Hs.29403	ESTs; Weakly similar to PROBABLE AT	5.3
106719	AA465171	Hs.236844	ESTs	5.6
106726	AA465339	Hs.3888	ESTs	10.1
106747	AA476473	Hs.171957	triple functional domain (PTPRF interacti	10.4
106759	AA477263	Hs.25584	ESTs	4.2
106765	AA477717	Hs.306117	interleukin 13 receptor; alpha 1	6.9
106784	AA478558	Hs.227913	API5-like 1	5.1
106831	AA482014	Hs.29463	centrin; EF-hand protein; 3 (CDC31 yeast	5.1
106836	AA482112	Hs.238707	ESTs	4.8
106840	AA482548	Hs.5534	ESTs	10.3
106856	AA486183	Hs.285123	ESTs; Weakly similar to similar to oxyste	6.2
106865	AA487228	Hs.19479	ESTs	4.5
106878	AA488872	Hs.12314	Homo sapiens mRNA; cDNA DKFZp586	7.9
106888	AA489101	Hs.24734	oxysterol binding protein	6.4
106895	AA489665	Hs.25245	ESTs	4.6
106909	AA490323	Hs.250747	SUMO-1 activating enzyme subunit 1	4.2
106919	AA490885	Hs.21766	ESTs	12.3
106920	AA490899	Hs.296323	ESTs	6.2
106941	AA496204	Hs.237971	ESTs	4
106942	AA496347	Hs.31314	retinoblastoma-binding protein 7	4.8
106948	AA496788	Hs.21077	KIAA0532 protein	4
106968	AA504631	Hs.26813	ESTs; Weakly similar to hypothetical 43.2	4.4
106973	AA505141	Hs.11923	Human DNA sequence from clone 167A1	5.4
106980	AA521121	Hs.8858	bromodomain adjacent to zinc finger dom	4.1
106981	AA521157	Hs.74101	ESTs	5.7
106998	AA598461	Hs.195464	insulin-like growth factor binding protein	16.7
107008	AA508710	Hs.23740	ESTs	6.2
107028	AA599214	Hs.24143	ESTs	4.1
107032	AA599472	Hs.247309	succinate-CoA ligase; GDP-forming; beta	5.3
107052	AA600134	Hs.12482	glyceronephosphate O-acyltransferase	4.8
107053	AA600147	Hs.5741	ESTs; Weakly similar to NADH-cytochro	5.8
107056	AA600310	Hs.18720	programmed cell death 8 (apoptosis-induc	4.9
107080	AA609210	Hs.19221	ESTs	8.4
107102	AA609723	Hs.30552	ESTs	8
107109	AA609943	Hs.32793	ESTs	9.5
107129	AA620553	Hs.4756	flap structure-specific endonuclease 1	4.9
107132	AA620598	Hs.9052	ESTs	5.3
107136	AA620795	Hs.8207	ESTs	4
107140	AA620889	Hs.170088	ESTs	6.7
107151	AA621169	Hs.8687	ESTs	19
107159	AA621340	Hs.10600	ESTs; Weakly similar to ORF YKR081c [	8.1
107174	AA621714	Hs.25338	ESTs	8.5
107217	D51095	Hs.35861	DKFZP586E1621 protein	7.2
107252	D59971	Hs.25925	ESTs	7.9
107295	T34527	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:po	5.6
107299	T40327	Hs.30661	lung resistance-related protein	8.4
107324	T81665	Hs.278422	DKFZP586G1122 protein	7.5
107372	U85625	Hs.8297	ribonuclease 6 precursor	4.7
107373	U85773	Hs.154695	phosphomannomutase 2	4.8
107481	W58247	Hs.279766	Homo sapiens kinesin superfamily motor	6.3
107531	Y13936	Hs.17883	protein phosphatase 1G (formerly 2C); ma	8.3
107859	AA024835	Hs.47584	potassium voltage-gated channel; delayed	7.3
107890	AA026030	Hs.61311	ESTs; Weakly similar to CALPAIN 2; LA	7.3
107908	AA026894	Hs.42826	ESTs	4.9
108039	AA041341	Hs.46670	ESTs	5.4
108040	AA041551	Hs.159971	ESTs	8.4
108102	AA046424	Hs.49433	ESTs; Weakly similar to HYPOTHETICA	6.6
108217	AA058686	Hs.62588	ESTs	7.7
108255	AA063157	Hs.172608	ESTs	4
108358	AA071514	Hs.1634	ESTs	4
108609	AA100694	Hs.69499	Human DNA sequence from BAC 15E1 o	5.5
108847	AA112398	Hs.44276	ESTs; Moderately similar to HOMEOBO	14.3
108876	AA115562	Hs.274417	Homo sapiens mRNA; cDNA DKFZp564	5.2
108687	AA120785	Hs.54347	ESTs	5.6
108695	AA121315	Hs.70823	KIAA1077 protein	10.5
108733	AA126422		zn84f1.s1 Stratagene lung carcinoma 9372	4.4

108774	AA128125	Hs.71040	ESTs; Moderately similar to CELL GROW	4.6
108828	AA131584	Hs.273344	DKFZP564O0463 protein	5.5
108872	AA134063	Hs.111680	ESTs	7.2
108884	AA134958	Hs.293591	ESTs	11.3
108893	AA135894	Hs.184691	retinoic acid induced 3	6.9
109008	AA156360	Hs.87128	ESTs	14.7
109010	AA156460	Hs.44229	dual specificity phosphatase 12	4.9
109011	AA156542	Hs.72127	ESTs	4.6
109042	AA169525	Hs.71779	Homo sapiens DNA from chromosome 19	7.2
109086	AA166695	Hs.270737	tumor necrosis factor (ligand) superfamily	4
109090	AA167006	Hs.70499	ESTs	5.9
109101	AA167708	Hs.52184	ESTs	4.2
109112	AA169379	Hs.257924	ESTs	4
109160	AA179387	Hs.301997	DKFZP434N126 protein	4
109166	AA179845	Hs.73825	RAB6 interacting; kinesin-like (rabkinesin	13.6
109178	AA181600	Hs.283707	ESTs	11.8
109179	AA181902	Hs.192789	ESTs; Weakly similar to !!!! ALU SUBFA	5.4
109261	AA195255	Hs.61779	ESTs	6.7
109270	AA195515	Hs.3585	ESTs; Weakly similar to alternatively spli	4.9
109277	AA196332	Hs.86043	ESTs	5.4
109313	AA206800	Hs.86276	ESTs; Moderately similar to zinc finger p	5.5
109415	AA227219	Hs.110826	trinucleotide repeat containing 9	20.1
109454	AA232255	Hs.295232	ESTs	4.7
109467	AA232904	Hs.63187	ESTs	6.8
109481	AA233342	Hs.269069	ESTs; Weakly similar to WD40 protein C	10.8
109508	AA233892	Hs.55902	ESTs; Weakly similar to !!!! ALU SUBFA	8
109514	AA234087	Hs.262346	ESTs; Weakly similar to ORF2: function	8.2
109572	F02027	Hs.171937	ESTs	4.8
109632	F04165	Hs.235873	ESTs; Weakly similar to K11C4.2 [C.eleg	5.2
109644	F04477	Hs.291531	ESTs; Moderately similar to GLYCERAL	6.6
109703	F09684	Hs.24792	ESTs; Weakly similar to ORF YOR283w	7.1
109726	F10009	Hs.9196	ESTs	5
109747	F10161	Hs.22969	ESTs	4.7
109799	F10770	Hs.180378	Homo sapiens clone 669 unknown mRNA	4.5
109814	F10979	Hs.153106	Homo sapiens clone 23728 mRNA sequen	8.7
110189	H20543	Hs.8278	DKFZP586B1821 protein	16.6
110240	H25577	Hs.176588	ESTs; Weakly similar to CYTOCHROME	6.2
110280	H29285	Hs.32468	ESTs	4.5
110520	H56965	Hs.4082	yr09l06.s1 Soares fetal liver spleen 1NFL	5.7
110561	H59617	Hs.5199	ESTs; Weakly similar to UBIQUITIN-CO	19.5
110707	H95079	Hs.15617	ESTs; Weakly similar to !!!! ALU SUBFA	6.2
110734	H98714	Hs.24131	ESTs	30.2
110770	N22262	Hs.131705	ESTs	5.8
110780	N23174	Hs.22891	solute carrier family 7 (cationic amino aci	8.2
110787	N24718	Hs.12244	ESTs; Weakly similar to C44B9.1 [C.eleg	6.7
110794	N25262	Hs.27931	ESTs	5.9
110799	N26101	Hs.323401	Human ring zinc-finger protein (ZNF127-	4
110818	N29454	Hs.27552	ESTs; Weakly similar to putative p150 [H	4.3
110839	N30856	Hs.30246	solute carrier family 19 (thiamine transpo	12.8
110844	N31952	Hs.167531	Homo sapiens mRNA full length insert cD	10.1
110854	N32919	Hs.27931	ESTs	4.7
110856	N33063		ESTs; Weakly similar to S164 [H.sapiens	4.2
110860	N33438	Hs.170065	ESTs	12.5
110897	N39148	Hs.6880	DKFZP434D156 protein	4
110915	N46252	Hs.29724	ESTs	23.2
110935	N48787	Hs.305979	protease inhibitor 1 (anti-elastase); alpha-	4.8
110970	N51374	Hs.96870	Homo sapiens mRNA full length insert cD	5.4
111006	N53375	Hs.166146	Homer; neuronal immediate early gene; 3	4.7
111008	N53388	Hs.7222	ESTs	13.3
111018	N54067	Hs.3628	mitogen-activated protein kinase kinase ki	5.7
111084	N59543	Hs.15456	PDZ domain containing 1	8.3
111100	N62522	Hs.20450	ESTs	14.3
111125	N63823	Hs.269115	ESTs	7.9
111132	N64378	Hs.83293	ESTs; Highly similar to unknown function	4.4
111139	N64883	Hs.290943	ESTs	6
111164	N66857	Hs.14808	ESTs; Weakly similar to !!!! ALU CLASS	4.1
111172	N67102	Hs.21851	Homo sapiens mRNA; cDNA DKFZp586	5.5

111178	N67227	Hs.24633	ESTs	5.7
111179	N67239	Hs.10760	ESTs	37
111181	N67278	Hs.171802	ESTs; Weakly similar to hypothetical pro	5.6
111184	N67437	Hs.243901	Homo sapiens mRNA; cDNA DKFZp564	8.7
111221	N68869	Hs.15119	ESTs	7.3
111223	N68921	Hs.297939	ESTs; Weakly similar to neogenin [H.sap	9
111229	N69113	Hs.110855	ESTs	8.9
111241	N69514	Hs.288880	ESTs; Weakly similar to CGI-82 protein [	6.9
111268	N70481	Hs.26118	Homo sapiens clone 24766 mRNA sequen	4.5
111285	N73275	Hs.21275	ESTs; Weakly similar to ubiquitin-conjug	5.6
111299	N73808	Hs.24936	ESTs	8.5
111335	N79565	Hs.29894	ESTs	6.7
111357	N91023	Hs.87128	ESTs	15
111370	N92915	Hs.94631	brefeldin A-inhibited guanine nucleotide-e	5.2
111806	R33468	Hs.279008	ESTs	10
111825	R35885	Hs.288148	stromal antigen 1	4.5
111836	R36228	Hs.25119	ESTs	7.2
111890	R38678	Hs.12365	ESTs	17.3
111923	R39995	Hs.25925	Homo sapiens clone 23860 mRNA sequen	7.3
111942	R40576	Hs.21590	ESTs	9.2
111987	R42036	Hs.6763	KIAA0942 protein	10.6
112101	R44793	Hs.296341	adenylyl cyclase-associated protein 2	5.3
112134	R46025	Hs.7413	ESTs	17.4
112197	R49482	Hs.5637	ESTs	4.4
112244	R51309	Hs.70823	KIAA1077 protein	11
112253	R51818		Homo sapiens mRNA; cDNA DKFZp566	9.3
112305	R54822	Hs.26244	ESTs	4.4
112449	R63802	Hs.124186	ring finger protein 2	6.3
112483	R66534	Hs.285885	ESTs	4.9
112519	R68631	Hs.11861	ESTs	14.3
112610	R79392	Hs.23843	ESTs	5.2
112693	R88741	Hs.91065	ESTs; Moderately similar to proliferation	4.6
112751	R93507	Hs.8207	ESTs	5.6
112801	R97486	Hs.157160	protein kinase; DNA-activated; catalytic p	8.7
112869	T03313	Hs.4747	dyskeratosis congenita 1; dyskerin	5.9
112871	T03352	Hs.12285	ESTs	5.8
112908	T10065	Hs.3530	TLS-associated serine-arginine protein	4.1
112968	T17119	Hs.102548	glucocorticoid receptor DNA binding fact	5.7
112971	T17185	Hs.83863	ESTs	6.4
112995	T23528	Hs.7155	ESTs; Weakly similar to TYKI protein [M	9.1
113047	T25867	Hs.7549	ESTs	5.4
113075	T34660	Hs.6986	ESTs; Weakly similar to IIII ALU SUBFA	5.7
113117	T47819	Hs.159153	ESTs	5.8
113206	T58044	Hs.241471	ESTs; Moderately similar to IIII ALU SU	6.4
113248	T63857		yc16e1.s1 Stratagene lung (#937721) Homo	4.6
113260	T64696	Hs.267420	ESTs	6.9
113277	T65797	Hs.11774	protein (peptidyl-prolyl cis/trans isomeras	5.6
113278	T65802	Hs.11135	yc11h10.s1 Stratagene lung (#937210) Ho	4.5
113440	T86121	Hs.191445	ESTs	6.4
113523	T90037	Hs.95549	ESTs	6.4
113604	T92735	Hs.296083	ESTs	8.7
113702	T97307		ESTs; Moderately similar to IIII ALU SU	9.5
113783	W19222	Hs.7041	ESTs; Weakly similar to IIII ALU SUBFA	5.2
113794	W37382	Hs.11090	ESTs	11.9
113808	W44735	Hs.9286	ESTs	16.7
113811	W44928	Hs.6994	ESTs	4
113822	W47350	Hs.17466	retinoic acid receptor responder (tazaroten	4.8
113823	W47388	Hs.55099	rab6 GTPase activating protein (GAP and	4
113836	W56792	Hs.12040	ESTs; Weakly similar to KIAA0881 prote	4.1
113857	W65477	Hs.5297	Homo sapiens mRNA; cDNA DKFZp564	4.3
113886	W72471	Hs.23920	ESTs	4.6
113895	W73738	Hs.12921	ESTs	7.1
113923	W80763	Hs.3849	ESTs; Weakly similar to FK506-binding p	6.8
113931	W81205	Hs.3496	ESTs	6.1
113950	W85765	Hs.30504	Homo sapiens mRNA; cDNA DKFZp434	14
113970	W86748	Hs.8109	ESTs	15
114051	W94942	Hs.177534	dual specificity phosphatase 10	5.4

114057	W96222	Hs.34192	ESTs	4.8
114086	Z38266	Hs.288849	Homo sapiens PAC clone DJ0777O23 fro	5.1
114098	Z38347	Hs.118338	ESTs; Weakly similar to similar to S. cere	6.2
114109	Z38435	Hs.184108	ribosomal protein L21	4.6
114124	Z38595	Hs.125019	ESTs; Highly similar to KIAA0886 prote	22
114138	Z38763	Hs.15740	amyloid beta (A4) precursor protein-bindi	8.8
114149	Z38814	Hs.27196	ESTs	4
114162	Z38909	Hs.22265	ESTs	7.2
114177	Z39062	Hs.23740	ESTs	5.3
114196	Z39211	Hs.150926	fucose-1-phosphate guanylyltransferase	4.4
114208	Z39301	Hs.7859	ESTs	5.1
114250	Z39897	Hs.13297	ESTs	7.2
114251	Z39898	Hs.21948	ESTs	14.7
114292	Z40715	Hs.184641	delta-6 fatty acid desaturase	19.4
114297	Z40758	Hs.173091	DKFZP434K151 protein	8.9
114334	Z41342	Hs.22941	ESTs	13.7
114460	AA024604	Hs.26102	ESTs	10.1
114471	AA028074	Hs.104613	ESTs	5.7
114480	AA032243	Hs.151878	UDP-N-acetyl-alpha-D-galactosamine:po	7.3
114518	AA046407	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like 1	4.3
114542	AA055768	Hs.293380	ESTs	11.7
114549	AA056484	Hs.292833	ESTs	7.3
114652	AA101416	Hs.107149	ESTs; Weakly similar to PTB-ASSOCIAT	6.1
114673	AA113303	Hs.95583	transmembrane 4 superfamily member (te	4.3
114698	AA126951	Hs.110857	ESTs; Highly similar to putative DNA-dir	7.1
114767	AA148885	Hs.154443	minichromosome maintenance deficient (S	5.3
114799	AA159323	Hs.109929	ESTs	4.2
114804	AA160363	Hs.269956	ESTs	4.8
114811	AA161161	Hs.95907	multiple inositol polyphosphate phosphata	7.1
114821	AA165313	Hs.55468	ESTs	4.4
114852	AA235035	Hs.38260	ESTs; Moderately similar to ubiquitin spe	5
114901	AA236276	Hs.196437	ESTs; Weakly similar to R26660_1; parti	16.9
114902	AA236359	Hs.39504	ESTs	5.1
114940	AA243012	Hs.75928	ESTs	8.5
114965	AA250737	Hs.72472	ESTs	35.1
115047	AA252627	Hs.82916	homeo box B5	5.7
115054	AA252863	Hs.87729	ESTs	6.2
115061	AA253217	Hs.41271	ESTs	13
115082	AA255557	Hs.198269	NADH dehydrogenase (ubiquinone) 1 alp	28.2
115116	AA256488	Hs.62275	ESTs	8.8
115140	AA258030	Hs.279938	ESTs; Weakly similar to supported by GE	4.1
115206	AA262470	Hs.284216	ESTs	8.3
115206	AA262491	Hs.186572	ESTs	5.1
115239	AA278650	Hs.73291	ESTs; Weakly similar to similar to the bet	4.6
115242	AA278755	Hs.283732	ESTs	6.3
115249	AA278961	Hs.71124	ESTs	10.1
115259	AA279071	Hs.13453	splicing factor 3b; subunit 1; 155kD	9.5
115285	AA279799	Hs.293736	ESTs	5.8
115291	AA279943	Hs.122579	ESTs	5.1
115357	AA281793	Hs.72988	ESTs	5
115377	AA282247	Hs.193063	ESTs	6.1
115400	AA283198	Hs.89113	ESTs	4.9
115439	AA284581	Hs.193090	ESTs	5.8
115471	AA287138	Hs.59346	ESTs; Weakly similar to ASPARTYL-TR	11.7
115506	AA292537	Hs.45207	Human DNA sequence from clone 620E1	6.8
115522	AA331393	Hs.47378	ESTs	5.8
115572	AA398392	Hs.59594	ESTs; Weakly similar to F33G12.3 gene p	9.7
115587	AA399264	Hs.283037	ESTs; Highly similar to HSPC039 protein	8.7
115600	AA400247	Hs.42173	ESTs	4
115612	AA400948	Hs.71243	ESTs; Weakly similar to zinc finger prote	8.4
115646	AA404352	Hs.305971	ESTs	5.3
115652	AA405098	Hs.38178	ESTs	16.1
115657	AA405820	Hs.55158	ESTs; Weakly similar to weak similarity t	4.7
115658	AA405625	Hs.183056	Human DNA sequence from clone 34B21	5.1
115675	AA406546	Hs.82065	Homo sapiens mRNA; cDNA DKFZp564	20.5
115721	AA417102	Hs.90960	ESTs	4.8
115763	AA421560		ESTs	7

115764	AA421582	Hs.91011	anterior gradient 2 (Xenopus laevis) homo	41.6
115835	AA428576	Hs.41371	ESTs	4.2
115844	AA430124	Hs.7773	ESTs	11.9
115875	AA433943	Hs.43946	ESTs; Weakly similar to Weak similarity	33.5
115888	AA435839	Hs.76591	KIAA0887 protein	7.2
115922	AA441911	Hs.71869	ESTs; Weakly similar to KIAA0926 prote	5.1
115941	AA443602	Hs.46679	ESTs	4.8
115947	AA443793	Hs.94761	ESTs	8.3
115948	AA443798	Hs.43445	poly(A)-specific ribonuclease (deadenylat	13.5
115951	AA443918	Hs.301048	cofilin 1 (non-muscle)	7.5
115967	AA446887	Hs.42911	ESTs	8.8
115984	AA447887	Hs.91109	ESTs	13.1
116009	AA449448	Hs.44238	ESTs	5.5
116024	AA451748	Hs.83883	Human DNA sequence from clone 718J7	7.5
116028	AA452112	Hs.42644	thioredoxin-like	12.7
116050	AA453656	Hs.88417	ESTs	7.2
116097	AA456099	Hs.176376	ESTs	11.8
116108	AA457566	Hs.26777	ESTs	4.5
116121	AA459254	Hs.48855	ESTs	4.5
116127	AA459703	Hs.279884	v-myc avian myelocytomatosis viral onco	4.3
116129	AA459956	Hs.49163	ESTs; Highly similar to putative ribonucle	7.6
116142	AA460649	Hs.39457	ESTs	4.8
116204	AA465701	Hs.108646	ESTs	6.6
116221	AA478397	Hs.50180	ESTs	4.9
116222	AA478415	Hs.89986	ESTs	4
116238	AA479352	Hs.47144	DKFZP586N0819 protein	4.6
116246	AA479961	Hs.250646	ESTs; Highly similar to ubiquitin-conjuga	4
116249	AA480886	Hs.86693	ESTs	16.5
116250	AA480975	Hs.44829	ESTs	10.8
116254	AA481146	Hs.41086	ESTs; Weakly similar to OXYSTEROL-B	9.1
116256	AA481256	Hs.88201	ESTs; Weakly similar to lysophospholipa	8.4
116264	AA482594	Hs.272239	Homo sapiens mRNA; cDNA DKFZp586	7.2
116265	AA482595	Hs.55189	ESTs; Weakly similar to F25B5.3 [C.eleg	11.1
116282	AA486550	Hs.204501	ESTs; Weakly similar to Wiskott-Aldrich	6.2
116298	AA489046	Hs.94109	ESTs	4.9
116300	AA489194	Hs.159471	ESTs; Weakly similar to snRNP protein B	4.6
116327	AA490959	Hs.28005	Homo sapiens mRNA; cDNA DKFZp564	5.8
116334	AA491457	Hs.48948	ESTs	4.3
116337	AA496127	Hs.44070	ESTs	8.4
116351	AA504116	Hs.82501	Homo sapiens mRNA; cDNA DKFZp434	5.3
116357	AA504806	Hs.90797	Homo sapiens clone 23620 mRNA sequen	5.2
116415	AA609204	Hs.27973	KIAA0874 protein	6.6
116443	AA620313	Hs.190488	ESTs; Weakly similar to KERATIN; TYP	4.5
116470	C13992	Hs.83484	ESTs	4.5
116480	C14088		glyceraldehyde-3-phosphate dehydrogena	5.6
116578	D51272	Hs.75337	nucleolar phosphoprotein p130	4.1
116579	D51276	Hs.81915	leukemia-associated phosphoprotein p18	5.8
116826	F02028	Hs.81907	ESTs	4.9
116847	F03069	Hs.15395	ESTs; Weakly similar to ARGINYL-TRN	6.1
116874	F04816	Hs.92127	ESTs	10.6
116880	F08813	Hs.273829	LINE retrotransposable element 1	4.2
116700	F09983	Hs.317589	ESTs	13
116724	F13565	Hs.65641	ESTs	8.5
116726	F13681	Hs.53913	ESTs	5.6
116732	F13779	Hs.165909	ESTs	11.6
116734	F13789	Hs.93796	DKFZP586D2223 protein	5.4
116760	H11054	Hs.155342	protein kinase C; delta	4.3
116780	H22566	Hs.30098	ESTs	5.7
116786	H25836	Hs.301527	tumor necrosis factor (ligand) superfamily	8.8
116787	H28581	Hs.15641	ESTs	8.6
116790	H29532	Hs.101174	microtubule-associated protein tau	22.2
116803	H47357	Hs.109701	ESTs; Moderately similar to weak similar	6.7
116877	H68116	Hs.168732	ESTs	6.5
116921	H72948	Hs.821	biglycan	20.7
117216	N20083	Hs.42792	ESTs	4.4
117232	N20579	Hs.61153	ESTs	7.4
117284	N22162	Hs.183779	ESTs; Weakly similar to cDNA EST yk33	4.1

117344	N24048	Hs.210706	ESTs	7.4
117367	N24954	Hs.42502	ESTs	10.5
117392	N26175	Hs.93405	ESTs	5.8
117394	N26257	Hs.39871	KIAA0727 protein	8.4
117412	N26722	Hs.42645	ESTs	18.1
117498	N31728	Hs.44268	ESTs; Highly similar to myelin gene expr	5.8
117557	N33920	Hs.44532	diubiquitin	12.3
117634	N36421	Hs.13323	ESTs; Weakly similar to SODIUM- AND	4.4
117639	N36923	Hs.44833	ESTs	6
117754	N47469	Hs.59757	ESTs	7.6
117852	N49408	Hs.136102	KIAA0853 protein	5.9
117879	N50050	Hs.303025	ESTs; Weakly similar to keratin; 67K typ	7.9
117924	N51056	Hs.38891	ESTs	7.9
117950	N51394	Hs.75478	KIAA0956 protein	5
117992	N52000	Hs.172089	Homo sapiens mRNA; cDNA DKFZp586	7
118138	N57773	Hs.93560	ESTs; Weakly similar to trg (R.norvegicu	4.8
118215	N62195	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A	13.4
118229	N62339	Hs.166254	heat shock 90kD protein 1; alpha	5.4
118265	N62827	Hs.48645	EST	4.2
118336	N63604	Hs.47166	ESTs	7.2
118363	N64168	Hs.48938	ESTs	6
118429	N66158	Hs.74849	ESTs	4.1
118470	N66769	Hs.291033	ESTs	5.4
118472	N66818	Hs.42179	ESTs	10.8
118475	N66845		ESTs; Weakly similar to IIII ALU CLASS	4.5
118493	N67149	Hs.50115	ESTs	5.3
118528	N67889	Hs.49397	ESTs	10.4
118542	N68010	Hs.49427	ESTs	7.9
118600	N69222		ESTs	9.2
118695	N71781	Hs.50081	Homo sapiens mRNA full length insert cD	9.8
118698	N72113	Hs.50187	ESTs	4.3
118901	N90719	Hs.84445	ESTs	8.1
118952	N92968		ESTs; Highly similar to CGI-90 protein [H	12.5
118976	N93629	Hs.93391	ESTs	5
118986	N94362	Hs.125830	ESTs	7.3
118989	N94439	Hs.45105	ESTs	8.2
119027	N99256	Hs.114611	ESTs	5
119042	R05316	Hs.5472	ESTs	4
119075	R36451	Hs.287820	fibronectin 1	6
119260	T15918	Hs.102950	ESTs; Highly similar to coat protein gamm	4.1
119271	T16387	Hs.65328	ESTs	12.1
119298	T23820	Hs.155478	cyclin T2	5.6
119302	T25725		ESTs	14.3
119341	T62571	Hs.146388	microtubule-associated protein 7	4
119495	W35390	Hs.55533	ESTs	5.3
119580	W42451	Hs.92260	high-mobility group protein 2-like 1	6.6
119602	W46288	Hs.233694	ESTs; Weakly similar to ZK1058.5 [C.ele	6.5
119620	W47620	Hs.56009	2'-5'oligoadenylate synthetase 3	8.1
119676	W60473	Hs.57787	ESTs	5.5
119717	W69134	Hs.57987	ESTs	4.6
119729	W69747	Hs.94808	KIAA1062 protein	4
119805	W73788	Hs.43213	ESTs	4
119859	W80702	Hs.58461	ESTs	4.8
119867	W80852	Hs.250696	KDEL (Lys-Asp-Glu-Leu) endoplasmic re	4.2
119873	W81129	Hs.44865	Homo sapiens mRNA; cDNA DKFZp586	4.8
119899	W84767	Hs.58698	ESTs	5.9
119940	W86779	Hs.272531	DKFZP586B0319 protein	9
119943	W86835	Hs.14158	copine III	4.8
119970	W87812	Hs.93581	Homo sapiens mRNA; cDNA DKFZp588	4
120131	Z38656	Hs.75887	coatomer protein complex; subunit alpha	4.2
120150	Z39549	Hs.153746	ESTs	11
120206	Z40805	Hs.91668	ESTs	8.2
120241	Z41815	Hs.65948	ESTs	15.6
120255	AA169752	Hs.5872	ESTs; Weakly similar to Similarity to Yea	4.2
120314	AA194166	Hs.221040	KIAA1038 protein	6.8
120325	AA195651	Hs.104108	ESTs	15.2
120352	AA211400	Hs.193172	ESTs	6.8

120428	AA236822	Hs.173694	KIAA1097 protein	5.6
120524	AA261852	Hs.192905	ESTs	5.6
120528	AA262107	Hs.104413	ESTs	4.5
120571	AA280738	Hs.34892	ESTs	4.9
120649	AA287115	Hs.192843	ESTs	4.5
120655	AA287347	Hs.238205	ESTs	6.7
120668	AA287833	Hs.292913	ESTs	8.3
120712	AA292654	Hs.102506	eukaryotic translation initiation factor 2 al	4.6
120713	AA292655	Hs.96557	ESTs	10.6
120724	AA293470	Hs.100747	ESTs	5.4
120873	AA358015		EST	7.1
120885	AA365515	Hs.301872	ESTs; Moderately similar to !!!! ALU SU	4.6
120919	AA381125	Hs.301444	ESTs	8.2
120948	AA397822	Hs.104650	ESTs; Highly similar to similar to mago n	8.6
120969	AA398116	Hs.129206	casein kinase 1; gamma 3	10.5
120977	AA398155	Hs.97600	ESTs	10.9
121103	AA398936	Hs.97697	EST	7.4
121291	AA401753	Hs.8186	lung cancer candidate	5.3
121320	AA403008	Hs.301927	T-cell receptor; alpha (V;D;J;C)	13.5
121463	AA411745	Hs.239681	ESTs; Weakly similar to KIAA0554 prote	8.9
121596	AA416740	Hs.174104	ESTs	22.6
121723	AA419622	Hs.104800	ESTs; Weakly similar to Mouse 19.5 mRN	8
121748	AA421171	Hs.234545	ESTs	5.6
122125	AA434411	Hs.98806	ESTs	5.3
122522	AA449444	Hs.98969	ESTs	4
122655	AA454756	Hs.97837	ESTs	4
122704	AA456326	Hs.99445	ESTs	6.2
122782	AA459894	Hs.99472	ESTs	5.3
122856	AA463740	Hs.75367	Src-like-adapter	13.1
122882	AA465381	Hs.108812	ESTs; Weakly similar to B0041.5 [C.eleg	5.5
122928	AA476578	Hs.101840	ESTs	6.3
122974	AA478625	Hs.194215	ESTs	6
122997	AA479295	Hs.106290	Kelch motif containing protein	12.5
123016	AA480103	Hs.323231	ESTs; Weakly similar to alternatively spli	4.4
123107	AA486071	Hs.104207	ESTs	8.3
123111	AA486273	Hs.191721	ESTs	4.2
123114	AA486407	Hs.129928	ESTs; Moderately similar to KIAA0454 p	5.2
123136	AA487449	Hs.194024	ESTs	4.2
123137	AA487458	Hs.100686	ESTs; Weakly similar to secreted cement	14.6
123169	AA488692		ESTs; Weakly similar to Gag-Pol polypro	4.5
123176	AA489020	Hs.69233	ESTs	5.2
123338	AA504249	Hs.187585	ESTs	4
123436	AA598714	Hs.223014	protease; serine; 15	7.3
123442	AA598803	Hs.111496	ESTs	5.9
123449	AA598899	Hs.112493	Homo sapiens mRNA; cDNA DKFZp564	4.1
123494	AA599786	Hs.112110	ESTs	4
123503	AA600121	Hs.293156	ESTs	12.8
123533	AA608751		ESTs; Weakly similar to !!!! ALU SUBFA	7.9
123619	AA609200		ESTs	23.1
123673	AA609471	Hs.158549	ESTs	6.6
123729	AA609778	Hs.278672	membrane component; chromosome 11; s	4.7
123819	AA620636	Hs.112264	ESTs	4
123960	AA821785	Hs.287733	methylmalonate-semialdehyde dehydroge	7.6
124000	D57317	Hs.74861	activated RNA polymerase II transcription	4.4
124006	D60302	Hs.270016	ESTs	20.6
124012	D80240	Hs.241471	HUM5G11A Human fetal brain (TFujiwa	8.7
124021	F02859	Hs.13974	ESTs	4.7
124049	F10523	Hs.74519	primase; polypeptide 2A (58kD)	4.7
124059	F13673	Hs.283713	ESTs	7.7
124243	H66710	Hs.133525	ESTs	5.5
124308	H93575	Hs.241507	Homo sapiens mRNA; cDNA DKFZp564	11.4
124314	H94877	Hs.215766	GTP-binding protein	13.7
124315	H94892	Hs.288757	v-ral simian leukemia viral oncogene hom	14
124350	N21359	Hs.101282	Homo sapiens mRNA; cDNA DKFZp434	8.6
124352	N21626	Hs.102406	ESTs	7.2
124357	N22401		yw37g07.s1 Morton Fetal Cochlea Homo	5.2
124390	N29325	Hs.7535	ESTs; Highly similar to COBW-like place	7.9

124438	N40188	Hs.11090	ESTs	9.5
124447	N48000		Homo sapiens mRNA; cDNA DKFZp586	4.8
124457	N50114	Hs.268175	ESTs	6.1
124539	N63172	Hs.146409	cell division cycle 42 (GTP-binding prote	5.6
124626	N74604	Hs.11090	ESTs	12.8
124632	N79515	Hs.306117	interleukin 13 receptor; alpha 1	6.4
124644	N91279	Hs.109654	ESTs; Moderately similar to outer membr	8.3
124676	R01037	Hs.181013	phosphoglycerate mutase 1 (brain)	12.3
124677	R01073		ESTs; Weakly similar to !!!! ALU CLASS	5.4
124724	R12405	Hs.112423	Homo sapiens mRNA; cDNA DKFZp586	6.6
124773	R40923	Hs.106604	ESTs	4.9
124777	R41933		ESTs	7.2
124792	R44357	Hs.48712	ESTs; Weakly similar to cDNA EST EMB	8.6
124857	R63652	Hs.137190	ESTs	4.9
124911	R88992	Hs.180612	ESTs	4.7
124955	T10598	Hs.324841	ESTs; Weakly similar to !!!! ALU SUBFA	4.4
124958	T11134	Hs.431	murine leukemia viral (bmi-1) oncogene h	12.6
125038	T78089	Hs.270134	ESTs	4.1
125092	T92544	Hs.137546	CD84 antigen (leukocyte antigen)	14.8
125132	W15495	Hs.129781	chromosome 21 open reading frame 5	6.7
125144	W37999	Hs.24336	ESTs	4.8
125154	W38419		ESTs	5.3
125243	W86423	Hs.105413	ESTs	6.6
125279	W93640	Hs.4779	ESTs; Moderately similar to similar to AD	5.8
125299	Z39436	Hs.102720	ESTs	12.2
125303	Z39821	Hs.288193	ESTs	10.2
125304	Z39833	Hs.124940	GTP-binding protein	6.8
125474	AA151216	Hs.75103	tyrosine 3-monooxygenase/tryptophan 5-m	8
125509	AA044232	Hs.288967	ESTs	5.4
125580	AA126504	Hs.267812	sorting nexin 4	4.1
125582	AA507383	Hs.74649	cytochrome c oxidase subunit VIc	11.5
125670	AI432621	Hs.82685	CD47 antigen (Rh-related antigen; integri	4
125698	AA748483	Hs.191356	general transcription factor IIH; polypepti	9.4
125745	AI283493	Hs.75722	ribophorin II	6.2
125852	H09290	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564	25.9
125972	AA434562	Hs.35406	ESTs	4.1
126160	N90960	Hs.265398	ESTs; Weakly similar to transformation-r	16.4
126257	N99838	Hs.124084	tumor necrosis factor receptor superfamily	9.5
126337	AI066486	Hs.40500	similar to S. cerevisiae RER1	5.8
126405	U46278	Hs.122489	ESTs	7.5
126537	W40262	Hs.146310	ESTs; Weakly similar to putative p150 [H	4.1
126590	W78958	Hs.181307	H3 histone; family 3A	4.5
126712	AA205862	Hs.7942	ESTs	5.2
126721	T72569	Hs.125359	Thy-1 cell surface antigen	4.4
126764	AI334393	Hs.102178	ESTs	4.6
126804	AI203334	Hs.160628	ESTs	11.7
126819	AA305536	Hs.279607	ESTs	4
126877	AI052047	Hs.26102	ESTs	7
126991	R31652	Hs.821	biglycan	5.6
127479	AA513722	Hs.179729	collagen; type X; alpha 1 (Schmid metaph	14.3
127514	AA826926	Hs.204214	ESTs	4.5
127663	W07286	Hs.10340	ESTs; Weakly similar to weak similarity i	5.1
127677	AA918752	Hs.264190	ESTs; Highly similar to MEM3 [M.muscu	17.3
127814	AA761755	Hs.136713	ESTs; Weakly similar to V4-1 [H.sapiens	4.1
127997	AI281549	Hs.311054	ESTs	5.5
128092	AA904617	Hs.166229	ESTs	5.8
128218	H02682	Hs.292154	ESTs; Moderately similar to recombinatio	5.8
128466	D59653	Hs.241471	EST	7.4
128482	U83908	Hs.296251	programmed cell death 4	5.8
128517	AA280617	Hs.100881	ESTs; Weakly similar to p60 katanin [H.s	8.3
128530	AA504343	Hs.183475	Homo sapiens clone 25061 mRNA sequen	6.6
128559	AA226801	Hs.101448	metastasis associated 1	5.2
128574	AA412048	Hs.38260	keratin 8	5.1
128595	U31875	Hs.152677	short-chain alcohol dehydrogenase family	27.1
128610	L38608	Hs.10247	activated leucocyte cell adhesion molecule	13.2
128629	AA399187	Hs.102708	DKFZP434A043 protein	8.7
128649	AA142853	Hs.103106	Homo sapiens mRNA for G7b protein (G	4.5

128651	AA446990	Hs.103135	ESTs	6.1
128653	R48943	Hs.10315	solute carrier family 7 (cationic amino aci	4.4
128656	AA458542	Hs.10326	coatomer protein complex; subunit epsilon	14.3
128717	T30617	Hs.104222	Homo sapiens mRNA; cDNA DKFZp566	24.5
128727	M64174	Hs.50551	Janus kinase 1 (a protein tyrosine kinase)	7.3
128764	N49308	Hs.104938	ESTs; Weakly similar to alpha 1(XVIII) c	9.2
128781	X85372	Hs.105465	small nuclear ribonucleoprotein polypepti	5.4
128793	W93562	Hs.105749	KIAA0553 protein	4.6
128835	W15528	Hs.106390	Homo sapiens mRNA; cDNA DKFZp586	4
128845	AA455658	Hs.10849	basement membrane-induced gene	6.9
128871	AA400271	Hs.106778	Homo sapiens mRNA for putative Ca2+-I	4.5
128922	AA252023	Hs.9589	ESTs; Weakly similar to HRIHFB2157 [H	6.4
128925	D61676	Hs.21851	Homo sapiens mRNA; cDNA DKFZp586	6.4
128938	AA410325	Hs.107260	ESTs	7
128946	N29353	Hs.107318	kynurenine 3-monooxygenase (kynurenin	5.2
128948	AA485655	Hs.223025	proteasome (prosome; macropain) subunit	13.1
128955	F10290	Hs.185807	Homo sapiens clone 24758 mRNA sequen	5.8
129005	AA460049	Hs.13323	ESTs; Weakly similar to SODIUM- AND	12.6
129009	AA131421	Hs.75607	ESTs	9.8
129017	H13108	Hs.107958	ESTs	13.9
129057	X62468	Hs.276770	CDW52 antigen (CAMPATH-1 antigen)	10.7
129075	AA129465	Hs.83765	ESTs	4.7
129095	L12350	Hs.108623	thrombospondin 2	4.4
129124	AA234530	Hs.108802	N-ethylmaleimide-sensitive factor	20.7
129160	AA131252	Hs.109007	ESTs	5.9
129184	AA282183	Hs.109045	ESTs	5.8
129180	R40556	Hs.318401	ESTs; Highly similar to HSPC039 protein	7.6
129224	X89109	Hs.109606	coronin; actin-binding protein; 1A	12
129229	AA211941	Hs.109643	polyadenylate binding protein-interacting	7.9
129240	W24360	Hs.237868	interleukin 7 receptor	5.3
129241	AA435665	Hs.109706	ESTs; Moderately similar to HN1 [M.mus	8.4
129243	H88033	Hs.109727	KIAA0733 protein	7.8
129247	AA151574	Hs.109733	pilin-like transcription factor	6.4
129259	AA090695	Hs.181385	ESTs	6.2
129270	Z35227	Hs.109918	ras homolog gene family; member H	5.4
129281	AA026318	Hs.289101	glucose regulated protein; 58kD	4.4
129300	C20976	Hs.110165	ESTs; Highly similar to ribosomal protein	5.7
129318	N93155	Hs.285976	calmodulin 1 (phosphorylase kinase; delta	7.7
129319	AA037467	Hs.30340	ESTs	6
129351	AA167268	Hs.62349	Human ras inhibitor mRNA; 3' end	9.3
129366	H18027	Hs.184697	plexin C1	18.2
129383	W92984	Hs.288224	ESTs	5.9
129388	AA151621	Hs.110964	ESTs	4.1
129391	T80814	Hs.11101	disc; large (Drosophila) homolog 3 (neur	10.9
129404	AA172056	Hs.317584	ESTs	5.3
129406	N23707	Hs.111138	KIAA0712 gene product	4
129426	AA412087	Hs.111323	EST; Highly similar to protein inhibitor o	8
129453	AA421213	Hs.111632	Lsm3 protein	5.5
129513	C00225	Hs.308163	ESTs; Weakly similar to fos39554_1 [H.s	5.5
129519	AA298786	Hs.112242	ESTs	6.8
129606	R21443	Hs.166254	heat shock 90kD protein 1; alpha	5
129622	AA278243	Hs.323949	ESTs	6.8
129626	AA447410	Hs.111334	ESTs; Weakly similar to !!!! ALU SUBFA	5.1
129627	AA258308	Hs.71968	Homo sapiens mRNA; cDNA DKFZp564	5.3
129628	U26727	Hs.1174	cyclin-dependent kinase inhibitor 2A (mel	8.2
129642	R50008	Hs.11806	7-dehydrocholesterol reductase	4.3
129683	AA442768	Hs.11866	translocase of inner mitochondrial membr	4.4
129685	M88458	Hs.118778	KDEL (Lys-Asp-Glu-Leu) endoplasmic re	4
129691	X06700	Hs.119571	collagen; type III; alpha 1 (Ehlers-Danlos	6
129783	AA454818	Hs.12479	associated molecule with the SH3 domain	6.4
129800	AA252436	Hs.12540	lysophospholipase I	7.7
129836	AA452161	Hs.206521	YME1 (S.cerevisiae)-like 1	5
129850	N20593	Hs.288932	GDP dissociation inhibitor 2	6.9
129869	AA102520	Hs.13015	ESTs; Weakly similar to heat shock prote	5
129896	AA043021	Hs.13225	UDP-GalbetaGlcNAc beta 1;4- galactosy	6.6
129982	M87789		immunoglobulin gamma 3 (Gm marker)	4
129985	AA450045	Hs.140452	cargo selection protein (mannose 6 phosp	5.8

130029	AA236412	Hs.236510	ESTs; Moderately similar to PFT27 [M.m	5.6
130033	M90696	Hs.181301	cathepsin S	5.4
130036	AA195260	Hs.125849	ESTs; Moderately similar to !!!! ALU SU	7.4
130069	AA055898	Hs.146428	collagen; type V; alpha 1	7.6
130077	T24055	Hs.91379	ribosomal protein L26	4
130080	X14850	Hs.147097	H2A histone family; member X	12.1
130098	AA223874	Hs.197955	KIAA0704 protein	5
130114	AA234717	Hs.14992	ESTs	7.8
130125	M36803	Hs.1504	hemopexin	7.2
130135	M61764	Hs.21635	tubulin; gamma 1	5.6
130170	AA610070	Hs.151469	calcium/calmodulin-dependent serine pro	7.5
130189	D43947	Hs.151761	KIAA0100 gene product	6.4
130208	AA620556	Hs.15250	peroxisomal D3;D2-enoyl-CoA isomerase	6.4
130211	D50840	Hs.23703	UDP-glucose ceramide glucosyltransferas	4.5
130235	X14046	Hs.153053	CD37 antigen	9.1
130276	S75295	Hs.169149	karyopherin alpha 1 (importin alpha 5)	6.6
130280	L13738	Hs.153937	activated p21cdc42Hs kinase	5
130313	AA620323	Hs.154320	ubiquitin-activating enzyme E1C (homolo	6.1
130314	D86967	Hs.154332	KIAA0212 gene product	10
130328	AA135673	Hs.154668	KIAA0391 gene product	6.1
130356	X84373	Hs.155017	nuclear receptor interacting protein 1	10.6
130387	Z38501	Hs.8768	ESTs; Weakly similar to !!!! ALU SUBFA	6.3
130378	T47333	Hs.155188	TATA box binding protein (TBP)-associa	7.1
130384	X66364	Hs.166071	cyclin-dependent kinase 5	5.6
130393	D13630	Hs.155291	KIAA0005 gene product	4.1
130399	AA449417	Hs.155358	Homo sapiens mRNA for putative glucosy	4.6
130407	N29888	Hs.155410	ESTs	7
130414	M21121	Hs.241392	small inducible cytokine A5 (RANTES)	4.1
130417	U58522	Hs.155485	huntingtin-interacting protein 2	7.9
130421	D21260	Hs.178710	clathrin; heavy polypeptide-like 2	4
130441	U35835	Hs.155637	protein kinase; DNA-activated; catalytic p	6.6
130455	X17059	Hs.155956	N-acetyltransferase 1 (arylamine N-acetyl	28.4
130498	L38951	Hs.180446	karyopherin (importin) beta 1	4.8
130499	AA416723	Hs.158286	Homo sapiens mRNA for KIAA0446 prot	6.1
130511	L32137	Hs.1584	cartilage oligomeric matrix protein (pseud	8.3
130553	AA430032	Hs.252587	pituitary tumor-transforming 1	7.5
130558	H96654	Hs.15984	ESTs; Weakly similar to gene pp21 protei	5.6
130568	AA232535	Hs.16085	ESTs; Highly similar to CGI-13 protein [H	4
130583	W24957	Hs.293907	ESTs; Moderately similar to similar to C.e	13.3
130585	H66211	Hs.16331	ESTs	10.1
130604	X03635	Hs.1657	estrogen receptor 1	39.9
130614	AA132007	Hs.16697	ESTs	5.1
130619	AA477739	Hs.12532	ESTs	5.9
130622	AA235247	Hs.16846	ESTs; Weakly similar to cytochrome P45	4.1
130625	F03969	Hs.260720	matrix metalloproteinase 2 (gelatinase A;	8.3
130627	L23808	Hs.1695	matrix metalloproteinase 12 (macrophage	10.3
130629	M60346	Hs.1697	ATPase; H+ transporting; lysosomal (vacu	7
130635	M87503	Hs.1706	interferon-stimulated transcription factor	5.5
130639	D59711	Hs.17132	ESTs	7.2
130677	H17851	Hs.17787	ESTs	13.5
130681	D82808	Hs.17820	Rho-associated; coiled-coil containing pro	6
130693	AA487202	Hs.17962	ESTs	6.1
130703	N63295	Hs.18103	ESTs	4.3
130706	AA488843	Hs.201673	comichon-like	4
130712	AA292066	Hs.279782	adenylate cyclase 7	5.1
130714	X92896	Hs.18212	DNA segment on chromosome X (unique)	8.4
130715	T98227	Hs.171952	occludin	5.7
130744	AA203527	Hs.18747	POP7 (processing of precursor; S. cerevis	6.2
130747	AA471293	Hs.6879	ESTs	8.2
130751	AA435833	Hs.18879	Homo sapiens clone 23965 mRNA sequen	8.3
130796	R39390	Hs.19525	ESTs	4.5
130800	AA223386	Hs.19574	ESTs; Weakly similar to katanin p80 subu	7.7
130855	AA425439	Hs.143323	putative DNA/chromatin binding motif	4.3
130859	AA287327	Hs.20478	ceroid-lipofuscinosis; neuronal 2; late infa	9.8
130866	M58028	Hs.2055	ubiquitin-activating enzyme E1 (A1S9T a	4.3
130880	D14678	Hs.20830	kinesin-like 2	4.5
130891	D31891	Hs.20991	SET domain; bifurcated; 1	4

130905	AA056489	Hs.129998	ESTs	8.7
130913	W03592	Hs.21198	translocase of outer mitochondrial membr	20.9
130919	AA291710	Hs.21276	collagen; type IV; alpha 3 (Goodpasture a	9
130921	AA074596	Hs.194688	bromodomain adjacent to zinc finger dom	5.3
130944	M97935	Hs.21486	signal transducer and activator of transcrip	18.8
130974	X57985	Hs.2178	H2B histone family; member Q	13.4
130987	R45698	Hs.21893	ESTs; Weakly similar to cAMP inductible	8.5
130999	N48963	Hs.21992	KIAA0689 protein	7.2
131010	AA435748	Hs.169341	ESTs; Weakly similar to phosphatidic acid	5.2
131046	X02530	Hs.2248	small inducible cytokine subfamily B (Cy	10.1
131091	T35341	Hs.22880	ESTs; Highly similar to dipeptidyl peptid	6.3
131153	H11760	Hs.23606	ESTs	7.3
131185	M25753	Hs.23960	cyclin B1	6.2
131200	AA609427	Hs.293732	ESTs; Moderately similar to !!!! ALU SU	4.3
131206	AA044078	Hs.24210	ESTs	5.5
131210	AA430047	Hs.95549	ESTs	7.1
131227	AA429472	Hs.236522	DKFZP434P106 protein	5.6
131244	D38076	Hs.24763	RAN binding protein 1	5.5
131245	AA620599	Hs.24766	DKFZP564E1962 protein	6.7
131257	AA256042	Hs.24908	ESTs	5.8
131319	U25997	Hs.25590	stanniocalcin	8.9
131339	AA463450	Hs.25812	Nijmegen breakage syndrome 1 (nibrin)	8.5
131388	R34531	Hs.92200	KIAA0480 gene product	9.2
131410	H84658	Hs.279836	ESTs	12.1
131472	AA608962	Hs.27258	calcyclin binding protein	18.1
131475	Z39053	Hs.27263	ESTs	7.5
131501	AA121127	Hs.8207	H3 histone; family 3A	5.5
131514	X02152	Hs.2795	lactate dehydrogenase A	5.1
131524	N39152	Hs.301804	ESTs	4.3
131528	D60856	Hs.28309	UDP-glucose dehydrogenase	8.4
131544	N33236	Hs.28555	ESTs; Weakly similar to B0511.8 [C.eleg	5.6
131557	D30948	Hs.28707	signal sequence receptor; gamma (transloc	8.7
131562	U90551	Hs.28777	H2A histone family; member L	18.8
131564	AA491465	Hs.28792	ESTs	11.8
131588	AA235385	Hs.26966	ESTs; Moderately similar to alternatively	4.7
131587	M15182	Hs.183868	glucuronidase; beta	5.2
131589	U52100	Hs.29191	epithelial membrane protein 2	4.4
131615	D14533	Hs.192803	xeroderma pigmentosum; complementatio	4.6
131664	AA136126	Hs.30327	mitogen-activated protein kinase-activated	4.3
131679	AA136660	Hs.30579	ESTs	9.4
131684	U26174	Hs.3066	granzyme K (serine protease; granzyme 3	9.7
131687	L11066	Hs.3069	heat shock 70kD protein 9B (mortalin-2)	6.2
131689	AA599653	Hs.30696	transcription factor-like 5 (basic helix-loo	8.3
131693	W60913	Hs.110798	ESTs; Weakly similar to cDNA EST yk45	9
131710	AA233225	Hs.30985	MRS1 protein	5.2
131716	D49738	Hs.31053	cytoskeleton-associated protein 1	6.6
131742	D31352	Hs.31433	ESTs	11
131762	H46831	Hs.107767	ESTs; Moderately similar to CaM-Kll inh	4.9
131781	AA460450	Hs.31989	DKFZP586G1722 protein	9.2
131795	N32724	Hs.32317	Sox-like transcriptional factor	4.5
131809	L76517	Hs.3260	presenilin 1 (Alzheimer disease 3)	5.4
131814	AA437226	Hs.157	interleukin 10 receptor; alpha	4
131838	AA091832	Hs.180628	dynamin-like protein	8.7
131877	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	5
131885	AA044095	Hs.3402	ESTs	11.1
131891	AA158258	Hs.30378	heterogeneous nuclear protein similar to r	5.8
131925	AA248470	Hs.183180	ESTs; Weakly similar to RING finger pro	4.5
131930	AA205460	Hs.69478	ESTs	14.3
131941	D62657	Hs.35086	ubiquitin-specific protease 1	6.2
131965	W90146	Hs.35962	ESTs	6.3
131970	D86960	Hs.3610	KIAA0205 gene product	4.2
131971	R70167	Hs.154938	ESTs	4.3
131974	AA410424	Hs.268122	Homo sapiens mRNA; cDNA DKFZp586	4.6
131977	F09788	Hs.3622	procollagen-proline; 2-oxoglutarate 4-diox	6.4
131994	AA478515	Hs.278882	Human DNA sequence from clone 703H1	12
131997	D82399	Hs.136644	Homo sapiens clone 23714 mRNA sequen	10
132017	W67251	Hs.267659	Homo sapiens vav 3 oncogene (VAV3) m	4.7

132021	T68246	Hs.306079	chaperonin containing TCP1; subunit 5 (e	5.2
132065	D82226	Hs.211594	proteasome (prosome; macropain) 26S sub	8.5
132085	D44466	Hs.3887	proteasome (prosome; macropain) 26S sub	13.5
132089	AA131971	Hs.39122	ESTs	4.8
132109	AA599801	Hs.40098	ESTs	6.2
132143	AA257056	Hs.7972	KIAA0871 protein	14.8
132149	T10822	Hs.324743	ESTs	5.3
132153	N90141	Hs.41068	ESTs; Moderately similar to ELONGATI	9.2
132160	AA281770	Hs.295923	seven in absentia (Drosophila) homolog 1	5.5
132164	U84573	Hs.41270	procollagen-lysine; 2-oxoglutarate 5-dioxy	8.1
132180	AA405569	Hs.418	fibroblast activation protein; alpha; sepras	15.4
132183	L19183	Hs.199695	hypothetical protein	12.2
132225	AA128980		ESTs	5.6
132227	AA412620	Hs.4248	ESTs	6.7
132235	F09058	Hs.42656	ESTs	6.2
132258	AA608856	Hs.431	murine leukemia viral (bmi-1) oncogene h	6
132298	N41849	Hs.7120	Homo sapiens cytokine receptor related p	5.6
132314	AA285290	Hs.44499	small EDRK-rich factor 2	6.8
132325	N37065	Hs.44858	ESTs	4.7
132384	AA479933	Hs.46967	Human DNA sequence from clone 167A1	4.2
132387	R70914	Hs.281434	heat shock 70kD protein 1	9.1
132393	W85888	Hs.47334	ESTs; Moderately similar to !!!! ALU SU	4
132406	F09979	Hs.4774	ESTs	15
132407	AA431459	Hs.47783	ESTs	6
132413	AA132969	Hs.260116	KIAA1104 protein	4
132446	AA426218	Hs.48764	ESTs	5.3
132465	AA047896	Hs.49169	ESTs	15.4
132482	AA429478	Hs.238126	ESTs; Highly similar to CGI-49 protein [H	9
132492	T03749	Hs.4990	KIAA1089 protein	8.5
132528	AA283006	Hs.50758	chromosome-associated polypeptide C	4.3
132540	AA488987	Hs.5097	synaptogyrin 2	9.8
132543	AA417152	Hs.5101	protein regulator of cytokinesis 1	10.1
132580	L37042	Hs.283738	casein kinase 1; alpha 1	5.9
132586	AA412452	Hs.52515	DKFZP434N024 protein	4.2
132608	AA199588	Hs.5321	ARP3 (actin-related protein 3; yeast) hom	4.2
132618	AA386264	Hs.283556	isocitrate dehydrogenase 2 (NADP+); mit	5.2
132617	AA171913	Hs.5338	carbonic anhydrase XII	10.1
132616	AA253330	Hs.279916	adaptor-related protein complex 1; gamma	4.8
132640	U33821	Hs.5437	Tax1 (human T-cell leukemia virus type I	5.7
132668	AA453614	Hs.5460	KIAA0776 protein	4.4
132694	M60830	Hs.5509	ecotropic viral integration site 2B	15.8
132700	N47109	Hs.5521	ESTs	7
132724	AA417952	Hs.55498	geranylgeranyl diphosphate synthase 1	5.6
132738	W42874	Hs.264636	ESTs; Moderately similar to neuronal thre	4.9
132742	AA490882	Hs.292812	ESTs; Weakly similar to C43H8.1 [C.eleg	7.9
132744	X54326	Hs.55921	glutamyl-prolyl-tRNA synthetase	4.1
132795	H99152	Hs.57079	ESTs	8
132807	AA331777	Hs.57301	mutL (E. coli) homolog 1 (colon cancer; n	8
132811	U25435	Hs.57419	transcriptional repressor	4
132817	AB004884	Hs.57553	tousled-like kinase 2	6.5
132840	N23817	Hs.5807	Homo sapiens clone 23675 mRNA sequen	5.6
132845	D62588	Hs.5813	ESTs	12.4
132847	T48195	Hs.58189	eukaryotic translation initiation factor 3; s	7
132858	W79885	Hs.58367	glypican 4	6.2
132869	N26855	Hs.203961	ESTs	6.5
132874	AA425776	Hs.58609	ESTs	5.6
132880	AA444369	Hs.177537	ESTs	7.2
132894	D82422	Hs.5944	ESTs	7.5
132900	N56451	Hs.5978	LIM domain only 7	4.4
132903	AA235404	Hs.5985	Homo sapiens clone 25186 mRNA sequen	9.1
132904	X83818	Hs.59889	3-hydroxy-3-methylglutaryl-Coenzyme A	10.7
132906	AA142857	Hs.234896	ESTs; Highly similar to geminin [H.sapie	10.2
132914	AA496037	Hs.60293	ESTs	4.7
132918	AA252605	Hs.6051	KIAA0616 protein	7.1
132936	AB002305	Hs.6111	KIAA0307 gene product	8.3
132951	U04209	Hs.61418	microfibrillar-associated protein 1	4.3
132957	AA234791	Hs.61469	Human gene from PAC 753P9; chromoso	13.2

132959	AA028103	Hs.61472	ESTs; Weakly similar to unknown [S.cere	18.9
132968	N77151	Hs.61638	myosin X	5.6
132984	H80409	Hs.62112	zinc finger protein 207	4.3
132990	AA458761	Hs.18387	transcription factor AP-2 alpha (activating	4.2
132994	AA505133	Hs.279905	solute carrier family 2 (facilitated glucose	28.4
132998	Y00062	Hs.170121	protein tyrosine phosphatase; receptor typ	4.4
133002	AF006082	Hs.42915	ARP2 (actin-related protein 2; yeast) hom	4.7
133005	C21400	Hs.278605	KIAA0970 protein	6.6
133015	AA047036	Hs.246315	ESTs	7.9
133016	W81298	Hs.5289	growth factor receptor-bound protein 2	5.2
133039	X62055	Hs.63469	protein tyrosine phosphatase; non-recepto	4
133050	S67325	Hs.63788	propionyl Coenzyme A carboxylase; beta	5.2
133056	AA071387	Hs.6396	jumping translocation breakpoint	5
133062	R33663	Hs.64056	ESTs	5.4
133083	N70633	Hs.6456	chaperonin containing TCP1; subunit 2 (b	6
133091	AA122147	Hs.64691	KIAA0483 protein	5
133093	AA598749	Hs.285996	ESTs	5.6
133124	AA156049	Hs.267923	ESTs	4.1
133126	D16469	Hs.6551	ATPase; H+ transporting; lysosomal (vacu	6.2
133196	R37367	Hs.6727	Ras-GTPase activating protein SH3 doma	5.1
133214	Y10659	Hs.285115	interleukin 13 receptor; alpha 1	6.2
133225	Z41415	Hs.6823	ESTs; Weakly similar to intrinsic factor-B	8.3
133228	N90029	Hs.6831	Homo sapiens clone 1400 unknown prote	4.7
133239	AA059405	Hs.179882	Homo sapiens clone 24655 mRNA sequen	5.5
133240	D31161	Hs.242894	ESTs	9
133257	AF006086	Hs.6895	actin related protein 2/3 complex; subunit	7.7
133264	W72187	Hs.69192	ESTs; Weakly similar to cDNA EST yk37	6.7
133274	AA488886	Hs.6949	ESTs	4.2
133281	AA421079	Hs.69594	ESTs; Weakly similar to Sox-like transcri	4.9
133283	AA410507	Hs.6968	ESTs	4.3
133287	L15702	Hs.69771	B-factor; properdin	9.3
133294	R79723	Hs.69997	zinc finger protein 238	30.4
133297	AA600057	Hs.70266	KIAA0905 protein	10.4
133318	AA256168	Hs.152316	ESTs	8.5
133362	H06195	Hs.7194	ESTs; Highly similar to CGI-59 protein [H	14
133370	AA156897	Hs.72157	DKFZP564I1922 protein	5
133391	X57579	Hs.727	inhibin; beta A (activin A; activin AB alp	13.9
133395	AA491296	Hs.72805	ESTs	4.3
133422	N79516	Hs.73287	ESTs; Weakly similar to eyelid [D.melano	4.5
133431	AA255438	Hs.7358	Homo sapiens mRNA; cDNA DKFZp566	8
133435	T23983	Hs.323966	ESTs	5
133449	AA094989	Hs.7381	voltage-dependent anion channel 3	8.7
133468	X03068	Hs.73931	major histocompatibility complex; class II	5
133484	X78710	Hs.211581	metal-regulatory transcription factor 1	5.3
133506	AA316668	Hs.74346	ESTs; Weakly similar to 140G11.h [D.me	6.8
133517	X52947	Hs.74471	gap junction protein; alpha 1; 43kD (conn	5.7
133551	D63480	Hs.278634	KIAA0146 protein	4.8
133569	AA313977	Hs.172772	transcription elongation factor B (SIII); po	9.5
133572	W94333	Hs.279915	translocase of inner mitochondrial membr	5
133577	F03717	Hs.75063	human immunodeficiency virus type I enh	7.4
133589	L37368	Hs.75104	RNA-binding protein S1; serine-rich dom	5
133608	D13315	Hs.75207	glyoxalase I	4.2
133617	AA148318	Hs.75249	KIAA0069 protein	4.5
133627	U09587	Hs.75280	glycyl-tRNA synthetase	10
133633	D21262	Hs.75337	nucleolar phosphoprotein p130	4.5
133634	U24166	Hs.234279	microtubule-associated protein; RP/EB fa	15.2
133640	D83004	Hs.75355	ubiquitin-conjugating enzyme E2N (homo	9.1
133644	D89077	Hs.75367	Src-like-adapter	6.4
133649	AA479139	Hs.75393	acid phosphatase 1; soluble	4.8
133652	AA287383	Hs.7540	ESTs	4.2
133874	AA458948	Hs.75497	ESTs	4.3
133700	K01396	Hs.297681	protease inhibitor 1 (anti-elastase); alpha-	8.3
133705	N21848	Hs.75659	MpV17 transgene; murine homolog; glom	4.6
133716	Y00282	Hs.75722	ribophorin II	7.5
133720	L27841	Hs.75737	pericentriolar material 1	9.4
133752	U49276	Hs.75875	ubiquitin-conjugating enzyme E2 variant	4.5
133765	D21255	Hs.75929	cadherin 11 (OB-cadherin; osteoblast)	6.4

133772	W73693	Hs.76038	isopentenyl-diphosphate delta isomerase	7.9
133774	Z23090	Hs.76067	heat shock 27kD protein 1	4.1
133776	J03473	Hs.177766	ADP-ribosyltransferase (NAD+; poly (AD	13
133784	AA214305	Hs.301064	ESTs	5.2
133814	M33882	Hs.76391	myxovirus (influenza) resistance 1; homol	11.7
133829	AA453783	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564	9.4
133834	AA147510	Hs.288660	serine protease; umbilical endothelium	4.8
133839	M59815	Hs.170250	complement component 4A	6.7
133842	U73477	Hs.285013	putative human HLA class II associated p	7.1
133845	T68510	Hs.76704	ESTs	6.3
133859	U86782	Hs.178761	26S proteasome-associated pad1 homolog	13.7
133867	D43948	Hs.76989	KIAA0097 gene product	4.1
133868	U58090	Hs.183874	cullin 4A	4
133871	AA454597	Hs.182783	ESTs	4.7
133893	X01060	Hs.77356	transferrin receptor (p90; CD71)	8.3
133914	N32811	Hs.77542	ESTs	5
133918	W72783	Hs.58382	ESTs; Weakly similar to C13F10.5 [C.ele	4.5
133944	AA045870	Hs.7780	Homo sapiens mRNA; cDNA DKFZp564	6.3
133946	AA156565	Hs.173878	4-nitrophenylphosphatase domain and non	6.4
133963	L34587	Hs.184693	transcription elongation factor B (SIII); po	6.3
133980	D00760	Hs.250811	proteasome (prosome; macropain) subunit	11.9
133990	C02374	Hs.7822	Homo sapiens mRNA; cDNA DKFZp564	6.2
133999	M28213	Hs.78305	RAB2; member RAS oncogene family	5.2
134030	J03077	Hs.78575	prosaposin (variant Gaucher disease and v	4.8
134032	Z81326	Hs.78589	protease inhibitor 12 (neuroserpin)	6.5
134045	S82470	Hs.78768	BB1	11.9
134046	D28473	Hs.172801	isoleucine-tRNA synthetase	5.2
134064	D87685	Hs.78893	KIAA0244 protein	7.3
134070	H98621	Hs.78946	cullin 3	4.7
134087	U51166	Hs.173824	thymine-DNA glycosylase	7
134090	M22382	Hs.79037	heat shock 60kD protein 1 (chaperonin)	4.5
134098	X06323	Hs.79086	ribosomal protein; mitochondrial; L3	9.4
134110	U41060	Hs.79136	LIV-1 protein; estrogen regulated	4.4
134132	U32519	Hs.220689	Ras-GTPase-activating protein SH3-doma	6.6
134168	AA398908	Hs.181634	Human Chromosome 16 BAC clone CIT9	8.6
134170	M63138	Hs.79572	cathepsin D (lysosomal aspartyl protease)	9.3
134208	U88871	Hs.79993	peroxisomal biogenesis factor 7	6.3
134258	L28010	Hs.808	heterogeneous nuclear ribonucleoprotein F	4.3
134288	AA430008	Hs.8117	ESTs	6.9
134310	AA313414	Hs.8148	Homo sapiens clone 24858 mRNA sequen	7.4
134326	U16306	Hs.81800	chondroitin sulfate proteoglycan 2 (versic	6.1
134329	D38551	Hs.81848	RAD21 (S. pombe) homolog	8.6
134331	AA452020	Hs.111222	ESTs; Weakly similar to CGI-128 protein	6.1
134351	R82074	Hs.82109	syndecan 1	4.4
134357	L43575	Hs.82171	Human clone 191B7 placenta expressed m	8.6
134363	M37033	Hs.82212	CD53 antigen	5.3
134367	X54199	Hs.82285	phosphoribosylglycinamide formyltransfe	4.8
134374	D62633	Hs.8236	ESTs	16.2
134375	AA412720	Hs.82389	ESTs; Highly similar to CGI-118 protein	7.2
134376	X02874	Hs.82396	2',5'-oligoadenylate synthetase 1	6.4
134381	U56637	Hs.184270	capping protein (actin filament) muscle Z-	4
134388	M15841	Hs.82575	small nuclear ribonucleoprotein polypepti	5.7
134395	L09717	Hs.8262	lysosomal-associated membrane protein 2	6.9
134399	H99801	Hs.82689	tumor rejection antigen (gp96) 1	4.5
134401	AA243746	Hs.211577	kinectin 1 (kinesin receptor)	11.2
134405	J04177	Hs.82772	collagen; type XI; alpha 1	15.3
134415	AA329274	Hs.82911	protein tyrosine phosphatase type IVA; m	4.1
134417	D87969	Hs.82921	solute carrier family 35 (CMP-sialic acid t	4.2
134419	L08044	Hs.82961	trefoil factor 3 (intestinal)	5.9
134421	AA122388	Hs.82985	collagen; type V; alpha 2	5.8
134423	W96151	Hs.83006	ESTs; Highly similar to CGI-139 protein	4.4
134438	AA449984	Hs.246857	ESTs; Highly similar to proteine kinase JN	7
134446	T25732	Hs.83419	KIAA0252 protein	4.6
134453	X70683	Hs.83484	SRY (sex determining region Y)-box 4	5.1
134470	X54942	Hs.83758	CDC28 protein kinase 2	20.3
134487	R38185	Hs.83954	Homo sapiens unknown mRNA	6
134495	D63477	Hs.84087	KIAA0143 protein	16.1

134498	M83180	Hs.84131	threonyl-tRNA synthetase	6.1
134506	U45328	Hs.84285	ubiquitin-conjugating enzyme E2I (homol	4.6
134529	H24460	Hs.848	FK506-binding protein 4 (59kD)	6.2
134570	U66615	Hs.172280	SWI/SNF related; matrix associated; actin	4.8
134582	AA234966	Hs.86041	CGG triplet repeat binding protein 1	4.7
134600	R58884	Hs.86347	ESTs; Weakly similar to predicted using G	5.8
134623	X74496	Hs.86978	prolyl endopeptidase	4.5
134654	W23625	Hs.8739	ESTs; Weakly similar to ORF YGR200c [	13.7
134655	AA454070	Hs.123090	ESTs	5.8
134675	AA250745	Hs.87773	protein kinase; cAMP-dependent; catalyti	8.9
134711	X04011	Hs.88974	cytochrome b-245; beta polypeptide (chro	6.8
134714	U89922	Hs.890	lymphotoxin beta (TNF superfamily; mem	35.7
134722	W47183	Hs.284226	ESTs; Weakly similar to neural F box pro	8.1
134776	J05582	Hs.89603	mucin 1; transmembrane	6.2
134806	Z49099	Hs.89716	spermine synthase	4.2
134810	M27394	Hs.89751	membrane-spanning 4-domains; subfamily	7
134840	U51477	Hs.89981	diacylglycerol kinase; zeta (104kD)	4.1
134843	H60595	Hs.90061	progesterone binding protein	4.7
134853	D82348	Hs.90280	5-aminoimidazole-4-carboxamide ribonuc	10.2
134866	U84011	Hs.904	amylo-1;6-glucosidase; 4-alpha-glucanotr	12.1
134868	Z39762	Hs.90419	KIAA0882 protein	6
134885	N27870	Hs.9071	progesterone membrane binding protein	5
134982	N46086	Hs.92308	ESTs	4.1
134989	AA236324	Hs.92381	Homo sapiens mRNA; chromosome 1 spe	16.8
134992	H05625	Hs.5831	ESTs	4
134993	AA282343	Hs.301005	purine-rich element binding protein B	4.4
135010	D59675	Hs.92927	ESTs	7
135015	U54999	Hs.278338	LGN protein	4.8
135029	AA224180		ESTs; Moderately similar to 17-beta-hydr	13.6
135032	AA243497	Hs.173685	Human DNA sequence from clone 30M3	4
135037	U77948	Hs.278589	general transcription factor II; I	8
135059	AA598449	Hs.93832	Homo sapiens clone 24483 unknown mRN	5.4
135071	L08069	Hs.94	heat shock protein; DNAJ-like 2	9.3
135083	AA495950	Hs.94262	ESTs	6.7
135117	W52493	Hs.94694	Homo sapiens clone 24837 mRNA sequen	10.2
135144	AA044842	Hs.95260	Homo sapiens mRNA; cDNA DKFZp586	6.6
135154	AA126433	Hs.267812	sorting nexin 4	7.4
135218	D31157	Hs.324277	ESTs; Weakly similar to growth factor-res	6.2
135237	AA454930	Hs.9691	ESTs	19.5
135243	AA215333	Hs.97101	putative G protein-coupled receptor	8.8
135335	H20989	Hs.198281	pyruvate kinase; muscle	12.4
135349	D83174	Hs.9930	collagen-binding protein 2 (colligen 2)	5.5
135367	AA480109	Hs.9963	TYRO protein tyrosine kinase binding pro	5.4
135389	U05237	Hs.99872	fetal Alzheimer antigen	7.8
135400	M23263	Hs.99915	androgen receptor (dihydrotestosterone re	9.1
135411	L10333	Hs.99947	reticulon 1	5.3
300019	M97935		AFFX control: STAT1	8.3
300021	M97935		AFFX control: STAT1	7
300022	M97935		AFFX control: STAT1	14
300089	AI199738	Hs.208275	ESTs; Weakly similar to III ALU CLASS	9.1
300107	AI594585	Hs.270464	ESTs; Weakly similar to III ALU CLASS	7.4
300254	AW079607	Hs.188417	ESTs; Weakly similar to ZnT-3 [H.sapien	30.1
300328	AW015860	Hs.224823	ESTs	11.9
300549	AA599328	Hs.298119	ESTs	5.5
300711	AI492179	Hs.166244	ESTs; Weakly similar to cDNA EST yk40	11
300921	AW283224	Hs.232165	ESTs	11
301124	T79326	Hs.298262	ESTs; Weakly similar to dJ88J8.1 [H.sapi	8.8
301165	N85789	Hs.150186	ESTs; Weakly similar to PTERIN-4-ALP	6
301578	AI682905	Hs.270431	ESTs; Weakly similar to III ALU SUBFA	4.7
301604	AA373124	Hs.24809	ESTs; Weakly similar to C17G10.1 [C.ele	8
301704	AA526313	Hs.293691	ESTs	4.2
301782	N99399	Hs.143046	EST cluster (not in UniGene) with exon h	18
301884	AA312082	Hs.105445	GDNF family receptor alpha 1	20.7
301936	NM_004694	Hs.114924	EST cluster (not in UniGene) with exon h	11.6
302002	AF013956	Hs.5637	chromobox homolog 4 (Drosophila Pc cla	9.2
302032	NM_001992	Hs.128087	EST cluster (not in UniGene) with exon h	4.3
302067	H05698	Hs.222399	ESTs; Weakly similar to protein-tyrosine	7.8

302145	NM_003613	Hs.151407	EST cluster (not in UniGene) with exon h	15.1
302236	AI128606	Hs.6557	zinc finger protein 161	25.8
302276	NM_004448	Hs.323910	EST cluster (not in UniGene) with exon h	21.6
302290	AL117607	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564	41.4
302326	NM_004271	Hs.184018	EST cluster (not in UniGene) with exon h	8.9
302342	AB023141	Hs.190386	KIAA0924 protein	5.4
302372	AL117406	Hs.200102	Homo sapiens mRNA; cDNA DKFZp434	8.9
302422	AB021227	Hs.3743	matrix metalloproteinase 24 (membrane-in	5.2
302431	AF129530	Hs.226434	EST cluster (not in UniGene) with exon h	5.3
302501	AF022726	Hs.251446	EST cluster (not in UniGene) with exon h	9.9
302505	AL049650	Hs.247874	multiple UniGene matches	4.3
302533	L36149	Hs.248118	chemokine (C motif) XC receptor 1	4.9
302638	AA463798	Hs.102696	ESTs; Weakly similar to C11D2.4 [C.eleg	5.3
302656	AW293005	Hs.70704	ESTs	8.4
302792	AA343696	Hs.46821	ESTs; Weakly similar to putative [H.sapie	4.5
302820	X04588	Hs.85844	EST cluster (not in UniGene) with exon h	6.8
302838	U66049	Hs.82171	EST cluster (not in UniGene) with exon h	8.4
302892	N58545	Hs.42346	histone deacetylase 3	22.8
302977	AW283124	Hs.315111	EST cluster (not in UniGene) with exon h	6.8
302989	N46408	Hs.84700	EST cluster (not in UniGene) with exon h	8.9
303007	AA478876	Hs.317714	palid (mouse) homolog; palikin	10.1
303052	AF140242	Hs.279926	EST cluster (not in UniGene) with exon h	24.4
303131	AW081081	Hs.103180	actin-like 6	6.3
303132	AI929819	Hs.4055	ESTs	17.7
303153	U09759	Hs.246857	mitogen-activated protein kinase 9	11.4
303387	AA908787	Hs.180799	ESTs	15.8
303499	AI815990	Hs.293515	ESTs	7.2
303502	AA488528		EST cluster (not in UniGene) with exon h	5.3
303576	T07216	Hs.301226	EST cluster (not in UniGene) with exon h	16.2
303620	AA397546	Hs.119151	ESTs	8.9
303634	AI953377	Hs.28444	ESTs; Weakly similar to predicted using G	12
303642	AW299459	Hs.111977	EST cluster (not in UniGene) with exon h	4.2
303654	AA436942	Hs.288529	ESTs	8.4
303733	AW502498	Hs.15220	ESTs; Weakly similar to zinc finger prote	5.2
303780	AI424014	Hs.18995	ESTs; Moderately similar to KIAA0458 p	28.4
303792	C75094	Hs.199839	ESTs; Highly similar to NG22 [H.sapiens	4.4
303842	AI337304	Hs.126268	ESTs; Weakly similar to similar to PDZ d	8.1
303951	AW475081	Hs.172928	collagen; type I; alpha 1	7.5
304465	AA421948		EST singleton (not in UniGene) with exon	6.5
304507	AA458426		EST	5.4
304591	AA505702		EST singleton (not in UniGene) with exon	9.8
304601	AA507875		EST singleton (not in UniGene) with exon	7.5
304659	AA533185		EST singleton (not in UniGene) with exon	7
305040	AA630582	Hs.169476	glyceraldehyde-3-phosphate dehydrogena	12.4
305134	AA653159	Hs.179681	EST singleton (not in UniGene) with exon	8.7
305415	AA725116	Hs.78465	EST singleton (not in UniGene) with exon	5.3
305453	AA738110		EST singleton (not in UniGene) with exon	4.1
305898	AA872838		keratin 8	7.7
305913	AA876109		EST singleton (not in UniGene) with exon	6.3
305950	AA884479		EST singleton (not in UniGene) with exon	5.6
306004	AA889992	Hs.2186	EST singleton (not in UniGene) with exon	13.2
306009	AA894560	Hs.283370	EST singleton (not in UniGene) with exon	4.4
306060	AA906181	Hs.76277	EST singleton (not in UniGene) with exon	4.6
306398	AA970548	Hs.297681	EST singleton (not in UniGene) with exon	7.8
306505	AA987722	Hs.172928	EST singleton (not in UniGene) with exon	19.7
306576	AA995781	Hs.276092	EST singleton (not in UniGene) with exon	5.5
307117	AI184111	Hs.76067	heat shock 27kD protein 1	7.7
307138	AI185516	Hs.172928	collagen; type I; alpha 1	8.8
307187	AI190870	Hs.276417	EST singleton (not in UniGene) with exon	4.1
307542	AI280859	Hs.62954	EST singleton (not in UniGene) with exon	6
307554	AI281603	Hs.172928	EST singleton (not in UniGene) with exon	10.8
307606	AI351739	Hs.276726	EST singleton (not in UniGene) with exon	4.7
308079	AI472733	Hs.270208	ESTs	4.2
308307	AI581398	Hs.172928	collagen; type I; alpha 1	5.4
308511	AI687580	Hs.169476	EST singleton (not in UniGene) with exon	10.1
308615	AI738593	Hs.101774	EST singleton (not in UniGene) with exon	15.1
308677	AI761173		EST singleton (not in UniGene) with exon	4.6

308852	AI829848	Hs.182937	peptidylprolyl isomerase A (cyclophilin A	5.9
308974	AI872290	Hs.300697	immunoglobulin gamma 3 (Gm marker)	4.5
308981	AI873242		EST singleton (not in UniGene) with exon	7.6
308995	AI880172		EST singleton (not in UniGene) with exon	6.6
309177	AI951118		EST singleton (not in UniGene) with exon	24.3
309186	AI952723	Hs.80207	EST singleton (not in UniGene) with exon	6.1
309198	AI955915		major histocompatibility complex; class I;	5.6
309226	AI969897		EST singleton (not in UniGene) with exon	6.2
309279	AI990102		EST singleton (not in UniGene) with exon	7.9
309583	AW170035		EST	64.5
309624	AW191929	Hs.252989	EST	5.3
309629	AW192764	Hs.172928	collagen; type I; alpha 1	6.9
309641	AW194230	Hs.253100	EST	11.4
309698	AW238461	Hs.73742	ribosomal protein; large; P0	4.3
309700	AW241170	Hs.179661	Homo sapiens clone 24703 beta-tubulin m	11.9
310073	AI335004	Hs.148558	ESTs	4.2
310094	AW450967	Hs.235240	ESTs	5.7
310373	AW080778	Hs.145582	ESTs	4.8
310438	AW022192	Hs.200197	ESTs	39.1
310470	AI281848	Hs.194691	ESTs	4.9
310583	AW205632	Hs.211198	ESTs	7
310877	T47784	Hs.188955	ESTs	4.1
311067	AI587332	Hs.209115	ESTs	11.2
311166	AI821294	Hs.118599	ESTs	24.1
311199	T57896	Hs.191095	EST cluster (not in UniGene)	5.7
311465	AI758660	Hs.206132	ESTs	15.7
311587	AI828254	Hs.271019	ESTs	6.4
311774	AA700870	Hs.14304	ESTs	6.2
311785	AI056769	Hs.133512	ESTs	5
311923	T60843	Hs.189679	ESTs	5.9
311935	AA216387		EST cluster (not in UniGene)	5.5
311972	N51511	Hs.188449	ESTs	5.2
312014	AI435650	Hs.128778	ESTs	4.3
312047	AA588275	Hs.180669	ESTs	14.7
312147	T89855	Hs.195648	EST cluster (not in UniGene)	9.8
312153	AA759250	Hs.153028	cytochrome b-561	27.1
312168	T92251	Hs.198882	ESTs	4.2
312172	AI222168	Hs.191168	ESTs	6.1
312226	AI796815	Hs.199993	ESTs; Weakly similar to ubiquitous TPR	5.5
312292	AW451893	Hs.151124	ESTs	18.4
312312	AI080505	Hs.134529	ESTs	11.9
312369	AA582039	Hs.173884	Homo sapiens mRNA; chromosome 1 spe	4
312407	R46180	Hs.153485	ESTs	13.6
312430	AW139117	Hs.117494	ESTs	4.1
312470	AW451347	Hs.175862	ESTs	4.8
312483	AI417526	Hs.7753	ESTs	15.3
312521	AA033609	Hs.319093	ESTs	12.5
312544	AI498371	Hs.183526	ESTs	14.6
312838	AW439196	Hs.256880	ESTs	5.3
312754	R99834	Hs.250383	ESTs	8.4
312772	H83791		EST cluster (not in UniGene)	4.3
312821	AA699325	Hs.269880	ESTs	8.3
312837	AW292286	Hs.255058	ESTs	7.1
312849	AA846353	Hs.194054	ESTs	5.9
312854	AA828713	Hs.321058	EST cluster (not in UniGene)	4.1
312992	AA088446	Hs.170298	ESTs	7.3
313096	AI422367	Hs.183533	ESTs	6.1
313112	AA732534	Hs.269099	ESTs	4.2
313126	AA720887	Hs.283313	EST cluster (not in UniGene)	18.1
313136	N59284	Hs.288010	ESTs	17
313197	AI738851	Hs.222487	ESTs	12.9
313219	N74924	Hs.182099	ESTs	7.1
313258	AW058358	Hs.183918	ESTs	13.7
313328	AW449211	Hs.105445	ESTs	27.9
313352	AW292127	Hs.144758	ESTs	9.8
313417	AA741151	Hs.137323	ESTs	8.2
313455	AW081702	Hs.98571	ESTs	6.9

313590	AA804410	Hs.291677	EST cluster (not in UniGene)	6.3
313663	AI953261	Hs.169813	ESTs	7.6
313667	U69201	Hs.13684	ESTs; Weakly similar to choline kinase is	12.5
313749	AW450376	Hs.119004	ESTs	5.5
313832	AW271022	Hs.133294	ESTs	4.3
313881	AA535580	Hs.16331	ESTs	7.7
313915	AI969390	Hs.163443	ESTs	27.1
313955	AI858884	Hs.270647	ESTs	5.7
313974	AI310151	Hs.173524	ESTs	4.3
314097	AA648744	Hs.269493	ESTs	14.5
314129	AA228366	Hs.115122	ESTs	9.5
314359	AA205569	Hs.194193	ESTs	5.4
314384	AA535840	Hs.162203	ESTs; Weakly similar to alternatively spli	5.3
314394	AI380563	Hs.130816	ESTs	13.2
314462	AA347951	Hs.326413	ESTs	8.2
314465	AA602917	Hs.158974	ESTs	18.1
314470	AI934422	Hs.30661	ESTs	4.2
314488	AA358265	Hs.182890	ESTs	6.1
314506	AA833655	Hs.206868	ESTs	27.8
314510	AI204418	Hs.190080	ESTs	9.5
314558	AI873274	Hs.190721	ESTs	22.5
314661	AA436432	Hs.324239	EST cluster (not in UniGene)	13.3
314691	AW207208	Hs.136319	ESTs	21.4
314754	AW026761	Hs.134374	ESTs	4.4
314775	AI149880	Hs.188609	ESTs	4.4
314943	AI476797	Hs.184572	cell division cycle 2; G1 to S and G2 to M	18.4
314961	AW008061	Hs.231994	ESTs	10.2
314963	AI689617	Hs.200934	ESTs	5.3
315006	AI538613	Hs.298241	ESTs	20.7
315010	AA531062	Hs.240049	ESTs	5
315019	AA532807	Hs.105822	ESTs	6.1
315033	AI493046	Hs.146133	ESTs	12
315036	AA534953	Hs.163297	ESTs	8.3
315037	AW205883	Hs.133988	ESTs; Weakly similar to gene MAC25 pr	6.1
315051	AW292425	Hs.163484	EST	12.7
315054	AI968598	Hs.78768	ESTs	7.6
315073	AW452948	Hs.257631	ESTs	13.9
315080	AA744550	Hs.136345	ESTs	4.4
315083	AI221325	Hs.206442	ESTs	5.1
315088	AA557351	Hs.152448	ESTs; Moderately similar to MULTIFUN	4.7
315175	AI025842	Hs.152530	ESTs	11.9
315196	AA972756	Hs.44898	ESTs	28.8
315296	AA876905	Hs.125286	ESTs	16.1
315303	AW194364	Hs.128022	ESTs; Weakly similar to FIG-1 PROTEIN	25.7
315352	AA604799	Hs.136528	ESTs; Moderately similar to !!!! ALU SU	12.3
315384	AA643602	Hs.155485	ESTs; Highly similar to serine protease [H	4.6
315388	AW291563	Hs.104696	ESTs	4.8
315390	AI801565	Hs.200113	ESTs; Weakly similar to alternatively spli	4.4
315408	AW273261	Hs.216292	ESTs	5
315458	AA872000	Hs.116104	ESTs	7.6
315472	AA828850	Hs.165469	ESTs	4.9
315478	AA665612	Hs.120874	ESTs	5.2
315498	AA628539	Hs.116252	ESTs; Moderately similar to !!!! ALU SU	4.6
315527	AI791138	Hs.116768	ESTs	4.4
315530	AI200852	Hs.127780	ESTs	22.4
315562	AA737415	Hs.152826	ESTs	5.9
315634	AA837085	Hs.220585	ESTs	8.8
315647	AA648983	Hs.212911	ESTs	15
315652	AI521489	Hs.3053	ESTs	6.3
315678	AW002565	Hs.124660	ESTs	9.2
315680	AA814309	Hs.123583	ESTs	8.1
315735	AI831760	Hs.155111	ESTs	13.4
315741	AA812168	Hs.122559	ESTs	5.4
315769	AA744875	Hs.189413	ESTs	4.4
315978	AA830893	Hs.119769	ESTs	10.4
315984	AI015862	Hs.131793	ESTs	5
316042	AW297979	Hs.170698	ESTs	14.7

316136	AA830808	Hs.124368	ESTs	4
316177	AI908272	Hs.293102	EST cluster (not in UniGene)	32.6
316313	AA741300	Hs.202599	ESTs	4.8
316405	AA757900	Hs.270823	ESTs	4.8
316480	AI749921	Hs.205377	ESTs	12.9
316564	AI743571	Hs.168799	ESTs; Weakly similar to IIII ALU SUBFA	8.1
316714	AA809792	Hs.123307	ESTs	5
316715	AI440266	Hs.170673	ESTs	4.2
316828	AA828116	Hs.173076	ESTs	5.2
316869	AI954880	Hs.134604	ESTs	13.3
316905	AW138241	Hs.210846	ESTs	6.2
316943	AW014875	Hs.137007	ESTs	5.3
316949	AA858749	Hs.124620	ESTs	7.2
317008	AW051597	Hs.143707	ESTs	4.1
317028	AA962623	Hs.189144	ESTs; Weakly similar to RENAL SODIU	4.2
317067	AI805392	Hs.325335	ESTs	4.5
317069	AI732892	Hs.190489	ESTs	6.4
317210	AA490718		EST cluster (not in UniGene)	4.4
317298	AI922374	Hs.158549	ESTs	5.9
317658	AW139077	Hs.202217	ESTs	4.6
317674	AW294909	Hs.132208	ESTs	5.2
317685	AI798830	Hs.149997	ESTs	4.3
317836	AA983913	Hs.128929	ESTs	12.4
317881	AI827248	Hs.224398	ESTs	12.1
317902	AI828602	Hs.211265	ESTs	8.8
317916	AI565071	Hs.159983	ESTs	12.6
318042	AW294522	Hs.149991	ESTs	5.8
318053	AI074465	Hs.133469	ESTs	4
318064	AW296888	Hs.170939	ESTs	5.2
318070	AI024594	Hs.248942	ESTs	4.7
318073	AW167087	Hs.131562	ESTs	15.7
318148	AI040125	Hs.150521	ESTs	5.9
318186	AW016773	Hs.3709	ESTs	5.3
318481	AI291584	Hs.145921	ESTs; Weakly similar to HYPOTHETICA	7.6
318566	AI335361	Hs.226376	ESTs	5.8
318617	AW247252	Hs.75514	nucleoside phosphorylase	11.1
318662	AI285898	Hs.294014	ESTs	16.3
318691	AW192139	Hs.181307	H3 histone; family 3A	4
318740	NM_002543	Hs.77729	EST cluster (not in UniGene)	21.3
318744	AI793124	Hs.144479	ESTs	35
318948	AA317274	Hs.13996	ESTs	11.7
319163	F15257	Hs.27	glycine dehydrogenase (decarboxylating;	7
319478	R06841	Hs.270307	EST cluster (not in UniGene)	8.9
319545	R83718	Hs.14355	ESTs	8.2
319688	NM_002731	Hs.87773	EST cluster (not in UniGene)	25.4
319783	AA460775	Hs.6295	ESTs	7
319913	AA179304	Hs.271586	ESTs; Moderately similar to IIII ALU SU	8.7
319936	W22152	Hs.282929	EST cluster (not in UniGene)	5.6
319951	AA307665	Hs.14559	ESTs	4.9
319962	H06350	Hs.135056	ESTs	9.2
319977	AA632632		EST cluster (not in UniGene)	4.6
320074	AA321166	Hs.278233	EST cluster (not in UniGene)	16.7
320092	AF022799	Hs.113292	calpain 9 (nCL-4)	5.4
320107	AA836461	Hs.291712	EST cluster (not in UniGene)	5.3
320133	D63271		EST cluster (not in UniGene)	5.5
320167	AA984373	Hs.90790	EST cluster (not in UniGene)	15
320187	T99949	Hs.303428	EST cluster (not in UniGene)	6.7
320211	AL039402	Hs.125783	DEME-6 protein	24.3
320401	U90449	Hs.152717	nucleoside diphosphate kinase type 6 (inh	10
320458	AI884396	Hs.24131	ESTs	5.4
320488	R31386	Hs.191791	EST cluster (not in UniGene)	4.9
320521	N31484	Hs.24743	ESTs	9.5
320661	AA864846	Hs.115175	EST cluster (not in UniGene)	6.6
320691	R61576	Hs.313951	hypothetical protein	5.9
320699	R63161	Hs.118249	EST cluster (not in UniGene)	4
320727	U96044	Hs.181125	EST cluster (not in UniGene)	45.3
320993	AL050145	Hs.225986	Homo sapiens mRNA; cDNA DKFZp586	7.2

321012	AA737314	Hs.194324	EST cluster (not in UniGene)	6.1
321050	AW393497		EST cluster (not in UniGene)	5
321051	AF134149	Hs.240395	EST cluster (not in UniGene)	11.4
321171	AI769410	Hs.221461	ESTs	7.7
321192	AA295304	Hs.297939	ESTs; Weakly similar to neogenin [H.sap	5.5
321354	AA078493		EST cluster (not in UniGene)	16.9
321387	H68014	Hs.141278	ESTs; Weakly similar to IIII ALU SUBFA	4.2
321412	AW366305	Hs.22891	EST cluster (not in UniGene)	6.3
321489	AW392474	Hs.172759	ESTs; Moderately similar to IIII ALU SU	9
321539	N98819	Hs.42915	ARP2 (actin-related protein 2; yeast) hom	11.3
321593	H84762	Hs.253197	ESTs	10.4
321666	D28390	Hs.272897	EST cluster (not in UniGene)	19.9
321891	AW157424	Hs.165954	ESTs	5.6
321910	H67065	Hs.271530	ESTs; Weakly similar to IIII ALU SUBFA	5.4
321953	AW068269	Hs.292833	ESTs; Weakly similar to IIII ALU CLASS	6.5
321978	N77342	Hs.21851	EST cluster (not in UniGene)	10.2
322017	AA310039	Hs.9192	ESTs	9.8
322026	AA233527	Hs.283675	low density lipoprotein receptor (familial	27.8
322035	AL137517	Hs.306201	EST cluster (not in UniGene)	40.2
322171	AF085968	Hs.48474	EST cluster (not in UniGene)	5.7
322175	AF085975		EST cluster (not in UniGene)	7.7
322238	AL134970	Hs.104222	follistatin-like 1	14.4
322303	W07459	Hs.157601	EST cluster (not in UniGene)	13.4
322735	AA036123	Hs.297856	EST cluster (not in UniGene)	7.6
322777	AA679082	Hs.269947	ESTs	4.4
322818	AW043782	Hs.293616	ESTs	21
322882	AW248508	Hs.279727	DiGeorge syndrome critical region gene 2	15.3
322975	C16391		EST cluster (not in UniGene)	21.3
322991	C18965	Hs.159473	ESTs	11.7
323011	AA580288		EST cluster (not in UniGene)	8.9
323091	AW014094	Hs.210761	ESTs	10.8
323107	AI301107	Hs.150790	ESTs	6.5
323138	AL120351	Hs.30177	EST cluster (not in UniGene)	5.5
323168	AL120862	Hs.124165	ESTs	17.9
323195	AI064982	Hs.117950	multifunctional polypeptide similar to SA	5.8
323201	AL049370	Hs.13350	Homo sapiens mRNA; cDNA DKFZp586	11.6
323203	AA203135	Hs.130188	ESTs	6.4
323243	W44372	Hs.110771	EST cluster (not in UniGene)	7.3
323244	T70731	Hs.193620	EST cluster (not in UniGene)	15.8
323328	AA228078	Hs.255096	EST cluster (not in UniGene)	4.8
323332	AI829520	Hs.227513	ESTs	20.2
323333	AA228883	Hs.208558	EST cluster (not in UniGene)	8.8
323570	AL038623	Hs.208752	ESTs; Weakly similar to IIII ALU SUBFA	5
323604	AI751438	Hs.41271	ESTs; Weakly similar to IIII ALU SUBFA	6.5
323685	AA344205	Hs.289088	EST cluster (not in UniGene)	7.1
323753	AA327102	Hs.70266	EST cluster (not in UniGene)	6.1
323817	AA410943		EST cluster (not in UniGene)	16.8
323845	AI684674	Hs.41127	ESTs; Weakly similar to waclaw [D.melan	10.1
323930	AA570698	Hs.8173	ESTs	8.4
323997	AA844907	Hs.274454	EST cluster (not in UniGene)	6
324047	AA378201	Hs.271340	EST cluster (not in UniGene)	8.3
324281	AL044891	Hs.269350	EST cluster (not in UniGene)	50.1
324302	AA543008	Hs.292471	ESTs; Weakly similar to IIII ALU SUBFA	5.7
324338	AL138357	Hs.145078	ESTs	9.5
324344	AW502000	Hs.46677	EST cluster (not in UniGene)	4.4
324432	AA464510	Hs.152812	EST cluster (not in UniGene)	16.7
324495	AW501411	Hs.122489	ESTs; Weakly similar to IIII ALU CLASS	5.5
324497	AW152624	Hs.136340	ESTs	5.4
324598	AA502659	Hs.163986	ESTs	8.8
324603	AW016378	Hs.292934	ESTs	23.1
324620	AA448021	Hs.94109	EST cluster (not in UniGene)	21.2
324727	AI610425	Hs.19597	ESTs	5
324774	AI031771	Hs.132586	ESTs	5
324783	AA640770	Hs.200894	EST cluster (not in UniGene)	4.1
324824	AI826999	Hs.224624	ESTs	6.3
324826	AA704808	Hs.143842	ESTs	11.7
324902	D31323	Hs.271492	ESTs	4.8

324961	AA613792		EST cluster (not in UniGene)	13.3
324987	T06882	Hs.172634	ESTs	19.6
324988	T06997	Hs.121028	EST cluster (not in UniGene)	24.5
325146	AI064690	Hs.171176	ESTs	4.6
325622			CH.14_hs gi|5867000	5.2
326213			CH.17_hs gi|5867224	8.1
326474			CH.19_hs gi|5867405	12.7
326816			CH.20_hs gi|6552458	9.4
326817			CH.20_hs gi|6552458	11.7
327110			CH.21_hs gi|6117842	14.7
327196			CH.01_hs gi|5867446	5.1
327283			CH.01_hs gi|5867478	4.3
327313			CH.01_hs gi|5867501	4.8
327450			CH.02_hs gi|5867766	4.1
328059			CH.06_hs gi|6117819	6.2
328304			CH.07_hs gi|6004478	5.4
328492			CH.07_hs gi|5868455	7
328857			CH.07_hs gi|6381927	5.2
329367			CH.X_hs gi|5868842	7.6
329373			CH.X_hs gi|6682537	12
329655			CH.14_p2 gi|5448516	4
329899			CH.15_p2 gi|5563505	4
329960			CH.16_p2 gi|5091594	7.6
330084			CH.19_p2 gi|6015302	4
330384	M23263		androgen receptor (dihydrotestosterone re	5.8
330385	AA449749		ESTs; Highly similar to secreted apoptosi	10.2
330387	H14624		ESTs; Highly similar to secreted apoptosi	4.4
330388	X03363		HER2 receptor tyrosine kinase (c-erbB-2;	17.7
330409	D50692	Hs.78221	c-myc binding protein	10.1
330460	TIGR:HT544		Hs.73946	Endothelial Cell Growth Factor 1 5.5
330488	M13755	Hs.833	interferon-stimulated protein; 15 kDa	67
330494	M29698	Hs.237868	interleukin 7 receptor	6
330500	M34423	Hs.79222	galactosidase; beta 1	13.1
330510	M75099	Hs.227729	FK506-binding protein 2 (13kD)	29
330513	M81057	Hs.180884	carboxypeptidase B1 (tissue)	38.5
330541	U22970	Hs.265827	multiple UniGene matches	7.4
330542	U23942	Hs.226213	cytochrome P450; 51 (lanosterol 14-alpha	15
330547	U32989	Hs.183671	tryptophan 2;3-dioxygenase	11
330551	U39840	Hs.299867	hepatocyte nuclear factor 3; alpha	6.5
330562	U49082	Hs.76460	transporter protein	7.7
330573	U62800	Hs.83393	cystatin E/M	4
330673	D57823	Hs.321403	Sec23 (S. cerevisiae) homolog A	10.5
330711	AA164687	Hs.177576	mannosyl (alpha-1;3-)-glycoprotein beta-1	24.3
330814	AA015730	Hs.265398	ESTs; Weakly similar to transformation-r	44.1
330850	AA075298	Hs.322710	ESTs	4.4
330874	AA127474	Hs.191157	ESTs; Weakly similar to IIII ALU SUBFA	8.1
330884	AA133457	Hs.102548	ESTs	5.2
330912	AA185938	Hs.82719	general transcription factor IIA; 1 (37kD a	5
330924	AA232136	Hs.159737	Homo sapiens mRNA; cDNA DKFZp434	9.1
330997	H55762	Hs.9302	ESTs	7.6
331014	H98597	Hs.30340	ESTs	13.5
331024	N32919	Hs.27931	ESTs	9.1
331048	N66563	Hs.191358	ESTs	10.5
331135	R61398	Hs.4197	ESTs	7.4
331145	R72427	Hs.129873	ESTs; Weakly similar to CYTOCHROME	41.9
331148	R73816	Hs.17385	ESTs	4.7
331222	T98531	Hs.173904	ESTs	4.1
331230	W69807	Hs.16537	hypothetical protein; similar to (U06944)	4.9
331308	AA252079	Hs.63931	dachshund (Drosophila) homolog	15.1
331327	AA281076	Hs.109221	ESTs	4.8
331337	AA287662	Hs.50495	ESTs	7.6
331341	AA303125	Hs.23240	ESTs; Weakly similar to IIII ALU SUBFA	13
331344	AA357927	Hs.126550	ESTs	12.4
331362	AA417956	Hs.40782	ESTs	6.5
331363	AA421562	Hs.91011	anterior gradient 2 (Xenopus laevis) homo	28.2
331376	AA443802	Hs.41007	ESTs; Weakly similar to cDNA EST yk47	15.1
331384	AA456001	Hs.93847	ESTs	7.9

331478	N26608	Hs.40639	ESTs	7
331526	N49967	Hs.46624	ESTs	19.8
331533	N51517	Hs.47282	ESTs	6.5
331681	W85712	Hs.119571	collagen; type III; alpha 1 (Ehlers-Danlos	13.6
331686	W86502	Hs.182258	ESTs	9.9
331750	AA284372	Hs.111471	ESTs	5.6
331751	AA284840	Hs.143816	ESTs	5.6
331760	AA292721	Hs.154434	ESTs; Weakly similar to unknown [H.sap	7.4
331763	AA312861	Hs.96704	ESTs	7.6
331825	AA411144	Hs.292882	ESTs	15.2
331890	AA432166	Hs.3577	succinate dehydrogenase complex; subuni	24.3
331952	AA454756	Hs.97837	ESTs	5
332015	AA487910	Hs.208800	ESTs; Weakly similar to IIII ALU CLASS	10.5
332043	AA490831	Hs.125056	ESTs	11.4
332060	AA504779	Hs.191402	ESTs	13.6
332071	AA598594	Hs.205293	ESTs	9.1
332093	AA608794	Hs.112592	ESTs	8.8
332139	AA620669	Hs.112879	EST	9
332219	N22508	Hs.139315	ESTs	7.1
332225	N33213	Hs.100425	ESTs	12.2
332246	N57927	Hs.120777	ESTs; Weakly similar to RNA POLYME	15.6
332247	N58172	Hs.109370	ESTs	16.9
332260	N70088	Hs.138467	ESTs	4
332269	N91279	Hs.109654	ESTs; Moderately similar to outer membr	8.2
332336	T96130	Hs.137551	ESTs	7.7
332340	W15495	Hs.129781	chromosome 21 open reading frame 5	14.1
332347	W60326	Hs.288684	ESTs	4.4
332362	W93640	Hs.4779	ESTs; Moderately similar to similar to AD	16.9
332467	AA489630	Hs.119004	KIAA0565 gene product	4.8
332499	M12036	Hs.323910	Human tyrosine kinase-type receptor (HE	10.4
332513	AA018182	Hs.154424	deiodinase; iodothyronine; type II	5.8
332526	AA281753	Hs.77515	inositol 1;4;5-triphosphate receptor; type	19
332532	N63192	Hs.1892	EST; Highly similar to PHENYLETHAN	15.3
332565	AA234896	Hs.25272	E1A binding protein p300	12.3
332607	R41791	Hs.36568	LIM domain kinase 1	11.1
332640	AA417152	Hs.5101	protein regulator of cytokinesis 1	18.2
332694	AA262768	Hs.243901	KIAA1067 protein	15.2
332702	H93968	Hs.75725	transgelin 2	4.7
332705	T59161	Hs.76293	thymosin; beta 10	5.5
332749	AA479968	Hs.88251	arylsulfatase A	9.8
332927			CH22_FGENES.38_1	17.7
332929			CH22_FGENES.38_3	4.7
332930			CH22_FGENES.38_4	7.4
332955			CH22_FGENES.48_12	5.4
332958			CH22_FGENES.48_15	17.8
332961			CH22_FGENES.48_18	10.6
332983			CH22_FGENES.54_5	4.3
333009			CH22_FGENES.61_1	5.2
333010			CH22_FGENES.61_2	8.1
333013			CH22_FGENES.61_5	8.5
333108			CH22_FGENES.79_14	5.6
333139			CH22_FGENES.83_16	6.3
333254			CH22_FGENES.118_2	6.8
333305			CH22_FGENES.137_2	11.4
333343			CH22_FGENES.139_12	5.1
333388			CH22_FGENES.144_3	12.7
333456			CH22_FGENES.157_5	4.2
333459			CH22_FGENES.157_8	7.6
333517			CH22_FGENES.173_2	8.2
333585			CH22_FGENES.203_4	5
333679			CH22_FGENES.247_6	4.3
333743			CH22_FGENES.264_1	13.4
333756			CH22_FGENES.268_1	4
333767			CH22_FGENES.271_6	5.6
333768			CH22_FGENES.271_7	12.2
333769			CH22_FGENES.271_8	48.3
333795			CH22_FGENES.275_1	6.1

333796	CH22_FGENES.275_3	6.8
333892	CH22_FGENES.292_14	4.4
333904	CH22_FGENES.294_2	6.5
333905	CH22_FGENES.294_3	8.3
333921	CH22_FGENES.296_12	9.6
333968	CH22_FGENES.307_4	15.9
334102	CH22_FGENES.327_60	7.1
334222	CH22_FGENES.360_3	6.7
334223	CH22_FGENES.360_4	33.5
334264	CH22_FGENES.367_15	18.5
334343	CH22_FGENES.375_25	6.1
334360	CH22_FGENES.378_5	6.1
334784	CH22_FGENES.432_9	4.8
334789	CH22_FGENES.432_14	5.1
334794	CH22_FGENES.434_2	7
334889	CH22_FGENES.452_3	12.4
335004	CH22_FGENES.472_8	7.9
335115	CH22_FGENES.496_2	18.8
335287	CH22_FGENES.526_11	4.5
335342	CH22_FGENES.536_1	5.3
335491	CH22_FGENES.570_23	24
335495	CH22_FGENES.570_28	7
335498	CH22_FGENES.571_7	12.2
335544	CH22_FGENES.576_5	8.4
335610	CH22_FGENES.583_4	12.9
335653	CH22_FGENES.590_4	6.7
335682	CH22_FGENES.595_2	12.1
335687	CH22_FGENES.596_2	13.9
335755	CH22_FGENES.604_4	11.5
335782	CH22_FGENES.609_4	17.9
335791	CH22_FGENES.611_7	27.3
335809	CH22_FGENES.617_6	19.2
335822	CH22_FGENES.619_7	19.1
335823	CH22_FGENES.619_8	4.5
335824	CH22_FGENES.619_11	40.2
335825	CH22_FGENES.619_12	34.3
335895	CH22_FGENES.635_3	10.2
335917	CH22_FGENES.638_13	6
335920	CH22_FGENES.638_16	8.8
336035	CH22_FGENES.678_6	5.9
336042	CH22_FGENES.679_4	5.8
336093	CH22_FGENES.691_2	11.6
336096	CH22_FGENES.691_5	7.6
336150	CH22_FGENES.706_6	8.3
336152	CH22_FGENES.706_9	10.5
336416	CH22_FGENES.823_38	5
336444	CH22_FGENES.827_10	4.8
336449	CH22_FGENES.829_6	13.6
336471	CH22_FGENES.829_30	6.9
336512	CH22_FGENES.834_7	21.4
336558	CH22_FGENES.842_3	8.2
336560	CH22_FGENES.842_5	9
336676	CH22_FGENES.43-4	9.4
336959	CH22_FGENES.367-13	19
337968	CH22_EM:AC005500.GENSCAN.103-2	13.4
338008	CH22_EM:AC005500.GENSCAN.127-9	15.2
338057	CH22_EM:AC005500.GENSCAN.160-1	13.9
338410	CH22_EM:AC005500.GENSCAN.341-6	6
338451	CH22_EM:AC005500.GENSCAN.359-3	11.6
338588	CH22_EM:AC005500.GENSCAN.432-1	10.3
338665	CH22_EM:AC005500.GENSCAN.464-2	4.8
338689	CH22_EM:AC005500.GENSCAN.475-3	6.7
338832	CH22_DJ246D7.GENSCAN.6-8	4.8
338980	CH22_DA59H16.GENSCAN.2-4	5.1
339352	CH22_BA354I12.GENSCAN.29-7	6.9
339373	CH22_BA232E17.GENSCAN.1-29	4.3

TABLE 13A

Table 13 A shows the accession numbers for those pkeys lacking unigeneID's for Table 13. For each probeset, we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT number	Accession
123619	371681_1	AA602964 AA609200
103207	30635_-4	X72790
103349	11052_-2	X89059
110856	19346_14	AA992380 N33063 N21418 H79958 R21911 H79957
113248	328628_1	T63857 AW971220 AA493469 T63699
123169	44573_2	AI950087 N70208 R97040 N36809 AI308119 AW967677 N35320 AI251473 H59397 AW971573 R97278 W01059 AW967671 AA908598 AA251875 AI820501 AI820532 W87891 T85904 U71456 T82391 BE328571 T75102 R34725 AA884922 BE328517 AI219788 AA884444 N92578 F13493 AA927794 AI560251 AW874068 AL134043 AW235383 AA663345 AW008282 AA488964 AA283144 AI890387 AI950344 AI741345 AI689062 AA282915 AW102898 AI872193 AI763273 AW173568 AW150329 AI653832 AI762688 AA988777 AA488892 AI356394 AW103813 AI339642 AA642789 AA856975 AW505512 AI961530 AW829970 BE612881 AW276997 AW513601 AW512843 AA044209 AW856538 AA180009 AA337499 AW961101 AA251669 AA251874 AI819225 AW205882 AI683338 AI858509 AW276905 AI833006 AA972584 AA908741 AW072529 AW513996 AA293273 AA969759 N75828 N22388 H84729 H60052 T92487 AI022058 AA780419 AA551005 W80701 AW613456 AI373032 AI564269 F00531 H83488 W37181 W78802 R66058 AI002839 R67840 AA300207 AW959581 T63226 F04005
123533	genbank_AA608751	AA608751
116480	genbank_C14088	C14088
132225	genbank_AA128980	AA128980
125154	genbank_W38419	W38419
118475	genbank_N66845	N66845
102919	25180_2	M21191 AL035748 AA021266 AA323126 AA180515 AI613029 D28356 NM_000034 M11560 AW401425 AW248248 AA012958 AA323294 W04965 H38759 AA206622 AA580747 AI541172 AA381075 AA354229 AW402353 AW405575 AW404021 AW406207 AA075752 AW176066 AA287222 AA195816 T20243 R87945 AA295539 AA402933 AA232419 AA224515 AW401583 AA331367 AW402140 AW249079 R31488 AA075757 X05236 AW239490 AA338038 AW239495 AA357262 AA431005 AA306726 R33804 AA216544 AW275288 AA227044 AL038124 AA243300 C03242 AA315615 AL035840 R64336 AA313917 AA018963 AA001385 AA054395 H30840 AW498825 AA068141 AI557324 AA121576 H39128 R77161 AA019688 AA380987 AA348140 AA348257 AW176086 AA362432 AA171389 AA362416 AA299938 AA319093 AA337972 C04921 AA345696 R89640 AA085425 AA481708 AA313637 AL039229 H84490 H86153 F00858 AA326668 AA347304 R65890 H41949 AA339309 AW402002 AW404854 AA192582 AA112802 H09248 N83165 H38367 AA356339 AA455783 R66853 AA294935 H85911 AA310414 H93438 N87014 AA001186 H83640 AA411328 AA317929 C04192 AW406268 U46335 AA323179 AA427649 AI368131 H14328 AA197161 AA379497 AA311818 AA017206 AA001137 AA017420 AA012990 AW163775 AA021397 AA295513 AA355248 AA374921 AW380419 AA345884 AA318058 AA371711 AA363255 AA057094 R88057 AA394045 AW362741 AA479579 AW382789 AW362775 AA223624 AW382809 AW362746 AW362753 AW380412 AA057104 AA295271 X06352 AW362771 X12447 R59553 R87925 AA292864 R83920 F01120 AA496740 AA852551 AL039209 AA093339 AA333961 N86416 C03325 C03831 AA194750 AA359270 AA359460 AW245492 AA339400 AA330784 AI908970 N89223 AW361938 AI940063 AA134323 AA371741 F01267 AW372970 AA341973 AA346098 AW372969 AA337549 AA327342 H93855 AI074079 F29118 AA852940 F35698 AA345963 AA079578 AA113785 C02989 AA095945 C03145 C05199 AA346024 AA190508 AW361859 AI909845 AW374374 AW374382 AW374401 AW374373 AW374370 AI909831 AW374387 AA353658 F01041 C02843 AA375948 AW374414 AA213946 AI525039 H13744 R31007 AA112044 AA134404 H47935 AW177018 AA429768 AA336873 AA112875 H46393 AA191267 D59131 AW406037 AA055244 AA341880 AA179024 AA308537 AW406985 AW327311 H30301 AA300705 H43788 AW364149 AA808213 AA481938 C04941 AW375289 M21190 AA410818 AA250940 AI354547 AA317422 AA250903 AI865497 AA890603 AA356197 AW498536 M78072 AW408481 C03092 F00308 H56486 AA336320 AW406501 AA354102 AA382942 AA098393 AW376830 AA383446 F01259 AW081388 T94038 AA379643 H43842 AI524063 AA621727 AA379099 AA371417 R66811 H44129 N84794 F01135 AA477852 AA293082 AW361595 H27194 AI831850 H43253 H24797 AI564880 AA380090 W20057 AI921586 AI192549 AW090808 H25987 AA918121 AI626060 H20221 AA812572 H42178 AA887222 H96000 C03180 F00946

C03986 AI318091 AI860172 AA582179 AI633388 AA557193 R68075 F24105 AW518239 W56622 AI625219 AI925243 AW468046 AI921828 AA339164 AI144391 AA643334 AA459631 AA873247 AW373432 AA604384 H27600 AI680458 AA159956 AA610835 AA364298 AW373435 AA604225 W73754 AW087924 AA599776 N89227 AI630871 AI633128 AW514329 AA010455 AA563928 AI571596 AI128394 W73707 AI423575 AA583809 AA657988 AI950837 AA169782 AA600009 AI885540 AA771884 AI978829 AA505408 AA533937 AA481469 AA610869 AA775241 AW273870 AW070909 AI905695 AA480115 AA574051 AI889185 AA773167 AA331375 AA001437 AA194324 AA194300 AA556632 AI038538 AA411329 AA781570 AI833176 AA935520 AW074197 AA583063 AW073099 AW001198 AA948025 AA587857 AA191540 AI460085 AA193244 AI538037 AA515572 AA758587 AI149311 AA508810 AA206409 AA534004 AA994600 AA827543 AI916349 AW245129 AW517804 D25663 AA781985 AA284538 AI819422 H16040 H27531 AA456564 AA845555 AI423596 AA012908 AA869439 AA715311 AA968868 AA320508 AA725731 AA834202 AA935997 AA724815 AA769353 AA594803 F00827 AI342442 AI003519 AI002503 AI347597 AI040946 AA197162 AA987883 AA292865 AW001944 AI640711 AW244044 AA456784 F30588 AA290829 H24754 AI978683 AA483686 AA583939 AA121382 AA833831 AA477102 AA977322 AA666379 F35456 AA993537 AI749610 AA226934 AA716204 AW513025 AA628543 AA583705 F25702 AI368748 AI124097 AI880086 AA477513 AI758834 AI690753 AA477746 F37761 AA642243 AA159957 AA250844 AA459406 AA427566 F25054 AI569314 AA861665 AI922050 AI759000 AA555236 AA514432 AA283474 AA001129 AA828789 AA841390 AA134405 F35585 AA477416 AW193359 AI361315 AA284988 F36340 AI361322 F26969 AA991922 AA021267 F26973 AI361314 F35891 AI918509 AA250964 AA190992 AA577139 AA855535 AA134324 AW192842 AI224046 F18975 AA779826 AA856894 AW269997 AW014614 H95554 F31378 AA374868 F26343 AA654007 AI830942 AA113195 F26432 W56552 AA464690 AA055263 AA340654 AA031448 AA976399 AA972526 AA063476 R83921 T16240 AA533290 N91545 H44053 AA883451 AA513761 AA086477 H09249 F20482 F26737 AA054148 AA857083 AA017259 AA179789 AA088908 H43704 AA194320 F35950 AI880127 F20441 F32878 AA962483 H39094 H56489 H44621 F19390 AI302232 F25162 AA826965 AA086052 AA917410 AA454513 R59554 AA186755 AA086369 AA079530 H28106 AA243301 AI025737 AA101239 AA088887 AI214910 AA974886 F16089 F26054 AA515092 F33436 F32829 M78061 AA235645 F19715 F37529 AI811549 AA665180 AA708200 F01124 F32382 AA346220 AA627361 F30741 F30010 F28543 AA211715 F20245 AA331222 F25634 F21996 W28215 F21911 R65793 AI192566 H20130 H84491 AA719223 AA557435 F16967 F26989 F30353 AA857159 AA291918 F28234 F20840 F25176 F22437 T27904 AA480355 F19528 R87926 H14286 F27532 AW337864 F28411 H13692 F25651 AA975454 F24229 F29657 F18024 AA464779 F17588 F34954 AA947328 F18063 AA657777 AA459644 N91455 F27850 F29808 F27206 F18418 F31459 F18564 F33498 F16376 F29740 F29843 F29904 F29868 F19135 AW276602 T40337 F24835 F34672 F26474 AI926215 AA464185 F18217 N26193 AL043256 T41197 F33055 F00386 F29500 F34191 F33297 AI937207 F22724 F15909 F26232 F18889 AA318627 F29085 AA872104 F17509 F23373 F15660 F17552 F17412 F16863 F34033 F21515 F17364 F18383 F16546 F17561 F17260 AA292000 F15723 T47438 F16798 F18046 F18319 F17978 F17566 F34230 F33258 F20860 F17998 AI695701

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108733 504187_1 AA121022 AA126422
101544 entrez_M31169 M31169
124447 genbank_N48000 N48000
124677 genbank_R01073 R01073
124777 genbank_R41933 R41933
119302 genbank_T25725 T25725

103680 entrez_Z93784 Z93784
135029 H58818_at H58818
112253 genbank_R51818 R51818

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322975	1510563_1	C16391 C16413
317210	211994_1	AW881145 AA490718 M85637 AA304575 T06067 AA331991
323817	233568_1	AA410943 AW946953 AA334202 AA332882
309583	1046029_-2	AW170035
324961	376239_1	AA613792 AW182329 T05304 AW858385
303502	325188_1	BE174240 AA468528 AL042253
320133	447553_1	BE151746 BE336853 D63271 T94955 AA774994
311935	174129_1	AA216387 T83548 AA228676
321050	502195_1	C05928 AW393497
319977	345248_1	AA534222 AA632632 T81234
312772	4380_7	AW962299 AA310349 AW962294 H63791 H63751
321354	116028_-2	AA078493
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336558	CH22_3892FG_842_3_LINK_DJ	
336560	CH22_3994FG_842_5_LINK_DJ	
329367	c_x_hs	
329373	c_x_hs	
336676	CH22_4154FG_43_4_	
338008	CH22_6490FG__LINK_EM:AC00	
338057	CH22_6558FG__LINK_EM:AC00	
329655	c14_p2	
336959	CH22_4764FG_367_13_	
329899	c15_p2	
329960	c16_p2	
338410	CH22_7087FG__LINK_EM:AC00	
338451	CH22_7124FG__LINK_EM:AC00	
338588	CH22_7331FG__LINK_EM:AC00	
338665	CH22_7438FG__LINK_EM:AC00	
338689	CH22_7484FG__LINK_EM:AC00	
308677	AI761173	
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338980	CH22_7859FG__LINK_DA59H18	
333009	CH22_233FG_61_1_LINK_EM:A	
333010	CH22_234FG_61_2_LINK_EM:A	
333013	CH22_237FG_61_5_LINK_EM:A	
308981	AI873242	
308995	AI880172	
333108	CH22_336FG_79_14_LINK_EM:	
333139	CH22_368FG_83_18_LINK_EM:	
333254	CH22_495FG_118_2_LINK_EM:	
333305	CH22_550FG_137_2_LINK_EM:	
333343	CH22_589FG_139_12_LINK_EM	
333388	CH22_634FG_144_3_LINK_EM:	
326213	c17_hs	
333456	CH22_706FG_157_5_LINK_EM:	
333459	CH22_709FG_157_8_LINK_EM:	
333517	CH22_773FG_173_2_LINK_EM:	
333585	CH22_846FG_203_4_LINK_EM:	
333679	CH22_941FG_247_6_LINK_EM:	
326474	c19_hs	
333743	CH22_1009FG_264_1_LINK_EM	
333758	CH22_1024FG_268_1_LINK_EM	
333767	CH22_1034FG_271_6_LINK_EM	
333768	CH22_1035FG_271_7_LINK_EM	
333769	CH22_1036FG_271_8_LINK_EM	
333795	CH22_1063FG_275_1_LINK_EM	
333796	CH22_1065FG_275_3_LINK_EM	
335004	CH22_2326FG_472_8_LINK_EM	
333892	CH22_1163FG_292_14_LINK_E	
335115	CH22_2447FG_496_2_LINK_EM	
333904	CH22_1176FG_294_2_LINK_EM	

333905 CH22_1177FG_294_3_LINK_EM
333921 CH22_1194FG_296_12_LINK_E
333968 CH22_1245FG_307_4_LINK_EM
328059 c_6_hs
335287 CH22_2629FG_526_11_LINK_E
326816 c20_hs
326817 c20_hs
335342 CH22_2689FG_536_1_LINK_EM
335491 CH22_2843FG_570_23_LINK_E
335495 CH22_2847FG_570_28_LINK_E
335498 CH22_2850FG_571_7_LINK_EM
328304 c_7_hs
305453 AA738110
335544 CH22_2899FG_576_5_LINK_EM
335610 CH22_2969FG_583_4_LINK_EM
335653 CH22_3013FG_590_4_LINK_EM
335682 CH22_3043FG_595_2_LINK_EM
335687 CH22_3048FG_596_2_LINK_EM
328492 c_7_hs
335755 CH22_3122FG_604_4_LINK_EM
335782 CH22_3151FG_609_4_LINK_EM
335791 CH22_3160FG_611_7_LINK_EM
335809 CH22_3181FG_617_6_LINK_EM
335822 CH22_3195FG_619_7_LINK_EM
335823 CH22_3196FG_619_8_LINK_EM
335824 CH22_3197FG_619_11_LINK_E
335825 CH22_3198FG_619_12_LINK_E
335895 CH22_3272FG_635_3_LINK_EM
335917 CH22_3294FG_636_13_LINK_E
335920 CH22_3297FG_636_16_LINK_E
305898 AA872838
305913 AA876109
305950 AA884479
328857 c_7_hs
330084 c19_p2
337968 CH22_6419FG__LINK_EM:AC00
309177 AI951118
309198 AI955915
309226 AI969897
339352 CH22_8317FG__LINK_BA35411
309279 AI990102
339373 CH22_8348FG__LINK_BA232E1
325622 c14_hs
334102 CH22_1380FG_327_60_LINK_E
332927 CH22_148FG_38_1_LINK_C20H
332929 CH22_150FG_38_3_LINK_C20H
332930 CH22_151FG_38_4_LINK_C20H
332955 CH22_178FG_48_12_LINK_EM:
332958 CH22_182FG_48_15_LINK_EM:
332961 CH22_185FG_48_18_LINK_EM:
332983 CH22_207FG_54_5_LINK_EM:A
334222 CH22_1506FG_360_3_LINK_EM
334223 CH22_1507FG_360_4_LINK_EM
334264 CH22_1551FG_367_15_LINK_E
327110 c21_hs
334343 CH22_1635FG_375_25_LINK_E
334360 CH22_1654FG_378_5_LINK_EM
327196 c_1_hs
327283 c_1_hs
327313 c_1_hs
304465 AA421948
304507 AA456426
327450 c_2_hs
304591 AA505702
304601 AA507875
304659 AA533185
334784 CH22_2096FG_432_9_LINK_EM

334789 CH22_2101FG_432_14_LINK_E
334794 CH22_2106FG_434_2_LINK_EM
336035 CH22_3420FG_678_6_LINK_DJ
336042 CH22_3427FG_679_4_LINK_DJ
336093 CH22_3481FG_691_2_LINK_DJ
336096 CH22_3484FG_691_5_LINK_DJ
334889 CH22_2205FG_452_3_LINK_EM
336150 CH22_3540FG_706_6_LINK_DA
336152 CH22_3543FG_706_9_LINK_DA
336416 CH22_3833FG_823_38_LINK_B
336444 CH22_3864FG_827_10_LINK_D
336449 CH22_3870FG_829_6_LINK_DJ
336471 CH22_3894FG_829_30_LINK_D

TABLE 13B

Table 13B shows the genomic positioning for those pkeys lacking unigene ID's and accession numbers in Table 13B. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
332955	Dunham, I. et.al.	Plus	2508896-2508992
332958	Dunham, I. et.al.	Plus	2516164-2516310
332961	Dunham, I. et.al.	Plus	2521424-2521555
333139	Dunham, I. et.al.	Plus	3369495-3369571
333254	Dunham, I. et.al.	Plus	2521424-2521555
333305	Dunham, I. et.al.	Plus	4630388-4630645
333388	Dunham, I. et.al.	Plus	4913749-4913805
333517	Dunham, I. et.al.	Plus	5570729-5570925
333585	Dunham, I. et.al.	Plus	6234778-6234894
333679	Dunham, I. et.al.	Plus	7068795-7068898
333767	Dunham, I. et.al.	Plus	7694407-7694623
333768	Dunham, I. et.al.	Plus	7695440-7695697
333769	Dunham, I. et.al.	Plus	7696625-7696707
333795	Dunham, I. et.al.	Plus	7807688-7807795
333796	Dunham, I. et.al.	Plus	7808253-7808319
333892	Dunham, I. et.al.	Plus	8156825-8157001
333921	Dunham, I. et.al.	Plus	8380325-8380441
333968	Dunham, I. et.al.	Plus	8681004-8681241
334102	Dunham, I. et.al.	Plus	9995140-9996373
334264	Dunham, I. et.al.	Plus	13234447-13234544
334343	Dunham, I. et.al.	Plus	13655828-13656307
334794	Dunham, I. et.al.	Plus	16374312-16374458
334889	Dunham, I. et.al.	Plus	19286024-19286515
335287	Dunham, I. et.al.	Plus	22299047-22299299
335491	Dunham, I. et.al.	Plus	24128651-24128827
335495	Dunham, I. et.al.	Plus	24140688-24140872
335498	Dunham, I. et.al.	Plus	24172082-24172181
335653	Dunham, I. et.al.	Plus	25329710-25329802
335687	Dunham, I. et.al.	Plus	25445952-25446064
335809	Dunham, I. et.al.	Plus	26310772-26310909
335822	Dunham, I. et.al.	Plus	26364087-26364196
335823	Dunham, I. et.al.	Plus	26365925-26366004
335824	Dunham, I. et.al.	Plus	26376860-26376942
335825	Dunham, I. et.al.	Plus	26378175-26378258
336035	Dunham, I. et.al.	Plus	29016748-29017410
336093	Dunham, I. et.al.	Plus	29556922-29557002
336096	Dunham, I. et.al.	Plus	29578878-29579047
336444	Dunham, I. et.al.	Plus	34190585-34190718
336959	Dunham, I. et.al.	Plus	13233040-13233126
338008	Dunham, I. et.al.	Plus	7697068-7697236
338057	Dunham, I. et.al.	Plus	8526397-8526522
338410	Dunham, I. et.al.	Plus	19292807-19292916
338568	Dunham, I. et.al.	Plus	22896767-22896920
338665	Dunham, I. et.al.	Plus	24472654-24472853
338832	Dunham, I. et.al.	Plus	27775128-27775290
338980	Dunham, I. et.al.	Plus	29896789-29896874
339352	Dunham, I. et.al.	Plus	33544784-33545121

332929	Dunham, I. et.al.	Minus	2020758-2020664
332930	Dunham, I. et.al.	Minus	2022565-2022497
332963	Dunham, I. et.al.	Minus	2631933-2631797
333009	Dunham, I. et.al.	Minus	2766043-2765856
333010	Dunham, I. et.al.	Minus	2768207-2768119
333013	Dunham, I. et.al.	Minus	2772278-2772039
333108	Dunham, I. et.al.	Minus	3240494-3240389
333343	Dunham, I. et.al.	Minus	4692886-4692753
333456	Dunham, I. et.al.	Minus	2631933-2631797
333459	Dunham, I. et.al.	Minus	5144548-5144344
333743	Dunham, I. et.al.	Minus	7573218-7573060
333758	Dunham, I. et.al.	Minus	7666413-7666091
333904	Dunham, I. et.al.	Minus	8217374-8217261
333905	Dunham, I. et.al.	Minus	8217796-8217670
334222	Dunham, I. et.al.	Minus	12732417-12732289
334223	Dunham, I. et.al.	Minus	12734365-12734269
334360	Dunham, I. et.al.	Minus	13728850-13728751
334784	Dunham, I. et.al.	Minus	16294548-16294360
334789	Dunham, I. et.al.	Minus	16306095-16305998
335004	Dunham, I. et.al.	Minus	20581911-20581794
335115	Dunham, I. et.al.	Minus	21388250-21388146
335342	Dunham, I. et.al.	Minus	22597448-22597284
335544	Dunham, I. et.al.	Minus	24650505-24650403
335610	Dunham, I. et.al.	Minus	25068943-25068841
335682	Dunham, I. et.al.	Minus	25421215-25421093
335755	Dunham, I. et.al.	Minus	25763806-25763747
335782	Dunham, I. et.al.	Minus	25908578-25908440
335791	Dunham, I. et.al.	Minus	25948563-25948411
335895	Dunham, I. et.al.	Minus	26975307-26975239
335917	Dunham, I. et.al.	Minus	27028481-27028377
335920	Dunham, I. et.al.	Minus	27034927-27034811
336042	Dunham, I. et.al.	Minus	29041694-29041500
336150	Dunham, I. et.al.	Minus	30150423-30150256
336152	Dunham, I. et.al.	Minus	30156053-30155870
336416	Dunham, I. et.al.	Minus	34047408-34047311
336449	Dunham, I. et.al.	Minus	34204707-34204577
336471	Dunham, I. et.al.	Minus	34215091-34214978
336512	Dunham, I. et.al.	Minus	34278373-34278275
336558	Dunham, I. et.al.	Minus	34375825-34375698
336560	Dunham, I. et.al.	Minus	34376814-34376696
336676	Dunham, I. et.al.	Minus	2022565-2022497
337958	Dunham, I. et.al.	Minus	7095797-7095680
338451	Dunham, I. et.al.	Minus	20174286-20174193
338689	Dunham, I. et.al.	Minus	24893073-24892972
339373	Dunham, I. et.al.	Minus	33860127-33860047
325822	5867000	Plus	69994-70075
329655	6448516	Minus	35565-35843
329899	6563505	Minus	111058-111783
329960	5091594	Minus	1031-1162
326213	5867224	Minus	60751-60927
326474	5867405	Plus	16995-18101
330084	6015302	Minus	57019-58337
326816	6552458	Plus	198354-198436
326817	6552458	Plus	199909-200001
327110	6117842	Plus	84608-84785
327196	5867446	Plus	180921-181333
327283	5867478	Minus	567-982
327313	5867501	Minus	89734-89838
327450	5867766	Minus	47928-48076
328059	6117819	Plus	37052-37204
328492	5868455	Minus	46094-46241
328304	6004478	Minus	3884-3952
328857	6381927	Minus	80557-81051
329367	5868842	Minus	87201-87587
329373	6682537	Minus	38950-39301

TABLE 14: Table 2 from BRCA 001-5 US

Table 14, a subset of table 13, depicts a preferred group of genes highly upregulated in breast cancer cells.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of tumor to normal breast tissue

Pkey	ExAccn	UniGene ID	Unigene Title	R1
100038	M97935		AFFX control: STAT1	16.7
100114	D00596	Hs.82962	thymidylate synthetase	15.9
100975	J02923	Hs.76506	lymphocyte cytosolic protein 1 (L-plastin)	30.1
101031	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B; 9	37.2
101104	L07615	Hs.169266	Human neuropeptide Y receptor Y1 (NPYY	18.3
101143	L12723	Hs.90093	heat shock 70kD protein 4	17.4
101332	L47276	Hs.156346	Homo sapiens (cell line HL-6) alpha topois	18.9
101378	M13755	Hs.833	interferon-stimulated protein; 15 kDa	18.1
101809	M86849	Hs.323733	Homo sapiens connexin 26 (GJB2) mRNA	22.5
102618	U65932	Hs.81071	extracellular matrix protein 1	23.2
102721	U79241	Hs.118666	Human clone 23759 mRNA; partial cds	15
102817	U90904	Hs.83724	Human clone 23773 mRNA sequence	15.2
102907	X06985	Hs.202833	heme oxygenase (decycling) 1	22.7
102985	X17644	Hs.2707	G1 to S phase transition 1	20.6
103060	X57766	Hs.155324	matrix metalloproteinase 11 (stromelysin 3	17.8
103180	X69433	Hs.5337	isocitrate dehydrogenase 2 (NADP+); mito	18.9
103208	X72755	Hs.77367	monokine induced by gamma interferon	15.1
103821	AA157623	Hs.198793	KIAA0750 gene product	23.3
104115	AA428090	Hs.26102	ESTs	26.7
104667	AA007234	Hs.30098	ESTs	16.6
105186	AA191512	Hs.28005	Homo sapiens mRNA; cDNA DKFZp564G	19.3
106103	AA421104	Hs.12094	ESTs	15.4
107151	AA621169	Hs.8687	ESTs	19
109415	AA227219	Hs.110826	trinucleotide repeat containing 9	20.1
110189	H20543	Hs.6278	DKFZP586B1621 protein	16.6
110561	H59617	Hs.5199	ESTs; Weakly similar to UBIQUITIN-CON	19.5
110734	H98714	Hs.24131	ESTs	30.2
110915	N46252	Hs.29724	ESTs	23.2
111179	N67239	Hs.10760	ESTs	37
111357	N91023	Hs.87128	ESTs	15
112134	R46025	Hs.7413	ESTs	17.4
113970	W88748	Hs.8109	ESTs	15
114124	Z38595	Hs.125019	ESTs; Highly similar to KIAA0886 protein	22
114292	Z40715	Hs.184641	delta-6 fatty acid desaturase	19.4
114901	AA236276	Hs.196437	ESTs; Weakly similar to R26660_1; partial	16.9
114965	AA250737	Hs.72472	ESTs	35.1
115652	AA405098	Hs.38178	ESTs	16.1
115875	AA433943	Hs.43946	ESTs; Weakly similar to Weak similarity t	33.5
116790	H29532	Hs.101174	microtubule-associated protein tau	22.2
116921	H72948	Hs.821	biglycan	20.7
117412	N26722	Hs.42645	ESTs	18.1
120241	Z41815	Hs.65946	ESTs	15.6
120325	AA195651	Hs.104106	ESTs	15.2
121598	AA416740	Hs.174104	ESTs	22.6
123619	AA609200		ESTs	23.1
124006	D80302	Hs.270016	ESTs	20.6
125852	H09280	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B	25.9
126160	N90960	Hs.265398	ESTs; Weakly similar to transformation-rel	16.4

127677	AA916752	Hs.264190	ESTs; Highly similar to MEM3 [M.musculi	17.3
128595	U31875	Hs.152677	short-chain alcohol dehydrogenase family m	27.1
128717	T30617	Hs.104222	Homo sapiens mRNA; cDNA DKFZp566L	24.5
129124	AA234530	Hs.108802	N-ethylmaleimide-sensitive factor	20.7
129366	H18027	Hs.184697	plexin C1	18.2
130455	X17059	Hs.155956	N-acetyltransferase 1 (arylamine N-acetylt	26.4
130604	X03635	Hs.1657	estrogen receptor 1	39.9
130913	W03592	Hs.21198	translocase of outer mitochondrial membra	20.9
130944	M97935	Hs.21486	signal transducer and activator of transcript	18.8
131472	AA608962	Hs.27258	calcyclin binding protein	18.1
131562	U90551	Hs.28777	H2A histone family; member L	18.8
132180	AA405569	Hs.418	fibroblast activation protein; alpha; seprase	15.4
132406	F09979	Hs.4774	ESTs	15
132465	AA047896	Hs.49169	ESTs	15.4
132994	AA505133	Hs.279905	solute carrier family 2 (facilitated glucose t	26.4
133294	R79723	Hs.59997	zinc finger protein 238	30.4
133634	U24168	Hs.234279	microtubule-associated protein; RP/EB fam	15.2
134374	D62633	Hs.8236	ESTs	15.2
134405	J04177	Hs.82772	collagen; type XI; alpha 1	15.3
134470	X54942	Hs.83758	CDC28 protein kinase 2	20.3
134495	D63477	Hs.84087	KIAA0143 protein	16.1
134714	U89922	Hs.890	lymphotoxin beta (TNF superfamily; memb	35.7
135237	AA454930	Hs.9691	ESTs	18.5
301884	AA312082	Hs.105445	GDNF family receptor alpha 1	20.7
302276	NM_004448	Hs.323910	EST cluster (not in UniGene) with exon hit	21.6
302290	AL117607	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564N	41.4
309177	AI951118		EST singleton (not in UniGene) with exon	24.3
309583	AW170035		EST	64.5
310438	AW022192	Hs.200197	ESTs	39.1
311166	AI821294	Hs.118599	ESTs	24.1
312153	AA759250	Hs.153028	cytochrome b-561	27.1
313915	AI969390	Hs.163443	ESTs	27.1
314508	AA833655	Hs.206868	ESTs	27.8
314558	AI873274	Hs.190721	ESTs	22.5
314691	AW207206	Hs.136319	ESTs	21.4
314943	AI478797	Hs.184572	cell division cycle 2; G1 to S and G2 to M	18.4
315196	AA972756	Hs.44898	ESTs	28.8
316177	AI908272	Hs.293102	EST cluster (not in UniGene)	32.6
318073	AW167087	Hs.131562	ESTs	15.7
318662	AI285898	Hs.294014	ESTs	16.3
318740	NM_002543	Hs.77729	EST cluster (not in UniGene)	21.3
318744	AI793124	Hs.144479	ESTs	35
319668	NM_002731	Hs.87773	EST cluster (not in UniGene)	25.4
320074	AA321166	Hs.278233	EST cluster (not in UniGene)	16.7
320211	AL039402	Hs.125783	DEME-6 protein	24.3
320727	U96044	Hs.181125	EST cluster (not in UniGene)	15.3
322818	AW043782	Hs.293616	ESTs	21
322882	AW248508	Hs.279727	DiGeorge syndrome critical region gene 2	15.3
324261	AL044891	Hs.269350	EST cluster (not in UniGene)	50.1
324432	AA464510	Hs.152812	EST cluster (not in UniGene)	16.7
324603	AW016378	Hs.292934	ESTs	23.1
324620	AA448021	Hs.94109	EST cluster (not in UniGene)	21.2
324988	T08997	Hs.121028	EST cluster (not in UniGene)	24.5
330388	X03363		HER2 receptor tyrosine kinase (c-erbB-2; E	17.7
330486	M13755	Hs.833	interferon-stimulated protein; 15 kDa	67
330814	AA015730	Hs.265398	ESTs; Weakly similar to transformation-rel	44.1
331145	R72427	Hs.129873	ESTs; Weakly similar to CYTOCHROME	41.9
331308	AA252079	Hs.83931	dachshund (Drosophila) homolog	15.1
331890	AA432166	Hs.3577	succinate dehydrogenase complex; subunit	24.3
332526	AA281753	Hs.77515	inositol 1;4;5-triphosphate receptor; type 3	19
332532	N63192	Hs.1892	EST; Highly similar to PHENYLETHANO	15.3
332694	AA262768	Hs.243901	KIAA1067 protein	15.2
332958			CH22_FGENES.48_15	17.8
333769			CH22_FGENES.271_8	48.3
333988			CH22_FGENES.307_4	15.9
334223			CH22_FGENES.360_4	33.5
334264			CH22_FGENES.367_15	18.5

335791	CH22_FGENES.611_7	27.3
336512	CH22_FGENES.834_7	21.4
338008	CH22_EM:AC005500.GENSCAN.127-9	15.2

TABLE 14A

Table 14A shows the accession numbers for those pkeys lacking unigeneID's for Table 14. For each probeset, we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT number	Accession
309583	1046029_-2	AW170035
336512	CH22_3941FG_834_7_LINK_DJ	
338008	CH22_8490FG__LINK_EM:AC00	
333769	CH22_1036FG_271_8_LINK_EM	
333968	CH22_1245FG_307_4_LINK_EM	
335791	CH22_3160FG_611_7_LINK_EM	
309177	AI951118	
332958	CH22_182FG_48_15_LINK_EM:	
334223	CH22_1507FG_360_4_LINK_EM	
334264	CH22_1551FG_367_15_LINK_E	
123819	371681_1	AA602984 AA609200

TABLE 14B

Table 14B shows the genomic positioning for those pkeys lacking unigene ID's and accession numbers in Table 14. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
332958	Dunham, I. et.al.	Plus	2516164-2516310
333769	Dunham, I. et.al.	Plus	7696625-7696707
333968	Dunham, I. et.al.	Plus	8681004-8681241
334264	Dunham, I. et.al.	Plus	13234447-13234544
338008	Dunham, I. et.al.	Plus	7697068-7697236
334223	Dunham, I. et.al.	Minus	12734365-12734269
335781	Dunham, I. et.al.	Minus	25948563-25948411
336512	Dunham, I. et.al.	Minus	34278373-34278275

TABLE 15: Table 3 from BRCA 001-5 US

Table 15 shows genes downregulated in breast cancer cells.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of normal breast tissue to tumor

Pkey	ExAccn	UniGene ID	Unigene Title	R1
100115	D00632	Hs.172153	glutathione peroxidase 3 (plasma)	1.7
100499	TIGR:HT1428	Hs.283108	Globin, Beta	1.5
100502	TIGR:HT1496	Hs.169228	Adrenal-Specific Protein Pg2	2.3
100615	TIGR:HT4268	Hs.9739	L-Glycerol-3-Phosphate:Nad+ Oxidoreduct	1.7
101125	L10373	Hs.82749	transmembrane 4 superfamily member 2	1.5
101367	M12963	Hs.4	alcohol dehydrogenase 1 (class I); alpha po	2.9
101397	M15856	Hs.180878	lipoprotein lipase	1.6
101883	M98399	Hs.75613	CD36 antigen (collagen type I receptor; thr	1.8
102227	U25138	Hs.93841	potassium large conductance calcium-activ	1.6
102857	X00129	Hs.76461	retinol-binding protein 4; interstitial	3
103211	X73079	Hs.288579	polymeric immunoglobulin receptor	1.8
103496	Y09267	Hs.132821	flavin containing monooxygenase 2	1.5
103562	Z21966	Hs.2815	POU domain; class 6; transcription factor 1	1.8
104672	AA007629		glycerol-3-phosphate dehydrogenase 1 (sol	2.4
105083	AA146619	Hs.18791	ESTs; Weakly similar to CALCIUM-BIND	1.7
105138	AA164519	Hs.15248	ESTs	1.5
106075	AA417915	Hs.25930	ESTs	1.5
106870	AA487576	Hs.26530	serum deprivation response (phosphatidyls	1.6
107099	AA609645	Hs.211568	eukaryotic translation initiation factor 4 gam	2.7
107616	AA004901	Hs.261164	ESTs	1.6
107937	AA037388	Hs.82223	Human DNA sequence from clone 141H5 o	1.7
108604	AA099820	Hs.49696	ESTs	2.4
111130	N64265	Hs.19515	yz44h12.s1 Morton Fetal Cochlea Homo sa	1.7
111837	R36447	Hs.24453	ESTs	1.6
112538	R70255		ESTs	1.9
112808	R97970	Hs.261022	EST	1.5
113086	T40652	Hs.209100	DKFZP434C171 protein	1.9
115740	AA418033	Hs.283559	ESTs	1.6
115949	AA443800	Hs.43125	ESTs	2
115985	AA446681	Hs.173233	ESTs	2.2
117224	N20300	Hs.218707	ESTs	1.7
117513	N32174	Hs.44317	SRY (sex-determining region Y)-box 10	1.7
119059	R15436	Hs.77889	Friedreich ataxia region gene X123	1.7
119175	R71792	Hs.301002	ESTs; Weakly similar to cell death activato	2.8
119359	T71021	Hs.285681	ESTs; Highly similar to WS basic-helix-loo	1.9
119798	W73386	Hs.249129	ESTs	3
120889	AA365784	Hs.97044	ESTs	1.6
121381	AA405747	Hs.97984	ESTs; Weakly similar to WASP-family pro	1.8
121750	AA421184	Hs.97549	ESTs	1.5
122127	AA434447	Hs.106771	ESTs	2.5
122348	AA443695	Hs.293410	ESTs	2.1
122485	AA448300	Hs.160318	phospholemman	1.5
123443	AA598841	Hs.187382	natriuretic peptide receptor A/guanylate cy	1.8
123505	AA600135		ESTs; Moderately similar to !!!! ALU SUB	1.5
125284	W94688	Hs.103253	perilipin	1.7
126300	D81972		HUM427D08B Human fetal brain (TFujiw	1.8
126747	R72515	Hs.160318	phospholemman	1.8
127218	AA309765	Hs.116017	ESTs; Weakly similar to KIAA0795 protei	1.5
127357	AA452788	Hs.75432	zx39g11.r1 Soares_total_fetus_Nb2HF8_9	1.7

127638	AA634405	Hs.122608	ESTs	1.5
128213	AA972780	Hs.129194	ESTs; Weakly similar to IIII ALU SUBFA	1.5
128351	AI092391	Hs.134886	ESTs	1.5
128842	N44757	Hs.20340	ESTs	1.6
128870	R71403	Hs.75309	eukaryotic translation elongation factor 2	1.7
129146	AA459944	Hs.108924	DKFZP586P1422 protein	1.5
129285	T62068	Hs.11006	ESTs	2.1
129331	N83465	Hs.279772	ESTs; Highly similar to CGI-38 protein [H	1.5
130085	M62402	Hs.274313	insulin-like growth factor binding protein 6	1.7
130400	M25079	Hs.283108	hemoglobin; beta	1.7
131267	AA211776	Hs.2504	myomesin 1 (skelemin) (185kD)	3.8
131277	AA131466	Hs.23767	ESTs	1.9
131282	M12272	Hs.4	alcohol dehydrogenase 3 (class I); gamma p	2.2
131304	AA295848	Hs.25475	aquaporin 7	1.7
131810	D49487	Hs.194236	leptin (murine obesity homolog)	2.5
132788	AA045503	Hs.56874	ESTs; Weakly similar to Homo sapiens p2	1.6
132931	Z41452	Hs.6090	deleted in bladder cancer chromosome regi	1.5
133120	X64559	Hs.65424	tetranectin (plasminogen-binding protein)	2
133314	U95367	Hs.70725	gamma-aminobutyric acid (GABA) A recep	1.5
133507	X74295	Hs.74369	integrin; alpha 7	1.7
133601	S95936	Hs.284176	transferrin	2.3
133702	N56898	Hs.75652	glutathione S-transferase M5	1.9
134111	N79674	Hs.8022	TU3A protein	4.6
134699	U56814	Hs.88646	deoxyribonuclease I-like 3	1.5
134749	L10955	Hs.89485	carbonic anhydrase IV	1.6
135173	M72885	Hs.95910	Human G0S2 protein gene; complete cds	1.9
300132	AW027556	Hs.156286	ESTs	1.7
300732	AI369956	Hs.257891	ESTs	1.5
300750	AA514805	Hs.293055	ESTs	1.8
301140	AI807692	Hs.129129	ESTs	1.6
301396	AA923549	Hs.224121	ESTs	2.1
302910	N77976	Hs.251577	hemoglobin; alpha 1	1.8
303798	V00505	Hs.36977	hemoglobin; delta	1.8
303831	T04868	Hs.46780	EST cluster (not in UniGene) with exon hit	1.7
303844	U94362	Hs.58569	glycogenin 2	1.5
304182	H91086		EST singleton (not in UniGene) with exon	1.5
304622	AA516384		EST singleton (not in UniGene) with exon	1.5
304682	AA550994		EST singleton (not in UniGene) with exon	1.7
305612	AA782347	Hs.272572	EST singleton (not in UniGene) with exon	1.5
306193	AA923457		EST singleton (not in UniGene) with exon	1.5
307206	AI192534		EST singleton (not in UniGene) with exon	1.6
307377	AI222691		EST singleton (not in UniGene) with exon	1.5
308023	AI452732	Hs.251577	EST singleton (not in UniGene) with exon	1.9
308359	AI612774	Hs.79372	retinoid X receptor; beta	1.5
309838	AW296073	Hs.255504	EST	1.5
310403	AI720978	Hs.148006	ESTs; Moderately similar to alternatively s	1.8
311671	AW241947	Hs.232478	ESTs	1.6
311794	AW238092	Hs.254759	ESTs	2.1
312082	T79860	Hs.118180	ESTs	1.9
312575	H25237	Hs.306814	ESTs	2.3
313076	N49684	Hs.143040	ESTs	1.8
313283	W32480	Hs.157099	ESTs	2.2
313374	AW328672	Hs.132760	ESTs	1.9
314701	AI754634	Hs.131987	ESTs	1.7
315391	AA759098	Hs.192007	ESTs	1.8
315688	AA680055	Hs.264885	ESTs	1.5
316249	AA948612	Hs.130414	ESTs	1.6
316586	AI205077	Hs.294085	ESTs	1.7
316890	AA837079	Hs.24647	ESTs	1.5
316983	AI480204	Hs.177131	ESTs	1.5
317604	AI650625	Hs.300756	ESTs	1.6
317951	AW206520	Hs.129621	ESTs	1.5
319400	W26902	Hs.154065	ESTs	1.7
320757	H22654	Hs.6382	EST cluster (not in UniGene)	1.5
321594	AA021402	Hs.11067	ESTs	1.7
322102	H45589		EST cluster (not in UniGene)	1.5
322814	AI824495	Hs.211038	ESTs	2.2

322929	AI365585	Hs.146246	ESTs	2.3
323831	AA335715	Hs.200299	ESTs	1.7
324044	AL045752	Hs.22350	ESTs	1.6
324675	AW014734	Hs.157969	ESTs	2.2
325272			CH.11_hs gi|5886902	1.5
325558			CH.12_hs gi|6056302	1.6
325658			CH.14_hs gi|6056305	1.6
326120			CH.17_hs gi|5887194	1.5
326139			CH.17_hs gi|5887203	1.5
326855			CH.20_hs gi|6552460	1.5
327438			CH.02_hs gi|6004454	1.6
329733			CH.14_p2 gi|6065783	1.6
330931	F01443	Hs.284256	ESTs	4.6
331591	N71677	Hs.42146	ESTs	1.9
332159	AA821393	Hs.112984	EST	1.5
332364	W94688	Hs.103253	pert2pin	2.1
332502	H21819	Hs.14896	Homo sapiens clone 24590 mRNA sequenc	1.5
334175			CH22_FGENES.349_10	1.5
334347			CH22_FGENES.375_31	1.8
334737			CH22_FGENES.424_12	1.8
335352			CH22_FGENES.539_5	1.5
335639			CH22_FGENES.584_19	1.6
336244			CH22_FGENES.746_2	1.5
336336			CH22_FGENES.814_8	1.7
336865			CH22_FGENES.305-1	1.6
337494			CH22_FGENES.799-12	1.8
337764			CH22_EM:AC000097.GENSCAN.119-1	1.8
337983			CH22_EM:AC005500.GENSCAN.110-1	2
338192			CH22_EM:AC005500.GENSCAN.228-1	1.5
339366			CH22_BA354I12.GENSCAN.34-2	1.5

TABLE 15A

Table 15A shows the accession numbers for those pkeys lacking unigeneID's for Table 15. For each probeset, we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT number	Accession
126300	250375_2	D81972 BE003132
112538	504579_1	AA908813 R70255
123505	genbank_AA600135	AA600135
104672	6735_7	AA349098 AI368018 F21390 F17759 R48772 AI421485 AI300352 H43971 AI378525 F33652 R47898 AI264177 F22289 N28263 AI276281 R48205 AI245302 AI190036 AI281050 AW242903 H42892 AA910870 AW473816 H25721 AW451438 F19647 F22375 H45809 F33447 AA774528 AA007629 H42537 C01077 F32388
322102	46708_1	H45589 H19807 AF075038 H19808 H42437
336865	CH22_4590FG_305_1_	
338192	CH22_6755FG__LINK_EM:AC00	
329733	c14_p2	
326120	c17_hs	
326139	c17_hs	
326855	c20_hs	
335352	CH22_2699FG_539_5_LINK_EM	
335839	CH22_2999FG_684_19_LINK_E	
307206	AI192534	
307377	AI222691	
337494	CH22_5727FG_799_12_	
337764	CH22_6115FG__LINK_EM:AC00	
337983	CH22_6438FG__LINK_EM:AC00	
339366	CH22_8336FG__LINK_BA354I1	
325272	c11_hs	
325558	c12_hs	
325656	c14_hs	
334175	CH22_1455FG_349_10_LINK_E	
304182	H91086	
334347	CH22_1640FG_375_31_LINK_E	
327438	c_2_hs	
304822	AA518384	
334737	CH22_2049FG_424_12_LINK_E	
304682	AA550994	
336244	CH22_3642FG_746_2_LINK_DA	
306193	AA923457	
336336	CH22_3745FG_814_8_LINK_BA	

TABLE 15B

Table 15B shows the genomic positioning for those pkeys lacking unigene ID's and accession numbers in Table 15. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
334347	Dunham, I. et.al.	Plus	13663814-13663926
334737	Dunham, I. et.al.	Plus	15998517-15998685
335639	Dunham, I. et.al.	Plus	25173591-25173696
337494	Dunham, I. et.al.	Plus	33339024-33339148
334175	Dunham, I. et.al.	Minus	11668659-11668597
335352	Dunham, I. et.al.	Minus	22681512-22681384
336244	Dunham, I. et.al.	Minus	31402729-31402583
336336	Dunham, I. et.al.	Minus	33797209-33797076
336865	Dunham, I. et.al.	Minus	8622405-8622289
337764	Dunham, I. et.al.	Minus	4035640-4035446
337983	Dunham, I. et.al.	Minus	7275495-7275271
338192	Dunham, I. et.al.	Minus	13248453-13248277
339366	Dunham, I. et.al.	Minus	33647431-33647293
325272	5866902	Minus	13247-13312
325558	6056302	Plus	70930-71030
325656	6056305	Minus	78190-78707
329733	6065783	Plus	163237-163450
326120	5867194	Plus	36116-36276
326139	5867203	Minus	218901-218960
326855	6552460	Minus	111390-111463
327438	6004454	Minus	199569-199692

TABLE 16: Table 4 from BRCA 001-5 US

Table 16, a subset of table 15, depicts a preferred group of genes highly downregulated in breast cancer cells.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of normal breast tissue to tumor

Pkey	ExAccn	UniGene ID	Unigene Title	R1
100502	TIGR:HT1496	Hs.169228	Adrenal-Specific Protein Pg2	2.3
101367	M12963	Hs.4	alcohol dehydrogenase 1 (class I); alpha	2.9
102857	X00129	Hs.76461	retinol-binding protein 4; interstitial	3
104672	AA007629		glycerol-3-phosphate dehydrogenase 1	2.4
107099	AA609645	Hs.211568	eukaryotic translation initiation factor 4 gam	2.7
108504	AA099820	Hs.49696	ESTs	2.4
115949	AA443800	Hs.43125	ESTs	2
115965	AA446661	Hs.173233	ESTs	2.2
119175	R71792	Hs.301002	ESTs; Weakly similar to cell death activator	2.8
119798	W73386	Hs.249129	ESTs	3
122127	AA434447	Hs.106771	ESTs	2.5
122348	AA443696	Hs.293410	ESTs	2.1
129265	T62068	Hs.11006	ESTs	2.1
131267	AA211776	Hs.2504	myomesin 1 (skelemin) (185kD)	3.8
131282	M12272	Hs.4	alcohol dehydrogenase 3 (class I); gamma	2.2
131810	D49487	Hs.194236	leptin (murine obesity homolog)	2.5
133120	X64559	Hs.65424	tetranectin (plasminogen-binding protein)	2
133501	S95936	Hs.284178	transferrin	2.3
134111	N79674	Hs.8022	TU3A protein	4.6
301396	AA923549	Hs.224121	ESTs	2.1
311794	AW238092	Hs.254759	ESTs	2.1
312575	H25237	Hs.306814	ESTs	2.3
313283	W32480	Hs.157099	ESTs	2.2
322814	AI824495	Hs.211038	ESTs	2.2
322929	AI365585	Hs.146246	ESTs	2.3
324675	AW014734	Hs.157969	ESTs	2.2
330931	F01443	Hs.284256	ESTs	4.8
332364	W94688	Hs.103253	perilipin	2.1
337983			CH22_EM:AC005500.GENSCAN.110-1	2

TABLE 16A

Table 16A shows the accession numbers for those pkeys lacking unigeneID's for Table 16. For each probeset, we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT number	Accession
104672	6735_7	AA349096 AI368018 F21390 F17759 R48772 AI421485 AI300352 H43971 AI378525 F33652 R47698 AI264177 F22289 N28283 AI276281 R48205 AI245302 AI190036 AI281050 AW242903 H42892 AA910870 AW473816 H25721 AW451438 F19647 F22375 H45809 F33447 AA774528 AA007629 H42537 C01077 F32386

TABLE 17: Table 1 from BRCA 014 P

Table 17 shows accession numbers representing 759 sequences of breast cancer genes or fragments thereof encoding breast cancer modulating proteins. For each overexpressed gene identified, a ratio of the relative amount of expression in breast tumors versus normal breast tissue.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of tumor to normal breast tissue

Pkey	ExAccn	UnigeneID	Unigene Title	R1
100227	AV654694	Hs.82316	interferon-induced, hepatitis C-associat	3
100405	AW291587	Hs.82733	nidogen 2	3.2
100406	AI962060	Hs.116397	AE-binding protein 1	3.6
100420	D86983	Hs.118893	Melanoma associated gene	3.2
100911	X83300	Hs.289103	SMA4	5.2
100960	J00124	Hs.117729	keratin 14 (epidermolysis bullosa simple	4.3
101011	BE387036	Hs.1211	acid phosphatase 5, tartrate resistant	3
101183	AA442324	Hs.795	H2A histone family, member O	3.2
101194	L20971	Hs.188	phosphodiesterase 4B, cAMP-specific (dun	3
101329	U66042	Hs.82171	Homo sapiens clone 191B7 placenta expres	4.1
101378	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	5.3
101474	R07566	Hs.73817	small inducible cytokine A3 (homologous	3.9
101491	M25809	Hs.64173	ATPase, H+ transporting, lysosomal (vacu	4.5
101530	M29874	Hs.1360	cytochrome P450, subfamily IIB (phenobar	9
101602	AA353776	Hs.901	CD48 antigen (B-cell membrane protein)	3.4
101663	NM_003528	Hs.2178	H2B histone family, member Q	5.6
101758	BE019494	Hs.79217	pyrroline-5-carboxylate reductase 1	3.5
101767	M81057	Hs.180884	carboxypeptidase B1 (tissue)	12
101817	M89907	Hs.152292	SWI/SNF related, matrix associated, acti	3.2
101851	BE260964	Hs.82045	midkine (neurite growth-promoting factor	4.1
101878	M97815	Hs.183650	cellular retinoic acid-binding protein 2	6.5
102209	NM_002038	Hs.265827	interferon, alpha-inducible protein (clo	3
102214	U23752	Hs.32964	SRY (sex determining region Y)-box 11	3
102297	NM_001504	Hs.198252	G protein-coupled receptor 9	3.7
102299	NM_005824	Hs.155545	37 kDa leucine-rich repeat (LRR) protein	3.7
102301	NM_005651	Hs.183671	tryptophan 2,3-dioxygenase	5.2
102305	AL043202	Hs.90073	chromosome segregation 1 (yeast homolog)	3.5
102369	U39840	Hs.299867	hepatocyte nuclear factor 3, alpha	3.9
102591	U62325	Hs.324125	amyloid beta (A4) precursor protein-bind	4
102721	H16648	Hs.118668	hypothetical protein PP591	3.5
102739	AA363025	Hs.155572	Human clone 23801 mRNA sequence	3.2
102791	AF080229		gb:Human endogenous retrovirus K clone 1	3
102804	NM_002318	Hs.83354	lysyl oxidase-like 2	3.2
102903	M73779	Hs.250505	retinoic acid receptor, alpha	3.3
103010	X52509	Hs.161640	tyrosine aminotransferase	12.4
103042	T81656	Hs.252259	ribosomal protein S3	4.5
103117	X63578	Hs.295449	parvalbumin	3
103207	X72790		gb:Human endogenous retrovirus mRNA for	5.9
103282	BE390551	Hs.77628	steroidogenic acute regulatory protein r	3.9
103284	AI751601	Hs.8375	TNF receptor-associated factor 4	3.3
103329	X85134	Hs.72984	retinoblastoma-binding protein 5	3.1
103364	X90872	Hs.279929	gp25L2 protein	3
103385	NM_007069	Hs.37189	similar to rat HREV107	3.4
103458	AA496425	Hs.9629	papillary renal cell carcinoma (transloc	3.2

103498	Y09306	Hs.30148	homeodomain-interacting protein kinase 3	3.4
103558	BE616547	Hs.2785	keratin 17	3.7
103563	L02911	Hs.150402	Activin A receptor, type I (ACVR1) (ALK	3.2
103612	BE336654	Hs.70937	H3 histone family, member A	4.5
103825	AI571835	Hs.55468	ESTs	4
104073	AW779318	Hs.88417	ESTs	3.8
104103	AW021102	Hs.21509	ESTs	4.3
104115	AF183810	Hs.26102	opposite strand to trichorhinophalangeal	7.6
104168	AA461618	Hs.31704	ESTs, Weakly similar to KIAA0227 [H.sapi	3.6
104173	AA084273	Hs.76561	ESTs, Weakly similar to S47072 finger pr	4
104181	AF173296	Hs.283740	DC6 protein	3
104189	AB040927	Hs.301804	KIAA1494 protein	3.2
104269	AI559444	Hs.293960	ESTs	4.3
104307	AI929700	Hs.111680	endosulfine alpha	3.1
104518	H20816	Hs.112423	Homo sapiens mRNA; cDNA DKFZp58811420 (f	3.2
104556	AV650851	Hs.96900	hypothetical protein; KIAA1830 protein	4.4
104658	AA360954	Hs.27268	Homo sapiens cDNA: FLJ21933 fis, clone H	3.2
104748	AA015879	Hs.33536	ESTs	3.2
104755	T49951	Hs.9029	DKFZP434G032 protein	4.5
104825	AA035613	Hs.141883	ESTs	6.9
104830	AW294092	Hs.21594	hypothetical protein MGC15754	11.1
104865	T79340	Hs.22575	B-cell CLL/lymphoma 6, member B (zinc fi	3.5
104906	BE298684	Hs.26802	protein kinase domains containing protei	6.5
104961	H78517	Hs.33905	ESTs	3.6
105038	AW503733	Hs.9414	KIAA1468 protein	4.5
105088	H58589	Hs.35156	Homo sapiens cDNA FLJ11027 fis, clone PL	3.8
105092	AA148982	Hs.29068	ESTs	3
105093	AL137566	Hs.32405	Homo sapiens mRNA; cDNA DKFZp586G0321 (f	4.8
105304	AW134924	Hs.190325	ESTs	8.2
105397	AA814807	Hs.7395	hypothetical protein FLJ23182	3.1
105409	AW505076	Hs.301855	DiGeorge syndrome critical region gene 8	4.2
105431	AA252033	Hs.242413	hypothetical protein DKFZp434K1421	4.4
105552	AA256750	Hs.28802	centaurin-alpha 2 protein	3.2
105598	AA279439	Hs.279763	hypothetical protein FLJ10504	3.5
105650	W16741	Hs.25635	HSPC003 protein	3.7
105688	AI299139	Hs.17517	ESTs	5.5
105808	AI133161	Hs.286131	CGI-101 protein	3.5
105809	AW973653	Hs.20104	hypothetical protein FLJ00052	3.3
105909	AA195191	Hs.5111	hypothetical protein FLJ20729	3.2
105965	AA131657	Hs.23830	ESTs	3.3
106135	AL117474	Hs.41181	Homo sapiens mRNA; cDNA DKFZp727C191 (fr	3.2
106184	W28948	Hs.10762	ESTs	3.3
106293	N39842	Hs.301444	KIAA1673	4.1
106400	BE397649	Hs.94109	Homo sapiens cDNA FLJ13634 fis, clone PL	3.1
106474	BE383668	Hs.42484	hypothetical protein FLJ10618	3.2
106484	AA351978	Hs.4943	hepatocellular carcinoma associated prot	7.6
106533	AL134708	Hs.145998	ESTs	3
106614	AA648459	Hs.335951	hypothetical protein AF301222	3.8
106636	AW958037	Hs.286	ribosomal protein L4	3.3
106681	AW499914	Hs.7579	hypothetical protein FLJ10402	3
106743	BE513328	Hs.21938	hypothetical protein FLJ12492	4.2
106844	AA485055	Hs.158213	sperm associated antigen 6	3.4
106864	AI311928		gb:qo89h04.x1 NCI_CGAP_Kid5 Homo sapiens	4.4
106865	AW192535	Hs.19479	ESTs	3.6
106871	AW472981	Hs.321130	hypothetical protein MGC2771	4.1
106942	AA995351	Hs.31314	retinoblastoma-binding protein 7	3.6
106968	AF216751	Hs.26813	CDA14	5.3
107105	AW963419	Hs.155223	stanniocalcin 2	3.4
107158	N32849	Hs.31844	hypothetical protein FLJ12586	3.1
107248	AW263124	Hs.315111	nuclear receptor co-repressor/HDAC3 comp	5.9
107265	BE379594	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN A	3.9
107630	AW961578	Hs.60178	ESTs	4.8
107710	AI955040	Hs.265398	ESTs, Weakly similar to transformation-r	3
107890	AA025386	Hs.61311	ESTs, Weakly similar to S10590 cysteine	3.1
107985	T40064	Hs.71968	Homo sapiens mRNA; cDNA DKFZp564F053 (fr	4.8
108000	AI263307	Hs.239884	H2B histone family, member L	3.3
108217	AA058686	Hs.62588	ESTs	3.8

108435	T82427	Hs.194101	Homo sapiens cDNA: FLJ20869 fis, clone A	3
108591	AB033073	Hs.43857	similar to glucosamine-6-sulfatases	3.3
108733	AA121022		gb:zn84f10.r1 Stratagene lung carcinoma	3.9
108771	AF068290	Hs.79741	hypothetical protein FLJ10116	6.1
108819	AA011449	Hs.271627	ESTs	3.6
108912	AA136674	Hs.118681	EST	3.9
109086	AF186114	Hs.270737	tumor necrosis factor (ligand) superfami	3.7
109124	AK000684	Hs.183887	hypothetical protein FLJ22104	3.1
109132	AI970536	Hs.16603	hypothetical protein FLJ13163	3.7
109163	N23235	Hs.30567	ESTs, Weakly similar to B34087 hypotheti	4.5
109277	AA196443	Hs.86043	Homo sapiens cDNA FLJ13558 fis, clone PL	3.7
109410	AW504732	Hs.21275	hypothetical protein FLJ11011	4.6
109454	AA232255	Hs.295232	ESTs, Moderately similar to A46010 X-lin	6.4
109514	AA234087	Hs.282346	ESTs, Weakly similar to 872482 hypotheti	4.8
109581	R45584	Hs.23025	ESTs, Weakly similar to ALU5_HUMAN ALU S	3.3
109632	AA325138	Hs.235873	hypothetical protein FLJ22672	3
109644	AW973964	Hs.291531	ESTs, Highly similar to 1203217A dehydro	3
109700	F09609		gb:HSC33H092 normalized infant brain cDN	3.2
109768	F06838	Hs.14763	ESTs	3.2
109807	R43646	Hs.12422	ESTs	3.8
109842	AW818436	Hs.23590	solute carrier family 16 (monocarboxylic	3.3
109895	AK001680	Hs.30488	DKFZP434F091 protein	3.6
110024	AW973152	Hs.31050	ESTs	4.2
110561	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	5.1
110675	H89355	Hs.249159	adrenergic, alpha-2A-, receptor	5.3
110707	AI239832	Hs.15617	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.7
110915	BE092285	Hs.29724	hypothetical protein FLJ13187	3.7
111139	N54683	Hs.290943	ESTs	4
111155	N56563	Hs.191358	ESTs	3.1
111199	AI767435	Hs.29822	ESTs	4.5
111336	AI457338	Hs.29894	ESTs	5.4
111510	R07856	Hs.16355	ESTs	3.2
111532	R08440		gb:yf19f09.s1 Soares fetal liver spleen	3.1
111689	AA602004	Hs.23260	ESTs	3.2
111823	R35252	Hs.24944	ESTs, Weakly similar to 2109260A B cell	3.3
111876	R38239	Hs.293246	ESTs, Weakly similar to putative p150 [H	3.1
111892	AA421081	Hs.12388	ESTs	3.4
111893	AF070526	Hs.13429	Homo sapiens clone 24787 mRNA sequence	3.3
112125	AW379029	Hs.118338	ESTs, Weakly similar to unnamed protein	4.4
112170	BE246743	Hs.288529	hypothetical protein FLJ22835	7.3
112267	AB033064	Hs.334806	KIAA1238 protein	3.2
112300	H24334	Hs.26125	ESTs	4.4
112303	R54797		gb:yg87b07.s1 Soares infant brain 1NIB H	3.4
112478	R56067	Hs.28664	ESTs	6.2
112561	AI791493	Hs.129873	ESTs, Weakly similar to A36036 cytochrom	5.5
112631	R82040		gb:yj06b06.s1 Soares placenta Nb2HP Homo	3.9
112637	R82331	Hs.164599	ESTs	5.4
112657	AW844878	Hs.19769	hypothetical protein MGC4174	3.2
112678	AI418466	Hs.33665	ESTs	4.7
112917	AA082485	Hs.125031	choline/ethanolaminephosphotransferase	3.7
113070	AB032977	Hs.6298	KIAA1151 protein	3.1
113095	AA828380	Hs.126733	ESTs	3.4
113117	AW813731	Hs.159153	ESTs, Moderately similar to S65657 alpha	3.4
113187	BE613410	Hs.31575	SEC63, endoplasmic reticulum translocon	3.2
113200	T57773	Hs.10263	ESTs	3.5
113208	BE262470	Hs.241471	RNB6	6.2
113374	T79925	Hs.269165	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.7
113440	U54727	Hs.191445	ESTs	3
113494	T91451	Hs.88538	ESTs	3.4
113518	AW367788	Hs.323954	postmeiotic segregation increased 2-like	3.1
113571	AI702609	Hs.15713	hypothetical protein MGC2776	3.1
113822	NM_004585	Hs.17468	retinoic acid receptor responder (tazaro	3.9
113835	AI912410	Hs.27475	Homo sapiens cDNA FLJ12749 fis, clone NT	3
113938	W81598		gb:zd88g02.s1 Soares_fetal_heart_NbHH19W	4.8
113947	W84768		gb:zh53d03.s1 Soares_fetal_liver_spleen_	3.1
113970	W27249	Hs.8109	hypothetical protein FLJ21080	6.9
114086	AA378778	Hs.288649	hypothetical protein MGC3077	4.3

114148	AW470411	Hs.288433	neurotrimin	4.1
114424	AW780192	Hs.267596	ESTs	3.4
114518	AW163267	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like	3.1
114563	AI979168	Hs.82226	glycoprotein (transmembrane) nmb	4.8
114985	AI733881	Hs.72472	BMP-R1B	10.1
114995	AA769268	Hs.193657	ESTs	3.6
115121	AI634549	Hs.88155	ESTs	3.2
115134	AW968073	Hs.194331	ESTs, Highly similar to A55713 inositol	4.2
115167	AA749209	Hs.43728	hypothetical protein	3
115253	BE149845	Hs.289038	hypothetical protein MGC4126	3.6
115277	AA814100	Hs.86593	ESTs	3.9
115327	N46436	Hs.109221	ESTs	3.4
115354	AA281636	Hs.334627	ESTs	4.8
115657	AA405620	Hs.55158	ESTs, Weakly similar to T29520 hypotheti	3.5
115676	AA953008	Hs.88143	ESTs	9.3
115709	AW293849	Hs.58279	ESTs, Weakly similar to ALU7_HUMAN ALU S	3.4
115729	AA417812	Hs.38775	ESTs	4
115787	AI126772	Hs.40479	ESTs	3.1
115830	AW970529	Hs.88434	hypothetical protein FLJ21816	3.6
115835	AA521410	Hs.41371	ESTs	3.1
115850	NM_014937	Hs.52463	KIAA0968 protein	3
115900	AK001500	Hs.165186	hypothetical protein FLJ13852	3.2
115935	AA354549	Hs.41181	Homo sapiens mRNA; cDNA DKFZp727C191 (fr	3
115948	AL042465	Hs.43445	poly(A)-specific ribonuclease (deadenyla	3.1
116092	AB041035	Hs.93847	NM_016931:Homo sapiens NADPH oxidase 4 (	8.7
116115	AL042355	Hs.70202	WD repeat domain 10	3.6
116184	AW450737	Hs.128791	CGI-09 protein	3.1
116192	AA464976	Hs.62528	ESTs, Moderately similar to A46010 X-lin	3.3
116208	AI219083	Hs.42532	ESTs, Moderately similar to ALU8_HUMAN A	3.2
116246	AF265555	Hs.250648	baculoviral IAP repeat-containing 6	3.6
116443	AW962186	Hs.321264	LBP protein 32	4.1
116470	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	4.1
116726	AK001114	Hs.53913	hypothetical protein FLJ10252	8.6
116845	AA849530		gb:ns44f06.s1 NCI_CGAP_Alv1 Homo sapiens	3.2
117026	H88256	Hs.50456	ESTs, Moderately similar to ZN75_HUMAN Z	3.5
117216	AI569804	Hs.42792	ESTs, Weakly similar to I78885 serine/th	3.1
117296	AL133427	Hs.42506	Homo sapiens mRNA full length insert cDN	3.2
117403	H84455	Hs.40639	ESTs	4.7
117691	AB040959	Hs.93835	DKFZP434N014 protein	3
118229	AW968941	Hs.166254	hypothetical protein DKFZp566I133	3.3
118363	AI183838	Hs.48938	hypothetical protein FLJ21802	4.3
118416	N56028	Hs.49105	FKBP-associated protein	3.1
118470	AW970584	Hs.291033	ESTs	3.4
118502	AL157488	Hs.50150	Homo sapiens mRNA; cDNA DKFZp564B182 (fr	5.2
118695	AK000465	Hs.50081	KIAA1199 protein	3.4
118925	N92293	Hs.206832	ESTs, Moderately similar to ALU8_HUMAN A	3.3
119025	BE003760	Hs.55209	Homo sapiens mRNA; cDNA DKFZp434K0514 (f	19.7
119036	R95872	Hs.117572	chemokine binding protein 2	3.7
119083	R16833	Hs.53106	ESTs, Moderately similar to ALU1_HUMAN A	4.1
119075	M10905	Hs.287820	fibronectin 1	3.2
119620	W47620	Hs.56009	2'-5'-oligoadenylate synthetase 3 (100 k	3.3
119741	AF041853	Hs.43670	kinesin family member 3A	3.1
119747	AI970797	Hs.64859	ESTs	5
119754	AL037824	Hs.194695	ras homolog gene family, member I	3.8
119905	AW449064	Hs.119571	collagen, type III, alpha 1 (Ehlers-Dant	3.1
120084	W94472	Hs.59529	ESTs, Moderately similar to ALU1_HUMAN A	8.4
120241	AA825686	Hs.321176	ESTs, Weakly similar to S85824 reverse t	3.6
120326	AA196300	Hs.21145	hypothetical protein RG083M05.2	3.2
120742	AA225084		gb:nc21d06.r1 NCI_CGAP_Pr1 Homo sapiens	3.6
120870	AA357172	Hs.292581	ESTs, Moderately similar to ALU1_HUMAN A	6.8
120885	AA365515	Hs.301872	hypothetical protein MGC4840	3
120970	AA398118	Hs.97579	ESTs, Weakly similar to A46010 X-linked	3.7
121054	AW976570	Hs.97387	ESTs	5.3
121095	AA320134	Hs.196029	Homo sapiens mRNA for KIAA1657 protein,	4
121103	AA368936	Hs.97697	EST	3.5
121121	AA399371	Hs.189095	similar to SALL1 (sal (Drosophila)-like	6.3
121337	AW885727	Hs.301570	ESTs	4.7

121351	AW206227	Hs.287727	hypothetical protein FLJ23132	5
121611	M31659	Hs.1735	inhibin, beta B (activin AB beta polypep	3.6
121643	AA640987	Hs.193767	ESTs	5.6
121770	NM_015902	Hs.278428	progestin induced protein	3.4
122125	AK000492	Hs.88805	hypothetical protein	4.1
122338	AA443311	Hs.98998	ESTs	3
122417	AA446965	Hs.112092	ESTs	4.7
122513	AI767879	Hs.99214	ESTs	3.8
122544	AW973253	Hs.292689	ESTs	3
122655	AA323296	Hs.97837	Homo sapiens mRNA; cDNA DKFZp547J047 (fr	5.6
122805	AA526911	Hs.82772	collagen, type XI, alpha 1	3.2
122851	AW205931	Hs.99598	hypothetical protein MGC5338	6.6
123105	AA487809	Hs.166011	catenin (cadherin-associated protein), d	3
123111	AA228776	Hs.191721	ESTs	6.9
123249	AA371307	Hs.125056	ESTs	3.6
123273	AA491253	Hs.173611	Empirically selected from AFFX single pr	7
123385	BE149685	Hs.17767	KIAA1554 protein	3.1
123419	T66087	Hs.112482	Homo sapiens unknown mRNA sequence	3.4
123485	AI308876	Hs.103849	hypothetical protein DKFZp761D112	3.1
123645	AI678944	Hs.188691	Homo sapiens cDNA FLJ12033 fis, clone HE	3.8
123819	AA580082	Hs.112264	ESTs	4.7
124012	AA352723	Hs.241471	RNB6	3.8
124243	H69125	Hs.133525	ESTs	4.1
124357	N22401		gb:yw37g07.s1 Morton Fetal Cochlea Homo	4.1
124359	N22508	Hs.139315	Homo sapiens cDNA: FLJ21479 fis, clone C	3.6
124567	AW451645	Hs.151504	Homo sapiens cDNA FLJ11973 fis, clone HE	3.1
124911	N34151	Hs.174195	interferon induced transmembrane protein	3.5
124972	R41396	Hs.101774	hypothetical protein FLJ23045	4.3
125006	BE065136	Hs.145696	splicing factor (CC1.3)	6
125042	T78906	Hs.269432	ESTs, Moderately similar to ALU1_HUMAN A	8.1
125184	W60326	Hs.288684	Homo sapiens cDNA FLJ11750 fis, clone HE	4.7
125243	AW970536	Hs.105413	ESTs	3.1
125286	AF086534	Hs.187561	ESTs, Moderately similar to ALU1_HUMAN A	3.3
125304	AL359573	Hs.124940	GTP-binding protein	3
125330	AW880562	Hs.114574	ESTs	3
125331	AI422996	Hs.161378	ESTs	3.2
125685	AI924630	Hs.4943	hepatocellular carcinoma associated prot	3.2
126257	N99638		gb:za39g11.r1 Soares fetal liver spleen	4
126474	AW975814	Hs.326714	Homo sapiens clone IMAGE:713177, mRNA se	4
126666	AA648886	Hs.151999	ESTs	3.8
126872	AW450979		gb:UI-H-BI3-ela-e-12-0-UI.s1 NCI_CGAP_Su	3
127431	AW771958	Hs.175437	ESTs, Moderately similar to PC4259 ferri	3.6
127980	AA961459	Hs.125644	ESTs	4.1
127997	AW068311	Hs.311054	Homo sapiens mRNA full length insert cDN	3.3
128420	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	4.6
128609	NM_003816	Hs.102456	survival of motor neuron protein interac	3.9
128946	Y13153	Hs.107318	kynurenine 3-monooxygenase (kynurenine 3	3.1
128955	AA775076	Hs.185807	Homo sapiens, Similar to PRO0478 protein	3.9
129092	D56365	Hs.63525	poly(rC)-binding protein 2	3.3
129270	AA357185	Hs.109918	ras homolog gene family, member H	3.1
129301	AF182277	Hs.330780	cytochrome P450, subfamily IIB (phenobar	3.9
129385	AA172106	Hs.110950	Rag C protein	6.2
129619	AA209534	Hs.284243	tetraspan NET-6 protein	3.4
129629	AK000398	Hs.11747	hypothetical protein FLJ20391	3
129725	X56411	Hs.1219	alcohol dehydrogenase 4 (class II), pi p	3.2
130069	AI754813	Hs.146428	collagen, type V, alpha 1	5.4
130092	X03363	Hs.323910	v-erb-b2 avian erythroblastic leukemia v	4.4
130288	AI347487	Hs.132781	class I cytokine receptor	4.6
130382	NM_003450	Hs.155204	zinc finger protein 174	5.6
130622	AI582291	Hs.16846	ESTs, Weakly similar to O4HUD1 debrisoqu	3
130703	R77776	Hs.18103	ESTs	3.8
130881	AA609875	Hs.25933	ESTs	4.2
130954	AB014544	Hs.21572	KIAA0644 gene product	4.7
131095	AI399653	Hs.22917	ESTs	4.3
131153	H09048	Hs.23808	ESTs	3.8
131253	R71802	Hs.24853	ESTs	3.5
131372	AW293399	Hs.144904	nuclear receptor co-repressor 1	3.6

131507	AI826268	Hs.27769	ESTs, Weakly similar to MCAT_HUMAN MITOC	3.2
131587	AI695549	Hs.183868	glucuronidase, beta	3.1
131739	AF017986	Hs.31386	secreted frizzled-related protein 2	3.2
131785	BE501849	Hs.32317	high-mobility group 20B	3.2
131970	D86960	Hs.3610	KIAA0205 gene product	3.6
131986	NM_002314	Hs.36566	LIM domain kinase 1	3.2
132093	AA400091	Hs.39421	ESTs	3.2
132122	AA426202	Hs.40403	Cbp/p300-interacting transactivator, wit	3
132159	D76435	Hs.41154	Zic family member 1 (odd-paired Drosophi	3.2
132333	AA192669	Hs.45032	ESTs	3.5
132406	AL133731	Hs.4774	Homo sapiens mRNA; cDNA DKFZp761C1712 (f	9.2
132482	AV660345	Hs.238126	CGI-49 protein	8.2
132543	BE568452	Hs.5101	protein regulator of cytokinesis 1	3.4
132624	AA326108	Hs.33829	bHLH protein DEC2	3.2
132700	AA319233	Hs.5521	ESTs	4.8
132725	NM_006276	Hs.184167	splicing factor, arginine/serine-rich 7	3.6
132769	W73311	Hs.169407	SAC2 (suppressor of actin mutations 2, y	3.2
132847	T48195	Hs.58189	eukaryotic translation initiation factor	3.5
132857	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to	4.4
132936	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear transl	4.8
133130	AI126606	Hs.6557	zinc finger protein 161	3.3
133142	AW952412	Hs.65874	ESTs, Weakly similar to A40348 Elav/Sex-	3.5
133167	AW162840	Hs.6641	kinesin family member 5C	4.5
133225	AW500291	Hs.6823	hypothetical protein FLJ10430	3.3
133274	AA085191	Hs.6949	hypothetical protein MGC11275	3
133275	Z93241	Hs.239934	CGI-96 protein	4.5
133287	AW797437	Hs.69771	B-factor, properdin	4.1
133376	BE618768	Hs.7232	acetyl-Coenzyme A carboxylase alpha	5.1
133462	AW675064	Hs.73875	fumarylacetoacetate hydrolase (fumarylac	3
133740	AW162919	Hs.170160	RAB2, member RAS oncogene family-like	3.4
133831	BE274552	Hs.76578	protein inhibitor of activated STAT3	3.9
133976	AI908165	Hs.169946	GATA-binding protein 3 (T-cell receptor	6.2
134666	BE391929	Hs.8752	transmembrane protein 4	3.1
134710	AI433797	Hs.8889	serine hydroxymethyltransferase 1 (soklb	3
134731	D89377	Hs.89404	msh (Drosophila) homeo box homolog 2	5.8
134776	J05582	Hs.89603	mucin 1, transmembrane	4
135230	AF064804	Hs.96757	suppressor of Ty (S.cerevisiae) 3 homolo	3.2
135303	R61253	Hs.98265	KIAA1877 protein	3.3
135400	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	4.8
135411	L10333	Hs.99947	reticulon 1	3.8
300089	AI199738	Hs.208275	ESTs, Weakly similar to ALUA_HUMAN !!!!	3.8
300233	AW614220	Hs.189402	ESTs	4.2
300254	AW183618	Hs.55610	solute carrier family 30 (zinc transport	9.9
300256	AW591433	Hs.298241	Transmembrane protease, serine 3	4.9
300378	Z45270	Hs.235873	hypothetical protein FLJ22672	3.4
300973	AA572949	Hs.207568	ESTs	3.5
301111	R10799	Hs.191990	ESTs	3.8
301341	AA887801	Hs.208229	G protein-coupled receptor	13.9
301548	AI091631	Hs.203845	two pore potassium channel KT3.3	4.4
301884	AA312082	Hs.105445	GDNF family receptor alpha 1	5.7
301936	U79745	Hs.114924	solute carrier family 16 (monocarboxylic	8.8
301976	T97905		gb:ye54c10.r1 Soares fetal liver spleen	3.9
302001	AB020711	Hs.278346	KIAA0904 protein	7.7
302067	BE542706	Hs.222399	CEGP1 protein	7.3
302094	AW749321	Hs.8788	ESTs	3.3
302099	AL049670	Hs.137576	ribosomal protein L34 pseudogene 1	4.2
302145	NM_003613	Hs.151407	cartilage intermediate layer protein, nu	7.9
302235	AL049987	Hs.166361	Homo sapiens mRNA; cDNA DKFZp564F112 (fr	5.6
302276	AW057736	Hs.323910	HER2 receptor tyrosine kinase (c-erb-b2,	5.4
302290	AA179949	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564N0763 (f	34.1
302372	AL117406	Hs.200102	ATP-binding cassette transporter MRP8	6.7
302378	AL109712	Hs.298506	Homo sapiens mRNA full length insert cDN	4
302384	AI678059	Hs.202676	synaptonemal complex protein 2	4.3
302385	AJ224172	Hs.204098	lipophilin B (uteroglobin family member)	13.8
302680	AW192334	Hs.38218	ESTs	9.6
302830	AI038997	Hs.132921	ESTs	5
302857	AF262265	Hs.44836	inner centromere protein antigens (135kD	3.4

302892	AW176909	Hs.42346	calcineurin-binding protein calsarcin-1	3.4
302970	W05608	Hs.312679	ESTs, Weakly similar to A49019 dynein he	5.1
303271	AA652587	Hs.96151	Human DNA sequence from clone RP5-1103G7	3.7
303289	AL121460	Hs.272673	hypothetical protein FLJ20508	4.1
303357	AW006352	Hs.159643	ESTs, Weakly similar to T32554 hypotheti	4.2
303540	AA355607	Hs.309490	ESTs, Weakly similar to putative WHSC1 p	4.3
303563	AA367699	Hs.10082	potassium intermediate/small conductance	3.3
303642	AW299459		gb:xs50d08.x1 NCI_CGAP_Kid11 Homo sapien	4.2
303780	AI424014	Hs.18995	KIAA1304 protein	3.6
303797	AW629759		gb:hh70e05.y1 NCI_CGAP_GU1 Homo sapiens	4.9
303852	R53434	Hs.90207	hypothetical protein MGC11138	3.7
304328	AA149951	Hs.62112	zinc finger protein 207	3
304782	AA582081		gb:nn32h08.s1 NCI_CGAP_Gas1 Homo sapiens	4.1
305913	AA876109		gb:nx24h01.s1 NCI_CGAP_GC3 Homo sapiens	3
305917	AA876469		gb:oe48b04.s1 NCI_CGAP_Pr25 Homo sapiens	3.1
307010	AI140014		gb:qa68f09.x1 Soares_fetal_heart_NbHH19W	3.5
307041	AI144243		gb:qb85b12.x1 Soares_fetal_heart_NbHH19W	3.9
308106	AI476803		gb:tj77e12.x1 Soares_NSF_F8_9W_OT_PA_P_S	4.3
308307	AI581398	Hs.172926	collagen, type I, alpha 1	4.6
308615	AK000142	Hs.101774	hypothetical protein FLJ23045	4.4
309177	AI951118	Hs.326736	Homo sapiens breast cancer antigen NY-BR	17.3
309328	AW024348	Hs.233191	EST, Weakly similar to A27217 glucose tr	3.2
309574	AW168083		gb:xg59g04.x1 NCI_CGAP_Ut4 Homo sapiens	3.1
309583	AW170035	Hs.326736	Homo sapiens breast cancer antigen NY-BR	57.6
310064	AI199712	Hs.148486	ESTs, Weakly similar to 1917210A Pro/Arg	4.6
310098	AI685841	Hs.161354	ESTs	3.6
310438	AW022192	Hs.200197	ESTs	4.6
310683	AI939456	Hs.160870	ESTs	3.2
310727	AK000703	Hs.323822	Homo sapiens mRNA for KIAA1551 protein,	3.6
310781	AI380797	Hs.158992	ESTs	10.2
310895	AI955121	Hs.165724	N-acetylgalactosamine-4-O-sulfotransfera	3.4
310955	AI476732	Hs.263912	ESTs	10.9
311117	AI871439	Hs.196029	Homo sapiens mRNA for KIAA1657 protein,	3.1
311166	AI821005	Hs.118599	ESTs	10.6
311237	AA641098	Hs.208809	ESTs, Moderately similar to ALU1_HUMAN A	4.3
311465	AI758860	Hs.206132	ESTs	4.4
311587	AI828254	Hs.271019	ESTs, Weakly similar to A47582 B-cell gr	5.1
311598	AW023595	Hs.232048	ESTs	5.8
311774	AA700870	Hs.14304	ESTs	3.3
311785	AI056769	Hs.133512	ESTs	3.9
311872	R12375	Hs.194600	ESTs	3.3
311889	AA767342	Hs.122483	ESTs, Weakly similar to PSF_HUMAN PTB-AS	3
311913	AI358522	Hs.270188	ESTs	3
311923	T60843	Hs.189679	ESTs	5.6
311935	AA216387		gb:nc16b02.s1 NCI_CGAP_Pr1 Homo sapiens	5.2
312019	AA373630	Hs.188750	ESTs	3
312021	AA759263	Hs.14041	ESTs	3.4
312067	T78968	Hs.14411	ESTs	3.5
312090	T60177	Hs.118064	similar to rat nuclear ubiquitous casein	3.8
312147	AI633744	Hs.195648	ESTs, Weakly similar to I38022 hypotheti	4.4
312153	BE261944	Hs.118825	hexokinase 1	5.2
312168	T92251	Hs.198882	ESTs	3.3
312182	T94344	Hs.326263	ESTs	3.3
312187	AA700439	Hs.188490	ESTs	3.4
312199	AW438602	Hs.191179	ESTs	3.9
312219	H73505	Hs.117874	ESTs	4
312226	AA315703	Hs.199993	ESTs, Weakly similar to ALUB_HUMAN !!!!	4.9
312299	AA972712	Hs.269737	ESTs	5.7
312544	AA516420	Hs.183526	ESTs, Weakly similar to I38022 hypotheti	6.3
312638	AW439195	Hs.256880	ESTs, Weakly similar to S65657 alpha-1C-	4.9
312826	AW291545	Hs.185018	ESTs	4.9
312837	AW292286	Hs.255058	ESTs	4.4
312980	AA497043	Hs.115685	ESTs	3.1
313070	AI422023	Hs.161338	ESTs	4.3
313079	N76497	Hs.1787	proteolipid protein 1 (Pelizaeus-Merzbac	3.3
313089	AF026944	Hs.293797	ESTs	5.8
313098	AW073310	Hs.183533	Homo sapiens cDNA FLJ14142 fis, clone MA	4.5

313126	AA746503	Hs.283313	ESTs	10
313166	AI801098	Hs.151500	ESTs	3.5
313197	AW979008	Hs.222487	ESTs	3.3
313280	AW960454	Hs.222830	ESTs	4.7
313325	AI420611	Hs.127832	ESTs	3.4
313328	AW449211	Hs.105445	GDNF family receptor alpha 1	12.4
313352	AW150945	Hs.144758	ESTs	4.1
313385	AI032087	Hs.269819	ESTs	3
313393	AI674685	Hs.200141	ESTs	5.2
313417	AA741151	Hs.137323	ESTs	3.5
313434	W92070		gb:zh48g05.r1 Soares_fetal_liver_spleen_	3.7
313569	AI273419	Hs.135148	hypothetical protein FLJ13984	3
313591	AA046309		gb:zf12f01.s1 Soares_fetal_heart_NbHH19W	5.6
313615	AI540978	Hs.301997	hypothetical protein FLJ13033	3.2
313915	C18863	Hs.163443	Homo sapiens cDNA FLJ11576 fis, clone HE	26.3
313975	AW175896	Hs.65114	keratin 16	3
313979	AI535895	Hs.221024	ESTs	4.9
313997	AV657317	Hs.288649	hypothetical protein MGC3077	3.9
314043	AA827082	Hs.291872	ESTs	3.1
314078	AW129357	Hs.329700	ESTs	8.3
314097	AA648744	Hs.269493	ESTs	6.6
314121	AI732083	Hs.187619	ESTs	6.2
314129	AA228366	Hs.115122	ESTs	4
314138	AA740616		gb:ny97f11.s1 NCI_CGAP_GCB1 Homo sapiens	5.9
314236	AA743396	Hs.189023	ESTs	3.1
314244	AL038450	Hs.103238	ESTs	4
314305	AI280112	Hs.125232	Homo sapiens cDNA FLJ13266 fis, clone OV	8
314306	AI697901	Hs.192425	ESTs	3.7
314322	AA907153	Hs.190060	ESTs	3.3
314394	AW961597	Hs.130818	ESTs, Moderately similar to I38022 hypot	4.2
314401	AI660412	Hs.234557	ESTs	3.3
314465	AA602917	Hs.156974	ESTs	4.7
314506	AA833655	Hs.206868	Homo sapiens cDNA FLJ14056 fis, clone HE	8.5
314510	AI204418	Hs.190080	ESTs	4
314546	AW007211	Hs.16131	hypothetical protein FLJ12876	3.4
314547	AA399272	Hs.144341	ESTs	6.7
314558	AI873274	Hs.190721	ESTs	27.4
314627	AA425310	Hs.155768	ESTs, Weakly similar to A47582 B-cell gr	4.4
314648	AW979268		gb:EST391378 MAGE resequences, MAGP Homo	4.6
314691	AW207208	Hs.136319	ESTs	20.7
314729	AA457367	Hs.191638	ESTs	3.6
314754	AW026761	Hs.134374	ESTs	3.8
314814	BE350122	Hs.157367	ESTs, Weakly similar to I78885 serine/th	4.9
314864	AW971198	Hs.294088	ESTs	4.3
314881	AI095087	Hs.152299	ESTs, Moderately similar to S65657 alpha	3.7
314882	AA628032	Hs.189076	ESTs	3.1
314981	AW972359	Hs.293334	ESTs	3
315006	AI538613	Hs.298241	Transmembrane protease, serine 3	10.9
315021	AA533447	Hs.312989	ESTs	5.3
315051	AW292425	Hs.163484	ESTs	12.9
315060	AA551104	Hs.189048	ESTs, Moderately similar to ALUC_HUMAN I	5.8
315073	AW452948	Hs.257631	ESTs	4.2
315080	AA744550	Hs.136345	ESTs	3.7
315175	AI025842	Hs.152530	ESTs	6
315183	AW136134	Hs.220277	ESTs	3.9
315193	AI241331	Hs.131765	ESTs, Moderately similar to I38937 DNA/R	4.4
315196	AI367347	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	8.2
315198	AI741508	Hs.165900	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.8
315240	R38772	Hs.172619	myelin transcription factor 1-like	3.4
315263	AW510994	Hs.220740	ESTs	3.4
315282	AI222165	Hs.144923	ESTs	4.9
315295	AA876905	Hs.125288	ESTs	4
315368	AB037745	Hs.104696	KIAA1324 protein	4.7
315397	AA218940	Hs.137516	fidgetin-like 1	3.1
315489	AI376817	Hs.191647	ESTs	3.1
315498	AA628539	Hs.116252	ESTs, Moderately similar to ALU1_HUMAN A	3.2
315526	AI193043	Hs.128685	ESTs, Weakly similar to T17226 hypotheti	4.1

315530	AW015415	Hs.127780	ESTs	8.9
315562	AA737415	Hs.152826	ESTs	5.5
315634	AA837085	Hs.220585	ESTs	6.3
315647	AA648883	Hs.212911	ESTs	3.6
315707	AI418055	Hs.161160	ESTs	5.1
315772	AW515373	Hs.271249	Homo sapiens cDNA FLJ13580 fis, clone PL	3.1
315850	AW270550	Hs.116957	ESTs	3.8
315858	AA737345	Hs.294041	ESTs	5
315878	AA683336	Hs.189046	ESTs	3.1
315977	AW865916	Hs.151206	ESTs	4.7
315978	AA830893	Hs.119769	ESTs	4.1
315995	AI217477	Hs.194591	ESTs	4.1
316012	AA764950	Hs.119898	ESTs	7
316042	AI469960	Hs.170698	ESTs	4.9
316052	AI982796	Hs.136754	ESTs	4.1
316072	AW517524	Hs.135201	NOD2 protein	3.2
316074	AW975114	Hs.293273	ESTs	3.8
316100	AW203986	Hs.213003	ESTs	3.2
316133	AI187742	Hs.125562	ESTs	3.7
316177	AI904982	Hs.293102	ESTs, Moderately similar to ALU1_HUMAN A	30.7
316186	AI433540		gb:ti69g05.x1 NCI_CGAP_Kid11 Homo sapien	3.1
316244	AI640761	Hs.224988	ESTs	3.5
316303	AA740994	Hs.209609	ESTs	3.8
316313	AA741300	Hs.202599	ESTs, Weakly similar to I38022 hypothet	4.4
316364	AA747807	Hs.149500	ESTs	3.2
316580	AA938198	Hs.146123	poly(A) polymerase gamma	9.4
316697	AW293174	Hs.252627	ESTs	4.4
316715	AI440266	Hs.170873	ESTs, Weakly similar to T24832 hypothet	3
316868	AI660898	Hs.195602	ESTs	3.2
316869	AI954880	Hs.134604	ESTs	3.2
316886	AA838331	Hs.134981	ESTs	4.4
316897	AA838114	Hs.221612	ESTs	3.7
316943	AW014875	Hs.137007	ESTs	4.6
317069	AI732892	Hs.190489	ESTs	5.9
317194	AW445187	Hs.126036	ESTs	4.1
317360	AI125252	Hs.126419	ESTs	3.5
317404	AI808867	Hs.126504	ESTs	5.1
317452	AA972965	Hs.135568	ESTs	6.9
317501	AI822034	Hs.137097	ESTs	4.6
317674	AW294909	Hs.132208	ESTs	4.3
317803	AW664964	Hs.128899	ESTs	6.1
317834	X56348	Hs.267270	ret proto-oncogene (multiple endocrine n	3.1
317850	AI681545	Hs.152982	hypothetical protein FLJ13117	3.4
317881	AI827248	Hs.224398	Homo sapiens cDNA FLJ11469 fis, clone HE	9.6
317902	AW102941	Hs.211265	ESTs	4.1
317916	AI565071	Hs.159983	ESTs	10.3
318042	AW294522	Hs.149991	ESTs	3.1
318223	AI077540	Hs.134090	ESTs	3.9
318327	AW294013	Hs.200942	ESTs	3
318332	AI093930	Hs.183440	Homo sapiens cDNA: FLJ21000 fis, clone C	4.4
318418	AF107493	Hs.118498	Homo sapiens LUCA-15 protein mRNA, splic	5.4
318558	AW402677	Hs.146381	RNA binding motif protein, X chromosome	4.4
318625	AA526235	Hs.193162	Homo sapiens cDNA FLJ11983 fis, clone HE	5.9
318634	T49598	Hs.158832	ESTs	4
318740	NM_002543	Hs.77729	oxidised low density lipoprotein (lectin	7.3
318744	AI793124	Hs.144479	ESTs	17.8
318781	F11802	Hs.6818	ESTs	3
319191	NM_012391	Hs.79414	prostate epithelium-specific Ets transcr	3.6
319478	AI524124	Hs.270307	ESTs	4.6
319510	W88532	Hs.254562	ESTs	3.3
319551	AA761668		gb:nz24c08.s1 NCI_CGAP_GCB1 Homo sapiens	3.2
319745	T79366	Hs.108258	actin binding protein; macrophin (microf	3.3
319834	AA071267		gb:zm61g01.r1 Stratagene fibroblast (937	6.2
319840	C19035	Hs.164259	ESTs	3.3
319977	AA534222		gb:nj21d02.s1 NCI_CGAP_AA1 Homo sapiens	4.3
320074	AA321166	Hs.278233	ESTs	3.4
320167	AA984373	Hs.90790	Homo sapiens cDNA: FLJ22930 fis, clone K	4.1

320187	T99949	Hs.303428	Homo sapiens cDNA FLJ14832 fis, clone OV	5.3
320211	AL039402	Hs.125783	DEME-6 protein	9.2
320416	AI026984	Hs.283662	ESTs	3.1
320588	U78082	Hs.167738	RNA polymerase II transcriptional regula	3.1
320635	N50617	Hs.80506	small nuclear ribonucleoprotein polypept	6.1
320654	AI160015	Hs.118112	ESTs	3.5
320742	AI801188	Hs.120910	ESTs	3
320832	AA214584	Hs.280167	ESTs	3.7
320915	AI359144	Hs.143688	Homo sapiens cDNA: FLJ23031 fis, clone L	3.1
321016	BE144167	Hs.49994	hypothetical protein similar to RNA-bind	3.3
321107	AI732643	Hs.144151	ESTs	12.3
321171	AI769410	Hs.221461	ESTs	3.3
321253	AA610649	Hs.333239	ESTs	3
321318	AB033041	Hs.137507	vang (van gogh, Drosophila)-like 2	3.9
321642	AI432199	Hs.247084	ESTs	3
321644	AW975944	Hs.237396	ESTs	11.7
321683	AI471598	Hs.197531	ESTs	3.8
321758	U29112	Hs.196151	ESTs	4.4
321811	D80830		gb:HUM091D02B Human fetal brain (TFujiwa	3.2
321828	R59690	Hs.83623	nuclear receptor subfamily 1, group I, m	3.1
321910	H67065	Hs.271530	ESTs, Weakly similar to ALU7_HUMAN ALU S	4.7
321937	AL049351	Hs.302058	Homo sapiens mRNA; cDNA DKFZp566C093 (fr	3.5
321978	N77342	Hs.21851	Homo sapiens cDNA FLJ12900 fis, clone NT	5
322035	AL137517	Hs.334473	hypothetical protein DKFZp564O1278	19
322136	AF075083		gb:Homo sapiens full length insert cDNA	3.6
322258	BE265745	Hs.194359	ESTs, Weakly similar to ALUC_HUMAN !!!!	3
322296	W76326		gb:zd60d04.r1 Soares_fetal_heart_NbHH19W	4.4
322303	AI357412	Hs.157601	ESTs	11.5
322476	AW983372	Hs.46677	PRO2000 protein	3
322520	T55958		gb:yb35f05.r1 Stratagene fetal spleen (9	3
322521	AF147347		gb:Homo sapiens full length insert cDNA	4.2
322567	AF155108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810	4
322595	W92147	Hs.118394	ESTs	5.4
322675	AA017656		gb:ze39h01.r1 Soares retina N2b4HR Homo	3.1
322768	AW068805	Hs.288467	Homo sapiens cDNA FLJ12280 fis, clone MA	5.2
322818	AW043782	Hs.293616	ESTs	7.6
322882	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035 fis, clone HE	5.9
322975	C16391		gb:C16391 Clontech human aorta polyA mRN	16.5
323091	AI902456	Hs.210761	ESTs, Weakly similar to I38022 hypothet	4
323131	AK002088	Hs.270124	Homo sapiens cDNA FLJ11226 fis, clone PL	3.3
323168	AL120862	Hs.124165	programmed cell death 9 (PDCD9)	6.3
323244	AW675572	Hs.193620	ESTs	4.6
323262	AL133990	Hs.190642	ESTs	10.5
323332	AI829520		gb:wi19c08.x1 NCI_CGAP_Ut1 Homo sapiens	8.2
323333	AV651680	Hs.208558	ESTs	4.3
323335	AI655499	Hs.161712	ESTs	9.2
323645	AW445014	Hs.197746	ESTs	3.1
323863	BE081058	Hs.243023	ESTs	4
323693	AA317962	Hs.249721	ESTs, Moderately similar to PC4259 ferri	3
323782	AW961560	Hs.97600	ESTs	3.2
323817	AA410943		BMP-R1B	8.4
323930	AL043683	Hs.8173	hypothetical protein FLJ10803	3.3
323974	AI825204	Hs.211408	ESTs	4.5
324001	AL044949	Hs.116298	ESTs	4.5
324036	AI472078	Hs.303662	ESTs	8.4
324261	BE069341		gb:QV3-BT0381-270100-073-c08 BT0381 Homo	49.4
324285	AA431159	Hs.122954	ESTs	3
324296	AI524039	Hs.192524	ESTs	3
324305	AA642007	Hs.116369	ESTs	3.3
324432	AA464510	Hs.152812	ESTs	16.5
324585	AI823969	Hs.132678	ESTs	3.3
324598	AW972227	Hs.163986	Homo sapiens cDNA: FLJ22765 fis, clone K	5
324603	AW993522	Hs.292934	ESTs	10.4
324631	AA937116	Hs.293683	ESTs, Weakly similar to I54374 gene NF2	3.3
324716	BE169748	Hs.12504	likely ortholog of mouse Arkadia	3.2
324748	AW974941	Hs.292385	ESTs, Weakly similar to I78685 serine/th	3
324771	AA631739	Hs.335440	EST	3

324774	AI031771	Hs.132586	ESTs	4.2	
324823	AW516704	Hs.208726	ESTs	3.4	
324824	AI826999	Hs.224824	ESTs	3.1	
324826	AA704806	Hs.143842	ESTs, Weakly similar to 2004399A chromos	4.4	
324961	AA613792		gb:nc97h03.s1 NCI_CGAP_Pr2 Homo sapiens	3.9	
324987	AI375572	Hs.172634	ESTs	18.8	
324994	AI805416	Hs.213897	ESTs	3.3	
325148	AI084690	Hs.171176	ESTs	4.2	
325372			Phase 2 & 3 Exons	4.4	
325544			Phase 2 & 3 Exons	5.7	
327075			Phase 2 & 3 Exons	3.8	
332798			C22000007:gi|12314195|emb|CAB99338.1| (A	4.3	
334223			NM_005080*:Homo sapiens X-box binding pr	26.2	
334447			NM_012429*:Homo sapiens SEC14 (S. cerevi	3.9	
335809			NM_014509*:Homo sapiens kraken-like (BK1	10.1	
335824			ENSP00000249072*:DJ222E13.1 (N-TERMINAL	20	
338255			NM_014323*:Homo sapiens zinc finger prot	9	
409430	R21945	Hs.166975	splicing factor, arginine/serine-rich 5	4	
428048	AW812795	Hs.155381	ESTs, Moderately similar to I38022 hypot	4.6	
432558	R97268	Hs.177269	ESTs	3.2	
436808	AA731602	Hs.120266	ESTs	3.9	
448569	BE382657	Hs.21486	signal transducer and activator of trans	4.1	
453542	AW836724	Hs.339660	Homo sapiens mRNA expressed only in plac	3.7	
	M97935		AFFX control: STAT1	3.2	
	M97935		AFFX control: STAT1	3	
	M55150		fumarylacetoacetate	3	
	M13755		interferon stimulated protein; 15 kDa	4.5	
	AI052047		ESTs	6.7	
	AA252033		ESTs; Weakly similar to IIII ALU SUBFAMILY J	3.2	
	AA401739		ESTs	3.3	
	H18459		hepatocellular carcinoma associated protein;	3	
	R48744		ESTs	4.2	
	M31682		inhibin; beta B (activin AB beta polypeptide)	3	
	AA416873		ESTs	3	
	D80240		HUM5G11A Human fetal brain (TFujiwara) Homo	4	
	R49590		ESTs	3.2	
			CH22_FGENES.678_5	16.8	
			CH22_FGENES.619_7	12.9	
			CH22_FGENES.619_12	11.3	
			CH22_EM:AC005500.GENSCAN.127 9	9.2	
			CH22_EM:AC005500.GENSCAN.304 2	8.5	
			CH22_FGENES.271_8	8.4	
			CH22_FGENES.619_13	8	
			CH22_FGENES.271_7	7.3	
			CH22_FGENES.617_7	7.2	
			CH.07_hs gi|6004473	7.1	
			CH22_FGENES.264_1	6.8	
	X03363		HER2 receptor tyrosine kinase (c erbB 2; ERBB2; neu)	6.6	
			CH22_FGENES.617_9	6.5	
			CH.07_hs gi|5868264	5.8	
			CH.19_hs gi|5867439	5.7	
			CH22_FGENES.6 3	5.3	
			CH.17_hs gi|5867230	5.1	
			CH.20_hs gi|8552458	5.1	
			CH22_EM:AC005500.GENSCAN.148 22	4.7	
			CH22_FGENES.669_10	4.6	
	AA034918		KIAA1028 protein	4.6	
			CH22_FGENES.48_12	4.5	
			CH22_FGENES.118_2	4.5	
	AF049569		ESTs	4.4	
	M13955		multiple UniGene matches	4.3	
			CH22_FGENES.619_8	4.3	
			CH22_FGENES.13 7	4.3	
	HG4126 HT4398		Zinc Finger Protein Hzf4	4.3	
			CH22_FGENES.360_3	4.3	
			CH22_FGENES.706_9	4.3	
			CH.21_hs gi|6531965	4.2	

	CH.17_hs gi|5867215	4.1	
	CH22_FGENES.669_8	4.1	
HG2614 HT2710		Collagen, Type VII, Alpha 1	4.1
	CH22_FGENES.48_18	4.1	
X83535	matrix metalloproteinase 14 (membrane-inserted)	4	
	CH22_FGENES.271_6	3.9	
	CH22_FGENES.617_3	3.9	
	CH22_FGENES.290_6	3.8	
HG4716 HT5158		Guanosine 5' Monophosphate Synthase	3.8
	CH22_FGENES.13 5	3.8	
	CH22_FGENES.13 2	3.8	
	CH.14_hs gi|6682474	3.8	
	CH.02_hs gi|5867750	3.8	
	CH22_FGENES.617_8	3.7	
HG4677 HT5102		Oncogene Ret/Ptc2, Fusion Activated	3.7
	CH22_DJ32I10.GENSCAN.23 39	3.7	
	CH22_FGENES.543_20	3.7	
	CH22_EM:AC005500.GENSCAN.98 1	3.7	
	CH22_FGENES.204_2	3.5	
	CH22_FGENES.619_4	3.5	
	CH.16_hs gi|5887087	3.5	
AA714311	EST cluster (not in UniGene)	3.4	
	CH22_EM:AC005500.GENSCAN.149 9	3.4	
	CH22_EM:AC005500.GENSCAN.421 5	3.4	
	CH22_FGENES.13 4	3.3	
	CH.07_hs gi|6004478	3.3	
	CH22_FGENES.360_1	3.3	
HG2465 HT4871		Dna Binding Protein Ap 2, Alt. Splice 3	3.3
	CH22_FGENES.6_2	3.3	
	CH22_C20H12.GENSCAN.16 2	3.2	
	CH22_C65E1.GENSCAN.8 1	3.2	
AA707750	ESTs; Weakly similar to cis Golgi matrix	3.1	
	CH22_FGENES.307_4	3.1	
	CH22_EM:AC005500.GENSCAN.248 14	3.1	
	CH.06_hs gi|5902482	3.1	
	CH22_FGENES.669_5	3.1	
	CH22_DJ32I10.GENSCAN.19 8	3.1	
	CH22_FGENES.527_6	3.1	
	CH22_FGENES.330_10	3.1	
	CH22_FGENES.14 2	3.1	
AA976074	ESTs	3	
	CH22_FGENES.226 7	3	
	CH22_FGENES.13 3	3	
	CH22_EM:AC005500.GENSCAN.209 12	3	
	CH22_FGENES.271_3	3	

TABLE 17A

Table 17A shows the accession numbers for those pkeys lacking unigeneID's for Table 17. For each probeset, we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT number	Accession
116845	393481_1	AA649530 AA659316 H64973
103207	30635_4	X72790
126257	182217_1	N99638 AW973750 AA328271 H90994 AA558020 AA234435 N59599 R94815
102791	37186_1	AF080229 AF080231 AF080230 AF080232 AF080233 AF080234 BE550633 AI636743 AW614951 BE467547 AI680833 AI633818 N29986 U87592 U87593 U87590 U87591 S46404 U87587 AA463992 AW206802 AI970376 AI583718 AI672574 N25695 AW665468 AI818326 AA126128 AI480345 AW013827 AA248638 AI214968 AA204735 AA207155 AA206262 AA204833 AW003247 AW496808 AI080480 AI631703 AI651023 AI867418 AW818140 AA502500 AI206199 AI671282 AI352545 BE501030 AI652535 BE465782 AA208331 AW451868 AA471088 AA206342 AA204834 AA206100 AW021681 AA332922 N56048 AA700396 H92278 AW139734 H92683 U87589 U87595 H89001 U87594 BE466420 AI624817 BE466611 AI206344 AA574397 AA348354 AI493192
126872	142698_1	AW450979 AA136653 AA136656 AW419381 AA884358 AA492073 BE168945 AA809054 AW238038 BE011212 BE011359 BE011367 BE011368 BE011362 BE011215 BE011365 BE011363
112631	1746257_1	R82040 R70934
120742	176835_1	AA225084 AA302713
106864	324239_1	AI311928 AA936030 T51931 AA609818 AA487195 AA564207
109700	genbank_F09609	F09609
111532	genbank_R08440	R08440
113938	genbank_W81598	W81598
113947	genbank_W84768	W84768
124357	genbank_N22401	N22401
108733	504187_1	AA121022 AA126422
112303	genbank_R54797	R54797
322138	46802_1	AF075083 H52291 H52528
322298	47334_1	W76328 AF086341 W72300
321811	1527481_1	D80830 D80896 D80895
314648	293660_1	AW979268 AA878419 AA431342 AA431828
322520	38918_1	T55958 T57205 AF147346
322521	38917_1	AF147347 T55426 T55503
322675	86787_1	AA017656 AA017374 AA019761
323332	179142_1	AI829520 AI791832 AA228414 AI791823 AA229211 AA229315
316186	425440_1	AI433540 AA728984 AA804981
322975	1510563_1	C16391 C16413
324261	273265_1	BE069341 AW748403 AL044891 AI808240 AA393080
323817	233566_1	AA410943 AW948953 AA334202 AA332882
301976	128835_1	T97905 AA101672
324981	376239_1	AA813792 AW182329 T05304 AW858385
303642	284260_1	AW299459 AA417112
303797	386384_1	AW629759 AW749955 AA833408 AI651005
319551	357371_1	AA761688 AA573621 R92814 R09670
311935	174129_1	AA216387 T63548 AA228676
319834	112523_1	AA071267 T65940 T64515 AA071334
319977	345248_1	AA534222 AA632632 T81234
314138	179960_1	AA740616 AA654854 AA229923
313591	103067_1	AA046309 AI283500 AA046397

308106	AM76803	
338255	CH22_6856FG__LINK_EM:AC00	
335809	CH22_3181FG_617_6_LINK_EM	
335824	CH22_3197FG_619_11_LINK_E	
307010	AI140014	
307041	AI144243	
305913	AA876109	
305917	AA876469	
309574	AW168083	
325372	c12_hs	
325544	c12_hs	
332798	CH22_14FG_6_5_LINK_C4G1.G	
334223	CH22_1507FG_360_4_LINK_EM	
327075	c21_hs	
334447	CH22_1746FG_387_7_LINK_EM	
304782	AA582081	
313434	441798_1	W92070 AW019952 W92053

TABLE 17B

Table 17B shows the genomic positioning for those pkeys lacking unigene ID's and accession numbers in Table 17. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
334447	Dunham, I. et.al.	Plus	14308764-14308824
335809	Dunham, I. et.al.	Plus	26310772-26310909
335824	Dunham, I. et.al.	Plus	26376860-26376942
332798	Dunham, I. et.al.	Minus	232147-231974
334223	Dunham, I. et.al.	Minus	12734365-12734269
338255	Dunham, I. et.al.	Minus	15242294-15242231
325372	5866920	Minus	1117081-1117304
325544	6682452	Plus	171228-171286
327075	6531965	Plus	4041318-4041431

TABLE 18: Table 2 from BRCA 014 P

Table 18 shows genes with atleast five times the expression in breast tumor tissue than is expressed in normal body tissues.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of tumor to normal body tissue

Pkey	ExAccn	UnigeneID	Unigene Title	R1
101378	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	5.3
101530	M29874	Hs.1360	cytochrome P450, subfamily IIB (phenobar	9
101767	M81057	Hs.180884	carboxypeptidase B1 (tissue)	12
101878	M97815	Hs.183650	cellular retinoic acid-binding protein 2	6.5
103010	X52509	Hs.161640	tyrosine aminotransferase	12.4
104115	AF183810	Hs.26102	opposite strand to trichorhinophalangeal	7.6
104825	AA035613	Hs.141883	ESTs	6.9
107105	AW963419	Hs.155223	stanniocalcin 2	5.3
108819	AA011449	Hs.271627	ESTs	6.1
112287	AB033064	Hs.334806	KIAA1238 protein	7.3
112561	AI791483	Hs.129873	ESTs, Weakly similar to A36036 cytochrom	8.2
112837	R82331	Hs.164599	ESTs	5.4
113206	BE262470	Hs.241471	RNB6	6.2
113970	W27249	Hs.8109	hypothetical protein FLJ21080	6.9
114985	AI733881	Hs.72472	BMP-R1B	10.1
118925	N92293	Hs.206832	ESTs, Moderately similar to ALU8_HUMAN A	19.7
119905	AW449064	Hs.119571	collagen, type III, alpha 1 (Ehlers-Dani	8.4
121811	M31669	Hs.1735	inhibin, beta B (activin AB beta polypep	5.6
129301	AF182277	Hs.330780	cytochrome P450, subfamily IIB (phenober	6.2
133976	AI908165	Hs.169946	GATA-binding protein 3 (T-cell receptor	6.2
134731	D89377	Hs.89404	msh (Drosophila) homeo box homolog 2	5.8
300254	AW183618	Hs.55610	solute carrier family 30 (zinc transport	8.9
301884	AA312082	Hs.105445	GDNF family receptor alpha 1	5.7
302001	AB020711	Hs.278346	KIAA0904 protein	7.7
302067	BE542708	Hs.222399	CEGP1 protein	7.3
302276	AW057736	Hs.323910	HER2 receptor tyrosine kinase (c-erb-b2,	5.4
302290	AA179949	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564N0763 (I	34.1
302372	AL117406	Hs.200102	ATP-binding cassette transporter MRP8	6.7
302385	AJ224172	Hs.204096	lipophilin B (uteroglobin family member)	13.8
309177	AI951118	Hs.326736	Homo sapiens breast cancer antigen NY-BR	17.3
309583	AW170035	Hs.326736	Homo sapiens breast cancer antigen NY-BR	57.8
310781	AI380797	Hs.158892	ESTs	10.2
311166	AI821005	Hs.118599	ESTs	10.8
311935	AA216387		gb:nc16b02.s1 NCI_CGAP_Pr1 Homo sapiens	5.2
312153	BE261944	Hs.118625	hexokinase 1	5.2
313328	AW449211	Hs.105445	GDNF family receptor alpha 1	12.4
313915	C18863	Hs.163443	Homo sapiens cDNA FLJ11576 fis, clone HE	26.3
314097	AA648744	Hs.289493	ESTs	6.6
314138	AA740816		gb:ny97f11.s1 NCI_CGAP_GCB1 Homo sapiens	5.9
314506	AA833655	Hs.206868	Homo sapiens cDNA FLJ14056 fis, clone HE	8.5
314558	AI873274	Hs.190721	ESTs	27.4
314691	AW207206	Hs.138319	ESTs	20.7
315006	AI538613	Hs.298241	Transmembrane protease, serine 3	10.9
315021	AA533447	Hs.312989	ESTs	5.3
315051	AW292425	Hs.163484	ESTs	12.9
315060	AA551104	Hs.189048	ESTs, Moderately similar to ALUC_HUMAN I	5.6

315196	AI367347	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	8.2
315530	AW015415	Hs.127780	ESTs	8.9
315634	AA837085	Hs.220585	ESTs	6.3
316012	AA764950	Hs.119898	ESTs	7
316177	AI904982	Hs.293102	ESTs, Moderately similar to ALU1_HUMAN A	30.7
316580	AA938198	Hs.146123	poly(A) polymerase gamma	9.4
317803	AW664964	Hs.128899	ESTs	6.1
317881	AI827248	Hs.224398	Homo sapiens cDNA FLJ11469 fis, clone HE	9.6
318740	NM_002543	Hs.77729	oxidised low density lipoprotein (lectin	7.3
318744	AI793124	Hs.144479	ESTs	17.8
320211	AL039402	Hs.125783	DEME-6 protein	9.2
321107	AI732643	Hs.144151	ESTs	12.3
321644	AW975944	Hs.237396	ESTs	11.7
321978	N77342	Hs.21851	Homo sapiens cDNA FLJ12900 fis, clone NT	5
322035	AL137517	Hs.334473	hypothetical protein DKFZp564O1278	19
322766	AW068805	Hs.288467	Homo sapiens cDNA FLJ12280 fis, clone MA	5.2
322818	AW043782	Hs.293616	ESTs	7.6
322975	C16391		gb:C16391 Clontech human aorta polyA mRN	16.5
323262	AL133990	Hs.190642	ESTs	10.5
323332	AI829520		gb:wi19c06.x1 NCI_CGAP_Ut1 Homo sapiens	6.2
323817	AA410943		BMP-R1B	8.4
324261	BE069341		gb:QV3-BT0381-270100-073-c08 BT0381 Homo	49.4
324432	AA464510	Hs.152812	ESTs	16.5
324598	AW972227	Hs.163986	Homo sapiens cDNA: FLJ22765 fis, clone K	5
324603	AW993522	Hs.292934	ESTs	10.4
324987	AI375572	Hs.172634	ESTs	18.8
325544			Phase 2 & 3 Exons	5.7
330388		Hs.46	HER2 receptor tyrosine kinase (c-erb-b2,	6.6
334223			NM_005080*:Homo sapiens X-box binding pr	26.2
335809			NM_014509*:Homo sapiens kraken-like (BK1	10.1
335824			ENSP00000249072*:DJ222E13.1 (N-TERMINAL	
	AI052047		ESTs; Weakly similar to CYTOCHROME P450	6.7
	R72427		CH22_EM:AC005500.GENSCAN.127 9	5.5
			CH22_FGENES.619_13	9.2
			CH22_FGENES.617_9	8
			CH22_FGENES.271_7	6.5
			CH22_FGENES.619_7	7.3
			CH22_FGENES.271_8	12.9
			CH22_FGENES.619_12	8.4
			CH22_EM:AC005500.GENSCAN.304 2	11.3
			CH.07_hs gi|6004473	8.5
			CH22_FGENES.617_7	7.1
			CH22_FGENES.678_5	7.2
			CH22_FGENES.678_5	16.8

TABLE 18A

Table 18A shows the accession numbers for those pkeys lacking unigeneID's for Table 18. For each probeset, we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT number	Accession
323332	179142_1	AI829520 AI791832 AA228414 AI791823 AA229211 AA229315
322975	1510563_1	C16391 C16413
324261	273265_1	BE069341 AW748403 AL044891 AI908240 AA393080
323817	233568_1	AA410943 AW946953 AA334202 AA332682
311935	174129_1	AA216387 T63548 AA228676
314138	179960_1	AA740516 AA654854 AA229923
335809	CH22_3181FG_617_8_LINK_EM	
335824	CH22_3197FG_619_11_LINK_E	
325544	c12_hs	
334223	CH22_1507FG_360_4_LINK_EM	

TABLE 18B

Table 18B shows the genomic positioning for those pkeys lacking unigene ID's and accession numbers in Table 18. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
335809	Dunham, I. et.al.	Plus	26310772-26310909
335824	Dunham, I. et.al.	Plus	26376860-26376942
334223	Dunham, I. et.al.	Minus	12734365-12734269
325544	6682452	Plus	171228-171286

TABLE 19: 1045 GENES UP-REGULATED IN BREAST CANCER COMPARED TO NORMAL ADULT TISSUES

Table 19 shows 1045 genes up-regulated in breast cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos-Hu03 GeneChip array such that the ratio of "average" breast cancer to "average" normal adult tissues was greater than or equal to 2.5. The "average" breast cancer level was set to the 90th percentile value. The "average" normal adult tissue level was set to the 90th percentile value amongst 144 non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst the 144 non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of tumor to normal body tissue

Pkey	ExAccn	UnigeneID	UnigeneTitle	R1
408591	AF015224	Hs.46452	mammaglobin 1	137.6
408964	M21305		gb:Human alpha satellite and satellite 3	71.0
400291	AA401389	Hs.190721	ESTs	68.4
407277	AW170035	Hs.326736	Homo sapiens breast cancer antigen NY-BR	64.2
449746	AI668594	Hs.176588	ESTs, Weakly similar to CP4Y_HUMAN CYTOC	46.4
426878	BE069341		gb:QV3-BT0381-270100-073-c08 BT0381 Homo	44.8
400292	AA250737	Hs.72472	BMP-R1B	37.4
427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	32.9
408045	AW138959	Hs.245123	ESTs	31.9
407178	AA195651	Hs.104108	ESTs	30.4
407377	C16391		gb:C16391 Clontech human aorta polyA mRN	27.7
450705	U90304	Hs.25351	iroquois homeobox protein 5	24.8
407212	AA412108	Hs.269350	ESTs	22.0
428848	NM_000230	Hs.194235	leptin (murine obesity homolog)	21.9
404561			trichorhinophalangeal syndrome I (TRPS1)	21.8
407980	AA046309		gb:zf12f01.s1 Soares_fetal_heart_NbHH19W	19.8
447350	AI375572	Hs.172634	ESTs	17.3
450375	AA009647	Hs.8650	a disintegrin and metalloprotehase doma	16.6
422109	S73265	Hs.1473	gastrin-releasing peptide	16.5
435496	AW840171	Hs.265398	ESTs, Weakly similar to transformation-r	16.0
453160	AI263307	Hs.239884	H2B histone family, member L	15.8
420813	X51501	Hs.89949	prolactin-induced protein	15.8
415989	AI267700	Hs.317584	ESTs	15.5
422505	AL120852	Hs.124165	programmed cell death 9 (PDCD9)	14.8
424399	AI905687	Hs.2533	aldehyde dehydrogenase 9 family, member	14.5
423575	C18863	Hs.183443	Homo sapiens cDNA FLJ11576 fis, clone HE	13.7
429441	AJ224172	Hs.204096	lipophilin B (uteroglobin family member)	13.6
431474	AL133990	Hs.190842	ESTs	13.5
448595	AB014544	Hs.21572	KIAA0644 gene product	13.0
427217	AA399272	Hs.144341	ESTs	12.8
402578			C1001134:gi|2117372|pir||I65981 fatty ac	12.6
422805	AA436989	Hs.121017	H2A histone family, member A	12.2
424634	NM_003613	Hs.151407	cartilage intermediate layer protein, nu	12.0
458207	AA193450		gb:zr40e07.r1 Soares_NhHMPu_S1 Homo sapi	11.9
424088	AI351010	Hs.102267	lysyl oxidase	11.9
459587	AA031956		gb:zk15e04.s1 Soares_pregnant_uterus_NbH	11.5

416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	11.5
429170	NM_001394	Hs.2359	dual specificity phosphatase 4	11.5
407276	AI951118	Hs.326736	Homo sapiens breast cancer antigen NY-BR	11.4
434377	AW137148	Hs.306593	Homo sapiens cDNA FLJ11382 fis, clone HE	11.3
448390	AL035414	Hs.21068	hypothetical protein	11.1
452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	11.0
421037	AI684808	Hs.197653	programmed cell death 9 (PDCD9)	10.9
452461	N78223	Hs.108106	transcription factor	10.7
443348	AW873598	Hs.182278	calmodulin 2 (phosphorylase kinase, delt	10.6
421155	H87879	Hs.102267	lysyl oxidase	10.5
402606			NM_024626:Homo sapiens hypothetical prot	10.4
409269	AA576953	Hs.22972	hypothetical protein FLJ13352	10.4
447268	AI370413	Hs.36563	hypothetical protein FLJ22418	10.3
447033	AI357412	Hs.157601	ESTs	10.2
400295	W72838	Hs.2533	aldehyde dehydrogenase 9 family, member	10.1
424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	10.1
432441	AW292425	Hs.163484	ESTs	9.9
427365	AI873274	Hs.190721	ESTs	9.9
438950	H23789	Hs.144530	EST	9.8
422835	BE218705	Hs.121378	metallothionein-like 5, testis-specific	9.7
425692	D90041	Hs.155956	N-acetyltransferase 1 (arylamine N-acety	9.7
411869	W20027	Hs.23439	ESTs	9.6
439820	AL360204	Hs.283853	Homo sapiens mRNA full length insert cDN	9.5
445730	AI624342	Hs.170042	ESTs	9.5
459583	AI907673		gb:IL-BT152-080399-004 BT152 Homo sapien	9.3
452744	AI267652	Hs.30504	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	9.2
432596	AJ224741	Hs.278461	matrilin 3	9.1
400297	AI127076	Hs.334473	hypothetical protein DKFZp564O1278	9.1
449448	D60730	Hs.57471	ESTs	9.1
423945	AA410943		gb:zd32h03.r1 Soares ovary tumor NbHOT H	9.1
408348			Target Exon	9.0
424735	U31875	Hs.272499	short-chain alcohol dehydrogenase family	9.0
453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11	9.0
433365	AF026944	Hs.293797	ESTs	8.8
405654	NA		C12001521:gi|7513934|pir||T31081 cca3 pr	8.8
418601	AA279490	Hs.86368	calmegin	8.8
451110	AI955040	Hs.265398	ESTs, Weakly similar to transformation-r	8.7
408771	AW732573	Hs.47584	potassium voltage-gated channel, delayed	8.5
409041	AB033025	Hs.50081	KIAA1199 protein	8.4
442353	BE379594	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN A	8.3
451561	N52812	Hs.177403	ESTs	8.2
424001	W67883	Hs.137476	paternally expressed 10	8.2
429859	NM_007050	Hs.225952	protein tyrosine phosphatase, receptor t	8.1
423887	AL080207	Hs.134585	DKFZP434G232 protein	8.1
405095	NA		Target Exon	8.1
419296	AA238115	Hs.120785	ESTs	8.0
447164	AF026941	Hs.17518	Homo sapiens clg5 mRNA, partial sequence	8.0
413472	BE242870	Hs.75379	solute carrier family 1 (glial high affi	8.0
416747	AW876523	Hs.15929	hypothetical protein FLJ12910	8.0
415385	R17798	Hs.7535	COBW-like protein	7.9
434424	AI811202	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	7.9
420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	7.9
406687	M31126	Hs.272620	matrix metalloproteinase 11 (MMP11; stro	7.8
400285	NA		Eos Control	7.7
437207	T27503	Hs.15929	hypothetical protein FLJ12910	7.6
427119	AW880562	Hs.114574	ESTs	7.5
429534	AW976987	Hs.183327	ESTs, Weakly similar to 2109260A B cell	7.5
433426	H69125	Hs.133525	ESTs	7.5
411078	AI222020	Hs.182364	CocoaCrisp	7.4
426214	H59846	Hs.128355	ESTs, Moderately similar to ALU7_HUMAN A	7.4
447475	AI380797	Hs.158992	ESTs	7.3
415263	AA948033	Hs.130853	ESTs	7.2
439569	AW602166	Hs.222399	CEGP1 protein	7.2
414142	AW368397	Hs.150042	Homo sapiens cDNA FLJ14438 fis, clone HE	7.1
426281	AW242243	Hs.168870	peroxisomal farnesylated protein	7.0
444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	6.9
445885	AI734009	Hs.127699	KIAA1603 protein	6.9

429432	AI678059	Hs.202676	synaptonemal complex protein 2	6.9
410781	AI375872	Hs.165028	ESTs	6.9
443788	AI732643	Hs.144151	ESTs	6.9
421373	AA808229	Hs.167771	ESTs	6.8
451398	AI793124	Hs.144479	ESTs	6.8
404253			NM_021058*:Homo sapiens H2B histone fami	6.8
441098	AI015591	Hs.131004	ESTs, Weakly similar to T17227 hypotheti	6.7
426215	AW963419	Hs.155223	stanniocalcin 2	6.6
428227	AA321649	Hs.2248	small inducible cytokine subfamily B (CX	6.6
422956	BE545072	Hs.122579	hypothetical protein FLJ10461	6.6
411111	AW818127		gb:CM1-ST0277-061299-059-b07 ST0277 Homo	6.6
434988	AI418055	Hs.161160	ESTs	6.6
442580	AI733682	Hs.130239	ESTs	6.6
449611	AI970394	Hs.197075	ESTs	6.6
408000	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	6.5
420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	6.5
431089	BE041395	Hs.283676	ESTs, Weakly similar to unknown protein	6.5
400301	X03635	Hs.1657	estrogen receptor 1	6.5
427356	AW023482	Hs.97849	ESTs	6.5
425704	U79293	Hs.159264	Human clone 23948 mRNA sequence	6.4
441134	W29092	Hs.7578	cellular retinoic acid-binding protein 1	6.4
424902	NM_003866	Hs.153687	inositol polyphosphate-4-phosphatase, ty	6.4
448693	AW004854	Hs.228320	hypothetical protein FLJ23537	6.4
431448	AL137517	Hs.334473	hypothetical protein DKFZp564O1278	6.2
444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	6.1
422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias	6.1
453331	AI240665	Hs.8895	ESTs	6.1
418007	M13509	Hs.83169	matrix metalloproteinase 1 (MMP1; intera	6.0
441233	AA972965	Hs.135568	ESTs	6.0
418092	R45154	Hs.106604	ESTs	6.0
430044	AA484510	Hs.152812	ESTs	5.9
432837	AA310693	Hs.87329	HSPC072 protein	5.9
433285	AW975944	Hs.237396	ESTs	5.9
450701	H39960	Hs.288467	Homo sapiens cDNA FLJ12280 fis, clone MA	5.9
425707	AF115402	Hs.11713	E74-like factor 5 (ets domain transcript	5.9
410785	AW803341		gb:IL2-UM0079-090300-060-D03 UM0079 Homo	5.9
425396	AL049689	Hs.156369	hypothetical protein similar to tenascin	5.8
414812	X72755	Hs.77367	monokine induced by gamma interferon	5.8
459371	R20991		gb:yg06h01.r1 Soares infant brain 1NIB H	5.8
411284	N28519	Hs.135191	ESTs, Weakly similar to unnamed protein	5.8
453511	AL031224	Hs.33102	transcription factor AP-2 beta (activati	5.8
451807	W52854	Hs.27099	hypothetical protein FLJ23293 similar to	5.7
430510	AW162916	Hs.241576	hypothetical protein PRO2577	5.7
415539	AI733881	Hs.72472	BMP-R1B	5.6
438199	AW016531	Hs.122147	ESTs	5.6
417866	AW067903	Hs.82772	collagen, type XI, alpha 1	5.5
430019	AA463893	Hs.220933	ESTs	5.5
439809	R41396	Hs.101774	hypothetical protein FLJ23045	5.5
423811	AW299598	Hs.50895	homeo box C4	5.4
434539	AW748078	Hs.214410	ESTs, Weakly similar to MUC2_HUMAN MUCIN	5.4
439138	AI742605	Hs.193696	ESTs	5.4
453931	AL121278	Hs.25144	ESTs	5.4
444078	BE246918	Hs.10290	U5 snRNP-specific 40 kDa protein (hPrp8-	5.4
447102	BE167434	Hs.98471	ESTs, Weakly similar to T18712 hypotheti	5.4
451821	AI879148	Hs.26770	fatty acid binding protein 7, brain	5.4
425238	AW067800	Hs.155223	stanniocalcin 2	5.3
421464	AA291553	Hs.190088	ESTs	5.3
450736	AW970080		gb:EST382140 MAGE resequences, MAGK Homo	5.3
428085	AA421081	Hs.12388	ESTs	5.3
452838	U65011	Hs.30743	preferentially expressed antigen in mela	5.3
445424	AB028945	Hs.12698	cortactin SH3 domain-binding protein	5.3
456938	X52509	Hs.161640	tyrosine aminotransferase	5.3
422867	L32137	Hs.1584	cartilage oligomeric matrix protein (COM	5.2
438167	R28363	Hs.24286	ESTs	5.2
433330	AW207084	Hs.132816	hypothetical protein MGC14801	5.2
449765	N92293	Hs.206832	ESTs, Moderately similar to ALU8_HUMAN A	5.2
416276	U41060	Hs.79136	LIV-1 protein, estrogen regulated	5.2

400300	X03363		HER2 receptor tyrosine kinase (c-erb-b2,	5.2
418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	5.2
439840	AW449211	Hs.105445	GDNF family receptor alpha 1	5.2
428771	AB028992	Hs.193143	KIAA1069 protein	5.2
455047	AW852530		gb:PM1-CT0243-071099-001-g08 CT0243 Homo	5.2
419169	AW851980	Hs.262346	ESTs, Weakly similar to S72482 hypotheti	5.2
453197	AI916269	Hs.109057	ESTs, Weakly similar to ALU5_HUMAN ALU S	5.1
400298	AA032279	Hs.61835	stx transmembrane epithelial antigen of	5.1
431023	AI283133	Hs.297420	ESTs	5.1
427666	AI791495	Hs.180142	calmodulin-like skin protein	5.1
427718	AI798680	Hs.25933	ESTs	5.1
434531	AA642007	Hs.118369	ESTs	5.1
429220	AW207206	Hs.135319	ESTs	5.1
405494	NA		C2001837*:gi|12697903|db|BAB21770.1| (A	5.1
452930	AW195285	Hs.194097	ESTs, Weakly similar to I38022 hypotheti	5.1
444910	AI201849		gb:xq76g04.x1 NCI_CGAP_Pr28 Homo sapiens	5.1
453310	X70697	Hs.553	solute carrier family 6 (neurotransmitte	5.0
444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	5.0
450603	R43646	Hs.12422	ESTs	5.0
416575	W02414	Hs.38383	ESTs	5.0
438504	AW665281	Hs.224625	ESTs	5.0
415209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	5.0
428804	AK000713	Hs.193736	hypothetical protein FLJ20706	5.0
420077	AW512260	Hs.87767	ESTs	4.9
450480	X82125	Hs.25040	zinc finger protein 239	4.9
437637	AJ003029	Hs.65792	syntrophin, gamma 2	4.9
431808	M30703	Hs.270833	amphiregulin (schwannoma-derived growth	4.9
418836	AI655499	Hs.161712	ESTs	4.8
442441	AI820682	Hs.129598	ESTs	4.8
435635	AF220050	Hs.181385	uncharacterized hematopoietic stem/proge	4.8
400286	NA		C16000922:gi|7499103|pir||T20903 hypothe	4.8
407508	U71600		gb:Human zinc finger protein zfp31 (zf31	4.8
420026	AI831190	Hs.166676	ESTs	4.8
441377	BE218239	Hs.202656	ESTs	4.8
457726	AI217477	Hs.194591	ESTs	4.8
412785	AW997558	Hs.78521	KIAA1717 protein	4.8
428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin	4.7
436026	AI349764	Hs.217081	ESTs	4.7
409110	AA191493	Hs.48778	niban protein	4.7
400284	NA		estrogen receptor 1	4.7
410102	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035 fis, clone HE	4.7
407819	R42185	Hs.274803	ESTs	4.7
430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	4.7
422695	AW961489	Hs.154116	ESTs	4.7
453818	NM_003462	Hs.33846	dynein, axonemal, light intermediate pol	4.7
427427	AF077345	Hs.177936	ESTs	4.6
421751	AW813731	Hs.159153	ESTs, Moderately similar to S65657 alpha	4.6
454074	R83503	Hs.28419	ESTs	4.6
405718			C4000799*:gi|6330365|db|BAA86508.1| (AB	4.6
444649	AW207523	Hs.197628	ESTs	4.6
429431	Z40313	Hs.106330	Homo sapiens clone IMAGE:23371, mRNA seq	4.6
427811	M81057	Hs.180884	carboxypeptidase B1 (tissue)	4.6
447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	4.6
430345	AK000282	Hs.239681	hypothetical protein FLJ20275	4.6
454307	AW855717		gb:RC1-CT0279-081299-013-b01 CT0279 Homo	4.6
400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	4.6
438180	AA808189	Hs.272151	ESTs	4.6
451340	AW936273		gb:OV0-DT0020-090200-107-g07 DT0020 Homo	4.6
458711	AL036877	Hs.282878	ESTs	4.6
457430	AA514660	Hs.128443	ESTs	4.6
416030	H15281	Hs.21948	ESTs	4.6
447233	AW248333	Hs.17901	Homo sapiens, clone IMAGE:3937015, mRNA,	4.6
445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6 (EGFL6)	4.5
424590	AW996399	Hs.46821	hypothetical protein FLJ20086	4.5
432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	4.5
423833	AW503329		gb:UI-HF-BN0-abx-e-02-0-UI.r1 NIH_MGC_50	4.5
408747	AI925153	Hs.217493	annexin A2	4.5

412102	H56435		gb:yq98e09.r1 Soares fetal liver spleen	4.5
431716	D89053	Hs.268012	fatty-acid-Coenzyme A ligase, long-chain	4.5
411050	AW814902		gb:MR1-ST0206-120400-022-f08 ST0206 Homo	4.5
401418	NA		C14000338*:gi|7459502|pir||S74665 outer	4.5
436194	AK001074	Hs.333435	Homo sapiens cDNA FLJ10212 fis, clone HE	4.5
438211	AK001581	Hs.334828	hypothetical protein FLJ10719; KIAA1794	4.4
414080	AA135257	Hs.47783	B aggressive lymphoma gene	4.4
424115	AA335497	Hs.293965	ESTs, Weakly similar to I38022 hypotheti	4.4
415788	AW419196	Hs.257924	hypothetical protein FLJ13782	4.4
442117	AW664964	Hs.128899	ESTs	4.4
452784	BE463857	Hs.151258	hypothetical protein FLJ21062	4.4
432731	R31178	Hs.287820	fibronectin 1	4.4
410534	AW905138		gb:QV0-NN1071-280400-207-g07 NN1071 Homo	4.4
405186	NA		C2000662*:gi|7512792|pir||T12482 hypothe	4.4
430217	N47863	Hs.336801	ribosomal protein S24	4.4
401793			C17001545:gi|5360127|gb|AAD42882.1|AF155	4.4
415747	AA381209		gb:EST94257 Activated T-cells I Homo sap	4.4
423679	AB007975	Hs.131454	KIAA0506 protein	4.4
400238	NA		C19000274*:gi|12741327|ref|XP_008833.2|	4.4
425627	AF019612	Hs.297007	membrane-bound transcription factor prot	4.4
400608			C10001899:gi|7508633|pir||T25392 hypothe	4.4
458634	AV657310	Hs.282898	ESTs	4.3
407771	AL138272	Hs.62713	ESTs	4.3
405906	NA		Target Exon	4.3
405925	NA		Target Exon	4.3
439382	BE247684	Hs.103070	ESTs	4.3
445263	H57646	Hs.42586	KIAA1580 protein	4.3
407162	N63855	Hs.142634	zinc finger protein	4.3
419536	AA603305		gb:np12d11.s1 NCI_CGAP_Pr3 Homo sapiens	4.3
454359	N71277		gb:za36e03.s1 Soares fetal liver spleen	4.3
411558	AA102670	Hs.70725	gamma-aminobutyric acid (GABA) A recepto	4.2
450715	AI266484	Hs.31570	ESTs, Weakly similar to KIAA1324 protein	4.2
421451	AA291377	Hs.50831	ESTs	4.2
452864	AA033714	Hs.287629	hypothetical protein FLJ14260	4.2
409757	NM_001898	Hs.123114	cystatin SN	4.2
413043	BE158766		gb:IL2-HT0397-071299-024-F02 HT0397 Homo	4.2
413499	BE144884		gb:CM0-HT0182-041099-065-e11 HT0182 Homo	4.2
444619	BE538082	Hs.8172	ESTs, Moderately similar to A46010 X-lin	4.2
408380	AF123050	Hs.44532	diubiquitin	4.2
406992	S82472		gb:beta -pol=DNA polymerase beta (exon a	4.2
404285	NA		C6001909:gi|704441|dbj|BAA18909.1| (D298	4.2
425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (MMP11; stro	4.2
428046	AW812795	Hs.155381	ESTs, Moderately similar to I38022 hypot	4.2
446163	AA026880	Hs.25252	prolactin receptor	4.2
421147	AW592167	Hs.293299	ESTs	4.2
426451	AI908165	Hs.169946	GATA-binding protein 3 (T-cell receptor	4.2
415227	AW821113	Hs.72402	ESTs	4.2
452176	AA024538	Hs.282990	Human DNA sequence from clone RP1-28H20	4.2
452862	AW378065	Hs.8587	ESTs	4.2
443646	AI085198	Hs.184226	ESTs	4.2
425523	AB007948	Hs.158244	KIAA0479 protein	4.1
424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	4.1
430009	AA894564	Hs.22242	ESTs	4.1
434469	AA634806		gb:ab28c02.r1 Stratagene lung (937210) H	4.1
451381	BE241831	Hs.172330	hypothetical protein MGC2705	4.1
450229	R18717	Hs.8929	hypothetical protein FLJ11362	4.1
455700	BE068115		gb:CM1-BT0368-061299-060-g07 BT0368 Homo	4.1
431924	AK000850	Hs.272203	Homo sapiens cDNA FLJ20843 fis, clone AD	4.1
438685	AI886658	Hs.184987	ESTs	4.1
401451			NM_004496*:Homo sapiens hepatocyte nucle	4.1
431676	AI885464		gb:tt88f04.x1 NCI_CGAP_Pr28 Homo sapiens	4.1
409092	AI735283	Hs.172608	ESTs	4.1
429270	W60379	Hs.57773	ESTs	4.1
443903	AI220547	Hs.135223	ESTs	4.1
427122	AW057736	Hs.323910	HER2 receptor tyrosine kinase (c-erb-b2,	4.1
410275	U85658	Hs.81796	transcription factor AP-2 gamma (activat	4.1
432912	BE007371	Hs.200313	ESTs	4.1

403585			Target Exon	4.1
438296	AI394151	Hs.37932	ESTs	4.1
420380	AA640891	Hs.102408	ESTs	4.1
431118	BE264901	Hs.250502	carbonic anhydrase VIII	4.1
416182	NM_004354	Hs.79069	cyclin G2	4.1
418994	AA296520	Hs.88546	selectin E (endothelial adhesion molecul	4.1
400555			Target Exon	4.1
410079	U94362	Hs.58589	glycogenin 2	4.0
427674	NM_003528	Hs.2178	H2B histone family, member Q	4.0
427131	AA448460	Hs.112017	GE36 gene	4.0
439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDN	4.0
429353	AL117408	Hs.200102	ATP-binding cassette transporter MRP8	4.0
421296	NM_002666	Hs.103253	perilipin	4.0
418819	AA228776	Hs.191721	ESTs	4.0
424188	AW954552	Hs.142634	zinc finger protein	4.0
455431	AW938484		gb:CM0-DT0057-290200-253-d06 DT0057 Homo	4.0
404142	NA		Target Exon	4.0
441143	AI027604	Hs.159650	ESTs	4.0
444540	AI693927	Hs.265165	ESTs	4.0
415579	AA165232	Hs.222069	ESTs	4.0
452891	N75582	Hs.212875	ESTs, Weakly similar to DYH9_HUMAN CILIA	4.0
414605	BE390440		gb:601283601F1 NIH_MGC_44 Homo sapiens c	4.0
452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	4.0
417801	AA417383	Hs.82582	integrin, beta-like 1 (with EGF-like rep	4.0
446232	AI281848	Hs.194691	retinoic acid induced 3	4.0
447377	X77343	Hs.334334	transcription factor AP-2 alpha (activat	4.0
437854	AL119723		gb:DKFZp761A2124_r1 761 (synonym: hamy2)	4.0
446140	AA356170	Hs.26750	hypothetical protein FLJ21908	4.0
452240	AI591147	Hs.61232	ESTs	4.0
459574	AI741122	Hs.101810	Homo sapiens cDNA FLJ14232 fis, clone NT	4.0
458673	N99626		gb:za39d11.r1 Soares fetal liver spleen	4.0
444858	AI199738	Hs.208275	ESTs, Weakly similar to ALUA_HUMAN !!!!	4.0
452166	AI948607	Hs.264680	ESTs	4.0
452681	AF153330	Hs.30248	solute carrier family 19 (thiamine trans	3.9
450192	AA263143	Hs.24596	RAD51-interacting protein	3.9
408554	NA		Target Exon	3.9
416259	AA573006	Hs.19173	ESTs	3.9
445813	Z42023	Hs.106576	alanine-glyoxylate aminotransferase 2-li	3.9
451024	AA442176		gb:zw63b08.r1 Soares_total_fetus_Nb2HF8_	3.9
413930	M86153	Hs.75618	RAB11A, member RAS oncogene family	3.9
401781			Target Exon	3.9
415296	F05086	Hs.328142	ESTs	3.9
452584	AA026777		gb:ze93c11.r1 Soares_fetal_heart_NbHH19W	3.9
442500	AI819068	Hs.209122	ESTs	3.9
419759	Z21336	Hs.135411	actin related protein	3.9
424638	AI472106	Hs.49303	Homo sapiens cDNA FLJ11663 fis, clone HE	3.9
439699	AF086534	Hs.187561	ESTs, Moderately similar to ALU1_HUMAN A	3.9
428042	AA418529	Hs.76391	myxovirus (influenza) resistance 1, homo	3.9
452501	AB037791	Hs.29716	hypothetical protein FLJ10980	3.9
453049	BE537217	Hs.30343	ESTs	3.9
443213	BE568414	Hs.145497	Homo sapiens cDNA: FLJ22097 fis, clone H	3.9
443489	AI073512	Hs.133916	ESTs	3.9
455092	BE152428		gb:CM0-HT0323-151299-126-b04 HT0323 Homo	3.9
401785			NM_002275*:Homo sapiens keratin 15 (KRT1	3.9
426427	M86699	Hs.169840	TTK protein kinase	3.9
446009	AI989885	Hs.231926	ESTs	3.9
436033	H75391	Hs.255748	ESTs	3.9
451067	BE172188		gb:MR0-HT0559-110300-005-h11 HT0559 Homo	3.8
419348	AA236845	Hs.98274	ESTs	3.8
444635	AI184268	Hs.339665	ESTs	3.8
412140	AA219691	Hs.73825	RAB6 interacting, kinesin-like (rabkines	3.8
403593	NA		Target Exon	3.8
442323	AW016869	Hs.29190	ESTs	3.8
419854	AW564873	Hs.87836	Homo sapiens PAC clone RP5-1087M19 from	3.8
433871	W02410	Hs.265555	ESTs	3.8
445253	AI217926	Hs.144762	ESTs	3.8
409542	AA503020	Hs.36563	hypothetical protein FLJ22418	3.8

443162	T49951	Hs.9029	DKFZP434G032 protein	3.8
458184	AW383618	Hs.265459	ESTs, Moderately similar to ALU2_HUMAN A	3.8
422475	AL359938	Hs.117313	Mels (mouse) homolog 3	3.8
440705	AA904244	Hs.153205	ESTs	3.8
447290	AI476732	Hs.263912	ESTs	3.8
403426			Target Exon	3.8
427821	AA470158	Hs.98202	ESTs	3.8
454288	BE222648	Hs.279458	ESTs, Highly similar to c380A1.1b [H.sap	3.8
443801	AW206942	Hs.253594	ESTs	3.8
410658	AW105231	Hs.192035	ESTs	3.8
410672	AW794600		gb:RC6-UM0014-170300-022-C05 UM0014 Homo	3.8
428579	NM_005756	Hs.184942	G protein-coupled receptor 64	3.8
445495	BE622641	Hs.38489	ESTs, Weakly similar to I38022 hypotheti	3.8
447995	AI742618	Hs.181733	ESTs, Weakly similar to nitrilase homolo	3.7
401747			Homo sapiens keratin 17 (KRT17)	3.7
420833	NM_014581	Hs.274480	odorant-binding protein 2A	3.7
423545	AP000692	Hs.129781	chromosome 21 open reading frame 5	3.7
433138	AB029496	Hs.59729	semaphorin sem2	3.7
434715	BE005346	Hs.116410	ESTs	3.7
428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	3.7
450951	AA018534	Hs.103334	ESTs	3.7
402696	NA		C3002523:gi|5688211|sp|Q27533|YH2M_CAEEL	3.7
446868	AW660737	Hs.135100	ESTs	3.7
458154	AW816379	Hs.335018	ESTs	3.7
422026	U80738	Hs.110826	trinucleotide repeat containing 9	3.7
419440	AB020689	Hs.90419	KIAA0882 protein	3.7
421524	AA312082	Hs.105445	GDNF family receptor alpha 1	3.7
417283	N62840	Hs.48648	ESTs	3.7
401508	NA		NM_024817:Homo sapiens hypothetical prot	3.7
410303	AA324597	Hs.21851	Homo sapiens cDNA FLJ12900 fis, clone NT	3.7
420362	U79734	Hs.97208	huntingtin interacting protein 1	3.7
433384	AI021992	Hs.124244	ESTs	3.7
434302	AA629085	Hs.116301	ESTs	3.7
443938	R55373	Hs.20884	ESTs	3.7
448420	BE523004		gb:601441282F1 NIH_MGC_72 Homo sapiens c	3.7
458712	AI347502	Hs.107872	hypothetical protein FLJ20761	3.7
433404	T32982	Hs.102720	ESTs	3.7
405232			NM_015832:Homo sapiens methyl-CpG bindin	3.7
430491	AL109791	Hs.241559	Homo sapiens mRNA full length insert cDN	3.7
455609	BE011668		gb:CM3-BN0223-100500-177-e04 BN0223 Homo	3.7
450164	AI239923	Hs.30098	ESTs	3.7
453948	AI970797	Hs.64859	ESTs	3.7
436061	AI248584	Hs.190745	Homo sapiens cDNA: FLJ21326 fis, clone C	3.7
401049	NA		Target Exon	3.6
416867	D31771	Hs.89404	msh (Drosophila) homeo box homolog 2	3.6
420179	N74530	Hs.21168	ESTs	3.6
458663	AW658444	Hs.280776	tankyrase, TRF1-interacting ankyrin-rela	3.6
437259	AI377755	Hs.120695	ESTs	3.6
428309	M97815	Hs.183650	cellular retinoic acid-binding protein 2	3.6
450522	AI698839		gb:wd31f02.x1 Soares_NFL_T_GBC_S1 Homo s	3.6
451952	AL120173	Hs.301663	ESTs	3.6
412209	AW001458		gb:RC0-NN1012-270300-031-c07 NN1012 Homo	3.6
425201	AA352111		gb:EST60081 Activated T-cells XX Homo sa	3.6
443830	AI142095	Hs.143273	ESTs	3.6
439255	BE164500		gb:RC4-HT0469-230300-014-e10 HT0469 Homo	3.6
414869	AA157291	Hs.21479	ubinuclein 1	3.6
409084	AA062954	Hs.141883	ESTs	3.6
407721	Y12735	Hs.38018	dual-specificity tyrosine-(Y)-phosphoryl	3.6
445135	AK000054	Hs.12347	hypothetical protein FLJ20047	3.6
404091	NA		Target Exon	3.6
409731	AA125985	Hs.58145	thymosin, beta, identified in neuroblast	3.6
405153			Target Exon	3.6
423248	AA380177	Hs.125845	ribulose-5-phosphate-3-epimerase	3.6
403639	NA		ENSP00000233023*:cDNA FLJ12662 fis, clon	3.6
404360			C7001385:gi|12082809|gb|AAG48618.1|AF315	3.6
422352	AA766298	Hs.99200	ESTs	3.6
423338	AB007961	Hs.127338	KIAA0492 protein	3.6

424202	BE350295	Hs.15032	RAN binding protein 17	3.6
431750	AA514986	Hs.283705	ESTs	3.6
439907	AA853978	Hs.124577	ESTs	3.6
453596	AA441838	Hs.62905	hypothetical protein FLJ14834	3.6
406446	NA		Target Exon	3.6
418454	AA315308	Hs.196870	hypothetical protein FLJ14991	3.6
434360	AW015415	Hs.127780	ESTs	3.6
409079	W87707	Hs.82065	interleukin 6 signal transducer (gp130,	3.6
440132	AI697121	Hs.202466	ESTs, Weakly similar to S65824 reverse t	3.6
448706	AW291095	Hs.21814	interleukin 20 receptor, alpha	3.6
440671	AW297920	Hs.130054	ESTs	3.5
407647	AW880158		gb:RC0-CT0379-290100-032-b04 CT0379 Homo	3.5
459023	AW968226	Hs.60798	ESTs	3.5
402820			NM_017646*:Homo sapiens tRNA isopentenyl	3.5
417009	AA191719	Hs.314714	ESTs	3.5
447048	AW393080	Hs.228320	hypothetical protein FLJ23537	3.5
449978	AI806335	Hs.200829	ESTs, Weakly similar to T30171 ninein -	3.5
428062	AA420683	Hs.98321	hypothetical protein FLJ14103	3.5
452909	NM_015368	Hs.30985	pannexin 1	3.5
400610	NA		Target Exon	3.5
417843	W07361	Hs.22545	Homo sapiens cDNA FLJ12935 fis, clone NT	3.5
419335	AW960146	Hs.284137	hypothetical protein FLJ12888	3.5
451592	AI805416	Hs.213897	ESTs	3.5
443270	NM_004272	Hs.337737	Homer, neuronal immediate early gene, 1B	3.5
423948	AW392342	Hs.283077	centrosomal P4.1-associated protein; unc	3.5
449424	AW448937	Hs.197030	ESTs	3.5
423841	AW753967		gb:RC2-CT0304-080100-011-h12 CT0304 Homo	3.5
416806	NM_000288	Hs.79993	peroxisomal biogenesis factor 7	3.5
422060	R20893	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	3.5
433104	AL043002	Hs.128246	ESTs, Moderately similar to unnamed prot	3.5
415778	H84847	Hs.49391	hypothetical protein LOC54149	3.5
413054	AW316843	Hs.66309	hypothetical protein MGC11061	3.5
416638	N32536	Hs.42645	solute carrier family 16 (monocarboxylic	3.5
424639	AI917494	Hs.8812	Homo sapiens cDNA FLJ14388 fis, clone HE	3.5
424827	AI057094	Hs.96867	Homo sapiens cDNA: FLJ23155 fis, clone L	3.5
437782	AI370876	Hs.79090	exportin 1 (CRM1, yeast, homolog)	3.5
411514	AW850178		gb:fL3-CT0219-271099-022-H12 CT0219 Homo	3.5
413783	AA314337	Hs.301547	ribosomal protein S7	3.5
421106	AA877124	Hs.172844	ESTs	3.5
431291	N25521	Hs.25275	Kruppel-type zinc finger protein	3.5
440623	AI935016	Hs.216639	ESTs	3.5
455838	BE145808		gb:MR0-HT0208-101299-103-f11 HT0208 Homo	3.5
458771	AW295151	Hs.163812	ESTs	3.5
442942	AW167087	Hs.131562	ESTs	3.5
436550	Z50158	Hs.270235	ESTs, Weakly similar to MMHUB1 laminin b	3.5
418849	AW474547	Hs.53565	Homo sapiens PIG-M mRNA for mannosyltran	3.5
424420	BE814743	Hs.146688	prostaglandin E synthase	3.5
430916	AW505021	Hs.88414	BTB and CNC homology 1, basic leucine zi	3.5
432030	AI908400	Hs.143789	ESTs	3.5
439405	AF086224	Hs.55238	ESTs	3.5
405917	NA		C17000675:gi|7290703|gb|AAF46150.1| (AE0	3.5
452727	AW993582	Hs.176220	ESTs	3.5
426320	W47595	Hs.169300	transforming growth factor, beta 2	3.4
421070	AA283185	Hs.19327	ESTs	3.4
424625	AW904466	Hs.321197	PDZ domain protein (Drosophila InaD-like	3.4
428508	BE252383	Hs.184668	SBBI31 protein	3.4
455651	BE064962		gb:RC1-BT0313-130400-016-c02 BT0313 Homo	3.4
410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma	3.4
447754	AW073310	Hs.163533	Homo sapiens cDNA FLJ14142 fis, clone MA	3.4
418636	AW749855		gb:OV4-BT0534-281299-053-c05 BT0534 Homo	3.4
404097	NA		C5000242*:gi|9369379|gb|AAF87128.1|AC006	3.4
434205	AF119861	Hs.283032	hypothetical protein PRO2015	3.4
421072	AI215069	Hs.89113	ESTs	3.4
402421	NA		C1001578*:gi|6759903|gb|AAF28099.1| (AF1	3.4
405248	NA		Target Exon	3.4
407638	AJ404672	Hs.334483	hypothetical protein FLJ23571	3.4
403000	BE247275	Hs.151787	U5 snRNP-specific protein, 116 kD	3.4

433393	AF038564	Hs.98074	itchy (mouse homolog) E3 ubiquitin prote	3.4
432239	X81334	Hs.2936	matrix metalloproteinase 13 (collagenase	3.4
458747	BE618395	Hs.257391	hypothetical protein DKFZp761J1523	3.4
442082	R41823	Hs.7413	ESTs; calsyntenin-2	3.4
417974	AA210765		gb:zr90c06.r1 NCI_CGAP_GCB1 Homo sapiens	3.4
446002	AI346468	Hs.145789	ESTs	3.4
448995	AI613276	Hs.5662	guanine nucleotide binding protein (G pr	3.4
436007	AI247718	Hs.232168	ESTs	3.4
424698	AA184366	Hs.151973	hypothetical protein FLJ23511	3.4
435202	AI971313	Hs.170204	KIAA0551 protein	3.4
410467	AF102546	Hs.83931	dachshund (Drosophila) homolog	3.3
405460	NA		Target Exon	3.3
441826	AW503603	Hs.129915	phosphotriesterase related	3.3
453472	AL037925		gb:DKFZp564M037_r1 564 (synonym: hfbr2)	3.3
447078	AW885727	Hs.301570	ESTs	3.3
441690	R81733	Hs.33106	ESTs	3.3
420092	AA814043	Hs.88045	ESTs	3.3
418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	3.3
408908	BE296227	Hs.250822	serine/threonine kinase 15	3.3
414737	AI160386	Hs.125087	ESTs	3.3
449650	AF055575	Hs.23838	calcium channel, voltage-dependent, L ty	3.3
418912	NM_000685	Hs.89472	angiotensin receptor 1	3.3
436405	AA160079	Hs.172932	Homo sapiens mRNA for partial 3'UTR, seq	3.3
453911	AW503857	Hs.4007	Sarcolemmal-associated protein	3.3
409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	3.3
429548	AW138872	Hs.135288	ESTs	3.3
420807	AA280627	Hs.57846	ESTs	3.3
409695	AA296981		gb:EST112514 Adrenal gland tumor Homo sa	3.3
445189	AI936450	Hs.147482	ESTs	3.3
402892	NA		Target Exon	3.3
426681	AA994896	Hs.22514	ESTs	3.3
458722	AA741545	Hs.282832	ESTs, Weakly similar to T24961 hypothet	3.3
409430	R21945	Hs.166975	splicing factor, arginine/serine-rich 5	3.3
443194	AI954968	Hs.279009	matrix Gla protein	3.3
445432	AV653771		gb:AV653771 GLC Homo sapiens cDNA clone	3.3
410908	AA121686	Hs.10592	ESTs	3.3
406151	NA		Target Exon	3.3
436461	AW511956	Hs.293261	ESTs	3.3
411171	AW820260		gb:QV2-ST0296-150200-040-c10 ST0296 Homo	3.3
432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	3.3
439310	AF086120	Hs.102793	ESTs	3.3
401575	NA		Target Exon	3.3
420900	AL045833	Hs.44269	ESTs	3.3
445628	AI344166	Hs.155743	ESTs	3.3
448243	AW369771	Hs.52820	integrin, beta 8	3.3
445102	AW204610	Hs.22270	ESTs	3.3
442118	AA976718	Hs.202242	ESTs	3.3
416783	AA206188	Hs.79889	monocyte to macrophage differentiation-a	3.3
435039	AW043921	Hs.130526	ESTs	3.3
451474	T70874	Hs.207636	ESTs	3.2
442559	T10213	Hs.159993	gycosyltransferase	3.2
453921	AI824009	Hs.44577	ESTs	3.2
420038	R60336	Hs.52792	Homo sapiens mRNA; cDNA DKFZp58611823 (f	3.2
435627	W88774	Hs.118370	ESTs	3.2
411598	BE336854	Hs.70937	H3 histone family, member A	3.2
446733	AA863360	Hs.26040	ESTs, Weakly similar to fatty acid omega	3.2
410153	BE311926	Hs.15830	hypothetical protein FLJ12691	3.2
403637	NA		C3001108*:gi|10047201|db|BAB13394.1| (A	3.2
405547			NM_018833*:Homo sapiens transporter 2, A	3.2
427878	C05766	Hs.181022	CGI-07 protein	3.2
451871	AI821005	Hs.118599	ESTs	3.2
410313	R10305	Hs.185683	ESTs	3.2
416858	N27833	Hs.269028	ESTs, Weakly similar to I38022 hypothet	3.2
449490	AI852777	Hs.197069	ESTs	3.2
450506	NM_004460	Hs.418	fibroblast activation protein, alpha	3.2
440684	AI253123	Hs.127356	ESTs, Highly similar to S21424 nestin (H	3.2
459055	N23235	Hs.30567	ESTs, Weakly similar to B34087 hypothet	3.2

452190	H26735	Hs.91668	Homo sapiens clone PP1498 unknown mRNA	3.2
430965	AA489732	Hs.154918	ESTs	3.2
405394			Target Exon	3.2
424693	BE169810	Hs.47557	ESTs	3.2
454265	H03556	Hs.300949	ESTs, Weakly similar to thyroid hormone	3.2
437687	AA765917	Hs.122840	ESTs	3.2
426372	AK000684	Hs.183887	hypothetical protein FLJ22104	3.2
414083	AL121282	Hs.257786	ESTs	3.2
411670	AW856552		gb:RC1-CT0294-080100-012-e04 CT0294 Homo	3.2
416283	NM_005429	Hs.79141	vascular endothelial growth factor C	3.2
437488	AA758239	Hs.180330	ESTs	3.2
428398	AI249368	Hs.98558	ESTs	3.2
452042	H38857	Hs.243901	Homo sapiens cDNA FLJ20738 fis, clone HE	3.2
421477	AI904743	Hs.104650	hypothetical protein FLJ10292	3.2
438078	AI016377	Hs.131693	ESTs	3.2
448816	AB033052	Hs.22151	KIAA1226 protein	3.2
419519	AI198719	Hs.176378	ESTs	3.2
404580			NM_014112*:Homo sapiens trichorhinophala	3.2
447048	AA326187	Hs.17170	G protein-coupled receptor 4	3.2
457473	AW974903	Hs.291231	ESTs	3.1
429838	AW904907	Hs.30732	hypothetical protein FLJ13409; KIAA1711	3.1
459702	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	3.1
400195	NA		NM_007057*:Homo sapiens ZW10 interactor	3.1
417860	AW408557	Hs.235498	hypothetical protein FLJ14075	3.1
417995	AW974175	Hs.188751	ESTs, Weakly similar to MAPB_HUMAN MICRO	3.1
422589	AA312735	Hs.30512	Homo sapiens mRNA for KIAA0556 protein,	3.1
435870	AA701327	Hs.17949	ESTs	3.1
440801	AA906366	Hs.190535	ESTs	3.1
426274	D38122	Hs.2007	tumor necrosis factor (ligand) superfami	3.1
423728	AW891294	Hs.132136	solute carrier family 4, sodium bicarbon	3.1
439677	R82331	Hs.164599	ESTs	3.1
452834	AI838627	Hs.105685	KIAA1688 protein	3.1
431349	AA503653	Hs.156942	ESTs, Moderately similar to ALU2_HUMAN A	3.1
417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	3.1
430264	AA470519		gb:nc71f10.s1 NCI_CGAP_Pr1 Homo sapiens	3.1
418827	BE327311	Hs.47166	HT021	3.1
410835	AW806906		gb:QV4-ST0023-160400-172-d12 ST0023 Homo	3.1
426269	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (f	3.1
405336	NA		Target Exon	3.1
437783	AI683150	Hs.201550	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.1
440931	AI583052	Hs.270058	ESTs	3.1
455945	BE160636		gb:PM1-HT0422-291299-002-c08 HT0422 Homo	3.1
430437	AI768801	Hs.189943	Homo sapiens cDNA FLJ13569 fis, clone PL	3.1
405848	NA		Target Exon	3.1
455685	BE066976		gb:PM0-BT0340-211299-003-c12 BT0340 Homo	3.1
406970	M29994		gb:Human alpha-I spectrin gene, exon 12.	3.1
409602	W26713	Hs.256972	ESTs	3.1
423518	D45027	Hs.129732	R3H domain (binds single-stranded nucleI	3.1
425653	AI065104	Hs.249718	ESTs, Weakly similar to A46010 X-linked	3.1
426326	BE165753	Hs.250528	Homo sapiens, clone IMAGE:4098694, mRNA,	3.1
433805	AA706910	Hs.112742	ESTs	3.1
437152	AL050027		gb:Homo sapiens mRNA; cDNA DKFZp566C03243.1	
448602	AI541305	Hs.48778	niban protein	3.1
452844	AW407181	Hs.218377	Homo sapiens cDNA FLJ11927 fis, clone HE	3.1
407366	AF026942		gb:Homo sapiens clg33 mRNA, partial sequ	3.1
408254	AW807227		gb:MR4-ST0062-180200-001-e10 ST0062 Homo	3.1
424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (40	3.1
416790	R83066	Hs.7043	succinate-CoA ligase, GDP-forming, alpha	3.1
420020	BE295866	Hs.94382	adenosine kinase	3.1
426119	W94997	Hs.189917	ESTs	3.1
426968	U07816	Hs.173034	amphiphysin (Stiff-Mann syndrome with br	3.1
457421	AL117431	Hs.112165	Homo sapiens cDNA FLJ12188 fis, clone MA	3.1
453403	BE466639	Hs.61779	Homo sapiens cDNA FLJ13591 fis, clone PL	3.1
454141	AW138413	Hs.139336	ATP-binding cassette, sub-family C (CFTR	3.1
426650	AA382814		gb:EST96097 Testis I Homo sapiens cDNA 5	3.1
450865	AI248013	Hs.106532	ESTs, Weakly similar to I38588 reverse t	3.1
407993	AW135274	Hs.12433	ESTs	3.1

446466	H38026	Hs.308	arrestin 3, retinal (X-arrestin)	3.1
457688	BE219794	Hs.293471	ESTs	3.1
420058	AK001423	Hs.94694	Homo sapiens cDNA FLJ10561 fis, clone NT	3.0
409248	AB033035	Hs.51965	KIAA1209 protein	3.0
452747	BE153855	Hs.81460	Ig superfamily receptor LNIR	3.0
418926	AA232658	Hs.105794	UDP-glucose:glycoprotein glucosyltransfe	3.0
419346	AI830417	Hs.44143	polybromo 1	3.0
429826	N93266	Hs.40747	ESTs	3.0
435147	AL133731	Hs.4774	Homo sapiens mRNA; cDNA DKFZp781C1712 (f	3.0
420139	NM_005357	Hs.95351	lipase, hormone-sensitive	3.0
405609	NA		ENSP00000241065*:CDNA	3.0
404274			NM_002944*:Homo sapiens v-ros avian UR2	3.0
449777	AI971362	Hs.231945	ESTs	3.0
415459	H07118	Hs.6099	ESTs	3.0
415245	N59650	Hs.27252	ESTs	3.0
406291	NA		Target Exon	3.0
414210	BE383592		gb:601297871F1 NIH_MGC_19 Homo sapiens c	3.0
432055	AW972359	Hs.293334	ESTs	3.0
442246	AI791988	Hs.129115	ESTs	3.0
451353	N21043	Hs.42932	ESTs	3.0
451177	AI969716	Hs.13034	ESTs	3.0
418026	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte	3.0
401326	NA		C10000447*:gi|1168375|sp|P43467|AGA1_PED	3.0
409920	BE169746	Hs.12504	likely ortholog of mouse Arkadia	3.0
432887	AI926047	Hs.162859	ESTs	3.0
411789	AF245505	Hs.72157	DKFZP564I1922 protein	3.0
401045			C11001883*:gi|6753278|ref|NP_033938.1| c	3.0
432162	AA584082	Hs.272798	hypothetical protein FLJ20413	3.0
434627	AI221894	Hs.39311	ESTs	3.0
442611	BE077155	Hs.177537	hypothetical protein DKFZp781B1514	3.0
425477	AW958879	Hs.270535	ESTs	3.0
457183	H91882	Hs.118569	Dvl-binding protein IDAX (inhibition of	3.0
433014	NM_014711	Hs.279912	KIAA0419 gene product	3.0
415542	R13474	Hs.290263	ESTs, Weakly similar to I38022 hypotheti	3.0
416173	R52782		gb:yg99d09.r1 Soares infant brain 1NIB H	3.0
408155	AB014528	Hs.43133	KIAA0628 gene product	3.0
453913	AW004683	Hs.78934	mutS (E. coli) homolog 2 (colon cancer,	3.0
435495	AI754212	Hs.21951	Homo sapiens Xq pseudoautosomal region;	3.0
423629	AW021173	Hs.18612	Homo sapiens cDNA: FLJ21909 fis, clone H	3.0
411836	AW901879	Hs.314453	ESTs	3.0
415030	D31118	Hs.191735	hypothetical protein MGC10520	3.0
419606	AW294795	Hs.198529	ESTs	3.0
440310	AA878939	Hs.125406	ESTs	3.0
443608	AI375957	Hs.289074	F-box only protein 22	3.0
414140	AA281279	Hs.23317	hypothetical protein FLJ14681	3.0
444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote	3.0
435393	AA701259	Hs.189299	ESTs	3.0
454071	AI041793	Hs.42502	ESTs	3.0
448922	BE175605		gb:RC5-HT0580-100500-022-H07 HT0580 Homo	3.0
446062	AW295923	Hs.255472	KIAA1843 protein	3.0
427711	M31659	Hs.180408	solute carrier family 25 (mitochondrial	3.0
450382	AA397658	Hs.60257	Homo sapiens cDNA FLJ13598 fis, clone PL	3.0
424868	W01938	Hs.337243	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.9
433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	2.9
420802	U22376	Hs.1334	v-myb avian myeloblastosis viral oncogen	2.9
445625	BE246743	Hs.288529	hypothetical protein FLJ22635	2.9
403677	NA		C4001462gi|4887715|gb|AAA79329.2| (L088	2.9
411093	BE067650		gb:MR4-BT0358-090300-003-e01 BT0358 Homo	2.9
435255	W87434	Hs.106015	ESTs, Moderately similar to ALU1_HUMAN A	2.9
443127	BE568102	Hs.180312	mitochondrial ribosomal protein S16	2.9
448104	AI674818	Hs.316433	Homo sapiens cDNA FLJ11375 fis, clone HE	2.9
427315	AA179949	Hs.175583	Homo sapiens mRNA; cDNA DKFZp564N0763 (f	2.9
430414	AW365665	Hs.120388	ESTs	2.9
423500	AI633559	Hs.310359	ESTs	2.9
458562	N34128	Hs.145268	ESTs	2.9
402109	NA		Target Exon	2.9
429529	BE501732	Hs.30622	Homo sapiens cDNA FLJ13010 fis, clone NT	2.9

442295	AI827248	Hs.224398	Homo sapiens cDNA FLJ11469 fis, clone HE	2.9
419752	AA249573	Hs.152618	ESTs, Moderately similar to ZN91_HUMAN Z	2.9
404721			NM_005596*:Homo sapiens nuclear factor I	2.9
445107	AI208121	Hs.147313	ESTs, Weakly similar to I38022 hypotheti	2.9
401987			NM_002737*:Homo sapiens protein kinase C	2.9
430566	AA481282	Hs.190149	ESTs	2.9
444517	AI939339	Hs.146883	ESTs	2.9
445563	AW873606	Hs.149006	ESTs	2.9
427691	AW194426	Hs.20726	ESTs	2.9
456581	AI868634	Hs.246358	ESTs, Weakly similar to T32250 hypotheti	2.9
401458			Target Exon	2.9
421039	NM_003478	Hs.101299	cullin 5	2.9
459504	BE514127		gb:601315974F1 NIH_MGC_8 Homo sapiens cD	2.9
424982	NM_012288	Hs.153954	TRAM-like protein	2.9
409617	BE003760	Hs.55209	Homo sapiens mRNA; cDNA DKFZp434K0514 (f	2.9
416931	D45371	Hs.80485	adipose most abundant gene transcript 1	2.9
413221	BE161151		gb:PM0-HT0425-141299-001-F08 HT0425 Homo	2.9
409732	NM_016122	Hs.56148	NY-REN-58 antigen	2.9
433687	AA743991		gb:my57g01.s1 NCI_CGAP_Pr18 Homo sapiens	2.9
434340	AI193043	Hs.128685	ESTs, Weakly similar to T17226 hypotheti	2.9
454529	Z45439	Hs.270425	ESTs	2.9
421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	2.9
452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisi	2.9
457402	AW452648	Hs.149342	activation-induced cytidine deaminase	2.9
449051	AW861400	Hs.333526	HER2 receptor tyrosine kinase (c-erb-b2,	2.9
408761	AA057264	Hs.238938	ESTs, Weakly similar to (define not ava	2.9
401093			C12000586*:gi|8330167|db|BAA88477.1| (A	2.9
435081	AI651474	Hs.163944	ESTs	2.9
447985	AI681475	Hs.200949	ESTs	2.9
449340	AW235786	Hs.195359	hypothetical protein MGC10954	2.9
426384	AI472078	Hs.303662	ESTs	2.9
411905	BE265067		gb:601193893F1 NIH_MGC_7 Homo sapiens cD	2.9
405953	NA		Target Exon	2.8
420854	AW296927		gb:UI-H-BW0-ajc-c-07-0-UI.s1 NCI_CGAP_Su	2.8
434265	AA846811	Hs.130554	Homo sapiens cDNA: FLJ23089 fis, clone L	2.8
428365	AA295331	Hs.183861	Homo sapiens cDNA FLJ20042 fis, clone CO	2.8
442861	AA243837	Hs.57787	ESTs	2.8
448337	AW206453	Hs.3782	ESTs	2.8
452554	AW452434	Hs.58006	ESTs, Weakly similar to ALU5_HUMAN ALU S	2.8
412248	BE176480		gb:RC3-HT0585-160300-022-c02 HT0585 Homo	2.8
449450	AL039852	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN A	2.8
434757	AI038997	Hs.132921	ESTs	2.8
409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	2.8
454545	AW806899		gb:QV4-ST0023-160400-172-c12 ST0023 Homo	2.8
439842	AI910898	Hs.132413	ESTs	2.8
428479	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to	2.8
424800	AL035588	Hs.153203	MyoD family inhibitor	2.8
411086	BE070800		gb:RC3-BT0502-251199-011-c07 BT0502 Homo	2.8
400250	NA		Eos Control	2.8
449168	NM_016206	Hs.23142	colon carcinoma related protein	2.8
456482	AA485224		gb:as41b12.s1 NCI_CGAP_GCB1 Homo sapiens	2.8
426044	AA502490	Hs.336695	ESTs	2.8
431854	AA383550	Hs.271699	polymerase (DNA directed) iota	2.8
405873	NA		Target Exon	2.8
440400	AA994364	Hs.125594	ESTs, Weakly similar to T25472 hypotheti	2.8
458265	AI075375	Hs.128193	ESTs, Weakly similar to IRX2_HUMAN IROQU	2.8
413708	BE158791		gb:IL2-HT0397-091299-025-D02 HT0397 Homo	2.8
423739	AA398155	Hs.97600	ESTs	2.8
424408	AI754813	Hs.148428	collagen, type V, alpha 1	2.8
453096	AW294831	Hs.11325	ESTs	2.8
421825	AA298758	Hs.183747	ESTs, Moderately similar to CALB_HUMAN C	2.8
417742	R64719		gb:EST22d11 WATM1 Homo sapiens cDNA clon	2.8
402765			C1003621*:gi|12407405|gb|AAG53491.1|AF22	2.8
444378	R41339	Hs.12569	ESTs	2.8
419172	AW338825	Hs.22120	ESTs	2.8
401497			Target Exon	2.8
402376			C19000763*:gi|1363912|pir|JC4296 dng f	2.8

405041	NA		C3001706*:gi|1345652|sp|P15989|CA38_CHIC	2.8
408758	NM_003686	Hs.47504	exonuclease 1	2.8
431917	D16181	Hs.2868	peripheral myelin protein 2	2.8
437583	AA761190	Hs.244627	ESTs	2.8
453737	AA744882	Hs.194293	ESTs, Weakly similar to I54374 gene NF2	2.8
458094	AF086325		gb:Homo sapiens full length insert cDNA	2.8
401283	NA		Target Exon	2.8
410784	AW803201		gb:IL2-UM0077-070500-080-E06 UM0077 Homo	2.8
417601	NM_014735	Hs.82292	KIAA0215 gene product	2.8
418236	AW994005	Hs.337534	ESTs	2.8
435532	AW291488	Hs.117305	Homo sapiens, clone IMAGE:3682908, mRNA	2.8
454714	AW815098		gb:QV4-ST0212-091199-023-f10 ST0212 Homo	2.8
418629	BE247550	Hs.86859	growth factor receptor-bound protein 7	2.8
442101	AI551930	Hs.135684	ESTs	2.8
405080	AK000375	Hs.88820	HDCMC28P protein	2.8
414681	T97401	Hs.21929	ESTs	2.8
425589	AI850633	Hs.143688	Homo sapiens cDNA: FLJ23031 fis, clone L	2.8
429638	AI916662	Hs.211577	kinectin 1 (kinesin receptor)	2.7
428824	W23624	Hs.173059	ESTs	2.7
421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	2.7
414596	BE386870		gb:601275271F1 NIH_MGC_20 Homo sapiens c	2.7
440868	R79707	Hs.263339	ESTs, Moderately similar to I38022 hypot	2.7
452943	BE247449	Hs.31082	hypothetical protein FLJ10525	2.7
443772	AV646449	Hs.282872	ESTs	2.7
432361	AI378562	Hs.159585	ESTs	2.7
430375	AW371048	Hs.93758	H4 histone family, member H	2.7
406504	NA		C5000558:gi|4504675|ref|NP_002175.1| int	2.7
423279	AW959861	Hs.290943	ESTs	2.7
424871	NM_004525	Hs.153595	low density lipoprotein-related protein	2.7
453619	H87648	Hs.33922	Homo sapiens, clone MGC:9084, mRNA, comp	2.7
423981	D13666	Hs.136348	osteoblast specific factor 2 (fasciclin	2.7
422156	N34524		gb:yy56d10.s1 Soares_multiple_sclerosis_	2.7
415752	BE314524	Hs.78776	putative transmembrane protein	2.7
419987	NM_005014	Hs.94070	osteomodulin	2.7
406182	NA		Target Exon	2.7
416495	X69970	Hs.79350	RYK receptor-like tyrosine kinase	2.7
444701	AI916512	Hs.198394	ESTs	2.7
408171	AA301228	Hs.43299	hypothetical protein FLJ12890	2.7
430153	AW988128	Hs.336679	ESTs	2.7
413383	AA128978	Hs.154708	hypothetical protein FLJ14817	2.7
414831	M31158	Hs.77439	protein kinase, cAMP-dependent, regulato	2.7
413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	2.7
433132	AB026264	Hs.284245	hypothetical protein IMPACT	2.7
437030	AA742577	Hs.303781	EST	2.7
439031	AF075079		gb:Homo sapiens full length insert cDNA	2.7
449532	W74653	Hs.271593	ESTs, Moderately similar to A47582 B-cel	2.7
406153			Target Exon	2.7
406625	Y13647	Hs.119597	stearoyl-CoA desaturase (delta-9-desatur	2.7
444698	AI188139	Hs.147050	ESTs	2.7
432326	AI572739	Hs.195471	6-phosphofructo-2-kinase/fructose-2,6-bi	2.7
429628	H09604	Hs.13268	ESTs	2.7
420149	AA255920	Hs.88095	ESTs	2.7
431207	AA495925	Hs.9394	ESTs	2.7
438394	BE379823	Hs.27693	peptidylprolyl isomerase (cyclophilin)-l	2.7
443304	AI050073	Hs.135338	ESTs	2.7
427660	AI741320	Hs.114121	Homo sapiens cDNA: FLJ23228 fis, clone C	2.7
408460	AA054726	Hs.265574	ESTs	2.7
416515	N91716	Hs.194140	ESTs, Weakly similar to I38022 hypotheti	2.7
429922	Z97630	Hs.226117	H1 histone family, member 0	2.7
418203	X54942	Hs.83758	CDC28 protein kinase 2	2.7
439509	AF086332	Hs.58314	ESTs	2.7
402184	NA		ENSP00000245238*:cDNA FLJ10922 fis, clon	2.7
450498	AW449251	Hs.257131	ESTs	2.7
451963	AI825440	Hs.224952	ESTs	2.7
457938	AI373838	Hs.133900	ESTs	2.7
441541	AA938683	Hs.199828	ESTs	2.7
441111	AI806867	Hs.126594	ESTs	2.7

423020	AA383092	Hs.1608	replication protein A3 (14kD)	2.7
445354	AV653485	Hs.6390	Homo sapiens clone FLB3344 PRO0845 mRNA,	2.7
427961	AW293165	Hs.143134	ESTs	2.7
410889	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalos	2.7
445234	AW137636	Hs.146059	ESTs	2.7
413903	AA496493	Hs.23136	ESTs	2.7
406069	NA		Target Exon	2.7
447410	AI470235	Hs.172698	EST	2.7
401256	NA		NM_024089*:Homo sapiens hypothetical pro	2.7
415139	AW975942	Hs.46524	ESTs	2.7
420218	AW958037	Hs.286	ribosomal protein L4	2.7
455511	BE144762		gb:CM0-HT0180-041099-085-b04 HT0180 Homo	2.7
438825	BE327427	Hs.79953	ESTs	2.6
409564	AA045857	Hs.54943	fracture callus 1 (rat) homolog	2.6
452837	AL121053	Hs.5534	Homo sapiens cDNA FLJ12961 fis, clone NT	2.6
434876	AF160477	Hs.61460	Ig superfamily receptor LNIR	2.6
421565	AK001122	Hs.105859	hypothetical protein FLJ10260	2.6
453279	AW893940	Hs.59698	ESTs	2.6
430785	Z30201		gb:HHEA22G Atrium cDNA library Human hea	2.6
456966	D38299	Hs.170917	prostaglandin E receptor 3 (subtype EP3)	2.6
433068	NM_006456	Hs.288215	sialyltransferase	2.6
421952	AA300900	Hs.98849	ESTs, Moderately similar to AF161511 1 H	2.6
429208	AA447990	Hs.190478	ESTs	2.6
430733	AW975920	Hs.283361	ESTs	2.6
441720	AI346487	Hs.28739	ESTs	2.6
418986	AI123555	Hs.81798	ESTs	2.6
432481	AW451645	Hs.151504	Homo sapiens cDNA FLJ11973 fis, clone HE	2.6
434338	AW754311		gb:CM1-CT0337-141299-068-f07 CT0337 Homo	2.6
417061	AI675944	Hs.188691	Homo sapiens cDNA FLJ12033 fis, clone HE	2.6
410530	M25809	Hs.84173	ATPase, H transporting, lysosomal (vacuo	2.6
456872	AK002016	Hs.114727	Homo sapiens, clone MGC:16327, mRNA, com	2.6
425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	2.6
408868	AW292286	Hs.255058	ESTs	2.6
451531	AA018311	Hs.114762	ESTs	2.6
405822			Target Exon	2.6
418301	AW976201	Hs.53913	hypothetical protein FLJ10252	2.6
417315	AI080042	Hs.336901	ribosomal protein G24	2.6
434699	AA843687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HE	2.6
443204	AW205878	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT	2.6
405638			Target Exon	2.6
452542	AW812256		gb:RC0-ST0174-191099-031-e07 ST0174 Homo	2.6
403943			C5000355:gi|4503225|ref|NP_000765.1| cyt	2.6
404535	Z25884	Hs.121483	chloride channel 1 , skeletal muscle (Th	2.6
402800	NA		Target Exon	2.6
449144	AI989503	Hs.233405	ESTs	2.6
454934	AW846080	Hs.314324	ESTs	2.6
424717	H03754	Hs.152213	wingless-type MMTV integration site fami	2.6
428303	AW974476	Hs.183601	regulator of G-protein signalling 16	2.6
427970	AA418187	Hs.330515	ESTs	2.6
450638	AK001826	Hs.25245	hypothetical protein FLJ11269	2.6
453034	BE246010	Hs.271468	Homo sapiens mRNA for FLJ00038 protein,	2.6
455097	AW855802		gb:RC1-CT0279-170200-023-d08 CT0279 Homo	2.6
427317	AB028955	Hs.175780	KIAA1032 protein	2.6
408875	NM_015434	Hs.48604	DKFZP434B168 protein	2.6
427510	Z47542	Hs.179312	small nuclear RNA activating complex, po	2.6
423201	NM_000163	Hs.125180	growth hormone receptor	2.6
408271			Target Exon	2.6
442696	BE566982	Hs.7063	Homo sapiens cDNA: FLJ20913 fis, clone A	2.6
454018	AW016892	Hs.100855	ESTs	2.6
435420	AI928513	Hs.59203	ESTs	2.6
434398	AA121098	Hs.3838	serum-inducible kinase	2.6
455708	BE069326		gb:QV3-BT0361-170100-080-g03 BT0361 Homo	2.6
439347	W24320	Hs.102941	Homo sapiens cDNA: FLJ21531 fis, clone C	2.6
407523	X64984		gb:H.sapiens mRNA HTPCRX10 for olfactory	2.6
425101	AA830431	Hs.180811	ESTs	2.6
435153	AA668763	Hs.291939	ESTs	2.6
409139	AI681917	Hs.3321	ESTs, Highly similar to IRX1_HUMAN IROQU	2.6

455100	BE160198		gb:QV1-HT0413-010200-059-h03 HT0413 Homo	2.6
414612	BE274552	Hs.76578	protein inhibitor of activated STAT3	2.6
440283	AI732892	Hs.190489	ESTs	2.6
423025	AA831267	Hs.12244	hypothetical protein FLJ20097	2.6
431473	AA825686	Hs.321176	ESTs, Weakly similar to S65824 reverse t	2.6
404440			NM_021048:Homo sapiens melanoma antigen,	2.6
403388	NA		C3001398*:gi|12248917|dbj|BAB20375.1| (A	2.6
403775	NA		Target Exon	2.6
405037	NA		NM_021628*:Homo sapiens arachidonate lip	2.6
407447	AF290544		gb:Homo sapiens aminopeptidase mRNA, par	2.6
420952	AA282067	Hs.68972	ESTs, Moderately similar to A46010 X-lin	2.6
435447	AI872932		gb:wm72e03.x1 NCI_CGAP_Ut2 Homo sapiens	2.6
440202	AW516211	Hs.125300	ring finger protein 21, interferon-respo	2.6
445854	AI702885	Hs.145568	ESTs	2.6
421247	BE391727	Hs.102910	general transcription factor IIH, polype	2.6
414870	N72264	Hs.300670	KIAA1204 protein	2.6
457411	AW085961	Hs.130093	ESTs	2.6
424676	Y08565	Hs.151678	UDP-N-acetyl-alpha-D-galactosamine:polyp	2.6
404443			C8001428*:gi|6572242|emb|CAB62951.1| (Z9	2.6
452268	NM_003512	Hs.28777	H2A histone family, member L	2.6
430832	AI073913	Hs.100686	ESTs, Weakly similar to JE0350 Anterior	2.6
444779	AI192105	Hs.147170	ESTs	2.6
408633	AW963372	Hs.46677	PRO2000 protein	2.6
459089	F13036	Hs.27373	Homo sapiens mRNA; cDNA DKFZp564O1763 (f	2.6
447197	R36075		gb:yh88b01.s1 Soares placenta Nb2HP Homo	2.6
454111	AW081681	Hs.269064	ESTs, Weakly similar to T42689 hypotheti	2.6
411165	NM_000169	Hs.69089	galactosidase, alpha	2.6
406922	S70284		gb:stearoyl-CoA desaturase (human, adipo	2.6
456045	H52943	Hs.154188	ESTs	2.6
413111	BE065837		gb:RC2-BT0318-110100-012-g12 BT0318 Homo	2.6
423123	NM_012247	Hs.124027	SELENOPHOSPHATE SYNTHETASE ; Human selen	2.6
432201	AI538613	Hs.298241	Transmembrane protease, serine 3	2.5
427032	AF012023	Hs.173274	integrin cytoplasmic domain-associated p	2.5
445417	AK001058	Hs.12680	Homo sapiens cDNA FLJ10196 fis, clone HE	2.5
422225	BE245652	Hs.118281	zinc finger protein 268	2.5
428330	L22524	Hs.2256	matrix metalloproteinase 7 (MMP7; uterin	2.5
410011	AB020641	Hs.57856	PFTAIRE protein kinase 1	2.5
428310	NM_000909	Hs.169268	neuropeptide Y receptor Y1	2.5
419589	AW973708	Hs.201925	Homo sapiens cDNA FLJ13446 fis, clone PL	2.5
437770	AA767881	Hs.122697	ESTs	2.5
442818	AK001741	Hs.8739	hypothetical protein FLJ10879	2.5
414251	AL042306	Hs.97689	VASA protein	2.5
428301	AW628666	Hs.98440	ESTs, Weakly similar to I38022 hypotheti	2.5
431956	AK002032	Hs.272245	Homo sapiens cDNA FLJ11170 fis, clone PL	2.5
455732	BE080908		gb:QV1-BT0631-280200-084-h07 BT0631 Homo	2.5
458624	AI362790	Hs.278639	KIAA1684 protein; likely homolog of mous	2.5
428257	BE394723	Hs.275243	S100 calcium-binding protein A6 (calcycl	2.5
418054	NM_002318	Hs.83354	lysyl oxidase-like 2	2.5
458652	AW375610	Hs.117102	hypothetical protein FLJ13048 similar to	2.5
458012	AI424899	Hs.188211	ESTs	2.5
422996	BE091089		gb:PM4-BT0724-130400-006-c07 BT0724 Homo	2.5
410804	U64820	Hs.66521	Machado-Joseph disease (spinocerebellar	2.5
457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	2.5
440029	AW089705	Hs.293711	ESTs, Weakly similar to S84329 probable	2.5
448141	AI471598	Hs.197531	ESTs	2.5
409163	AA065081		gb:zm13a03.s1 Stratagene pancreas (93720	2.5
431385	BE178536	Hs.11090	membrane-spanning 4-domains, subfamily A	2.5
414569	AF109298	Hs.118258	prostate cancer associated protein 1	2.5
439983	AW247529	Hs.6793	platelet-activating factor acetylhydrola	2.5
455935	BE158687		gb:CM0-HT0395-280100-169-b09 HT0395 Homo	2.5
425025	AW953168	Hs.12407	ESTs	2.5
415589	AA652687	Hs.96151	Human DNA sequence from clone RP5-1103G7	2.5
404826			Target Exon	2.5
422938	NM_001809	Hs.1594	centromere protein A (17kD)	2.5
421991	NM_014918	Hs.110488	KIAA0990 protein	2.5
417404	NM_007350	Hs.82101	pleckstrin homology-like domain, family	2.5
448516	AW898595		gb:RC1-NN0073-260400-011-g09 NN0073 Homo	2.5

403356	NA		ENSP00000251525*:Hypothetical protein KI	2.5
404983			ENSP00000252242*:Keratin, type II cytosk	2.5
418282	AA215535	Hs.98133	ESTs	2.5
427409	AW467143	Hs.135411	actin related protein	2.5
431806	AF186114	Hs.270737	tumor necrosis factor (ligand) superfami	2.5
443357	AW071349	Hs.215937	ESTs	2.5
421246	AW582962	Hs.102897	CGI-47 protein	2.5
439217	AF086041	Hs.42975	ESTs	2.5
400925			Target Exon	2.5
404552	NA		ENSP00000220888*:ZINC FINGER TRANSCRIPTI	2.5
417168	AL133117	Hs.81376	Homo sapiens mRNA; cDNA DKFZp586L1121 (f	2.5
418841	NM_002332	Hs.89137	low density lipoprotein-related protein	2.5
426853	U32974	Hs.172777	baculoviral IAP repeat-containing 4	2.5
427738	NM_000318	Hs.180612	peroxisomal membrane protein 3 (35kD, Ze	2.5
457384	AA501760	Hs.15806	Homo sapiens mRNA; cDNA DKFZp434H2019 (f	2.5
447128	AI271898	Hs.164868	cyclin K	2.5
454693	AW813428		gb:MR3-ST0192-010200-210-c05 ST0192 Homo	2.5
434657	AA641876	Hs.191840	ESTs	2.5
402077	NA		Target Exon	2.5
400289	X07820	Hs.2258	matrix metalloproteinase 10 (MMP10; str	2.5
409723	AW885757	Hs.257862	ESTs	2.5
447020	T27308	Hs.16988	hypothetical protein FLJ11046	2.5
455068	AI807894	Hs.47274	Homo sapiens mRNA; cDNA DKFZp564B176 (fr	2.5
431232	AI024353	Hs.131755	hypothetical protein FLJ14298	2.5
408938	AA059013	Hs.22607	ESTs	2.5
411571	AA122393	Hs.70811	hypothetical protein FLJ20516	2.5
426504	AW162919	Hs.170160	RAB2, member RAS oncogene family-like	2.5
428248	AI126772	Hs.40479	ESTs	2.5
408813	AI580090	Hs.48295	RNA helicase family	2.5
423504	N80077	Hs.24792	chromosome 12 open reading frame 5	2.5
425441	AA449644	Hs.193063	Homo sapiens cDNA FLJ14201 fis, clone NT	2.5
443066	AW297921	Hs.255703	ESTs	2.5
443556	AA256769	Hs.94949	methylmalonyl-CoA epimerase	2.5
428943	AW086180	Hs.37838	ESTs, Weakly similar to KIAA1392 protein	2.5
425320	U29344	Hs.83190	fatty acid synthase	2.5
430388	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 2	2.5
423242	AL039402	Hs.125783	DEME-6 protein	2.5
416241	N52839	Hs.32683	ESTs	2.5
440244	AI743977	Hs.205144	ESTs	2.5
409239	AA740875	Hs.44307	ESTs, Moderately similar to I38022 hypot	2.5
452484	AW500507	Hs.192619	KIAA1600 protein	2.5
410718	AI920783	Hs.191435	ESTs	2.5
408877	AA479033	Hs.130315	ESTs, Weakly similar to A47582 B-cell gr	2.5
445150	AI446747	Hs.338704	olfactory receptor, family 7, subfamily	2.5
407756	AA116021	Hs.38260	ubiquitin specific protease 18	2.5
407633	NM_007069	Hs.37189	similar to rat HREV107	2.5
449754	H00820	Hs.30977	ESTs, Weakly similar to B34087 hypothetl	2.5
419316	AA238255	Hs.298419	ESTs	2.5
429118	H20669	Hs.35406	ESTs, Highly similar to unnamed protein	2.5
440331	AL046412	Hs.202151	ESTs	2.5
449344	AI640355	Hs.312591	ESTs	2.5
459006	AW298631	Hs.27721	Wolf-Hirschhorn syndrome candidate 1-lik	2.5
423165	AI937547	Hs.124915	hypothetical protein MGC2601	2.5
411337	AW837349		gb:QV2-LT0038-270300-108-d12 LT0038 Homo	2.5
438290	AA843719	Hs.122341	ESTs	2.5
406414			C5000506*:gi|124941|sp|P16814|ITA1_RAT I	2.5
424498	AB033043	Hs.149377	hypothetical protein DKFZp761L0424	2.5
443464	BE548446	Hs.5167	Homo sapiens mRNA; cDNA DKFZp434F152 (fr	2.5
424856	AA347746	Hs.9521	ESTs, Weakly similar to ZN43_HUMAN ZINC	2.5
440304	BE159984	Hs.125395	ESTs	2.5
409045	AA635062	Hs.50094	Homo sapiens mRNA; cDNA DKFZp434O0515 (f	2.5
422848	D86983	Hs.118893	Melanoma associated gene	2.5
428819	AL135623	Hs.193914	KIAA0575 gene product	2.5
412520	AA442324	Hs.795	H2A histone family, member O	2.5
430602	D13752	Hs.184927	cytochrome P450, subfamily XIB (steroid	2.5
408031	AA081395	Hs.42173	Homo sapiens cDNA FLJ10366 fis, clone NT	2.5
403133			Target Exon	2.5

413189	BE070231		gb:QV4-BT0407-260100-087-f12 BT0407 Homo	2.5
400346	AB041269	Hs.272263	Homo sapiens mRNA for keratin 19, partia	2.5
435509	AI458679	Hs.181915	ESTs	2.5
458145	AI239457	Hs.130794	ESTs	2.5

TABLE 19A

Table 19A shows the accession numbers for those pkeys lacking unigeneID's for Table 19. For each probeset, we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT number	Accessions
407647	1007366_1	AW860158 AW862385 AW860159 AW862386 AW862341 AW821869 AW821893 AW062660 AW062656
407980	103087_1	AA046309 AI263500 AA046397
408254	1049346_1	AW807227 AW807576 AW807137 AW807157 AW807495 AW807494 AW807417 AW807083 AW845786 AW845801 AW807130 AW807335 AW807081 AW807349 AW807339 AW807164 AW807341 AW807224 AW845903 AW177424 AW807159 AW807123 BE141576 AW807340 AW807334 AW807520 AW807205 AW807505 BE141574 AW807390 AW807395 AW845789 AW807101 AW807089 AW807519 AW807239 AW807509 AW807356 AW807526 AW807098 AW807307 AW807153 AW807295 AW807313 AW807322 AW807265 AW807513 AW807516 AW807166 AW807501 AW807120 AW807168 AW807121 AW807527 AW807151 AW807203 AW807489 AW807511 AW807158 AW845800 AW807507 AW845793 AW845796 AW807298 AW845781 AW807444 AW845871 AW807512 AW807242 AW807141 AW807522 AW807487 AW807514 AW807142 AW807232 AW807379 AW807114 AW807518 AW807199 AW807211 AW807498 AW807086 AW807492 AW807218 AW807082 AW807525 AW807493 AW807523 AW807087 AW845784 AW807037 AW807128 AW807080 AW807118 AW845807 AW807524 AW845803 AW807249 AW845795 AW807160 AW807343 AW807515 AW807233 AW807289 AW177102 AW807352 AW807394 AW177105 AW807176 AW177103 AW845870 AW177099 AW177101 AW807528 AW807338 AW807038 AW177100 AW807411 AW807088 AW845865 AW807226 AW807517 AW807397 AW807303 AW807177 AW807154 AW807138 AW807146 AW807085 AW807521 AW807488 AW807385 AW807355 AW807223 AW807155
409183	110418_1	AA065081 AA075017 AA084791 AA071015 AA081560 AA071459 AA545727 AA083100 AA085366 AA115845 AA075457 AA084704 AA082878 AA075742 AA069162
409695	114876_1	AA296961 AA296889 AA076945 AA077528 AA077497
410534	1207247_1	AW905138 AW753008 R13818 Z43519
410672	1214882_1	AW794600 AW794730
410784	1221005_1	AW803201 BE079700 BE062940
410785	1221055_1	AW803341 AW803265 AW803403 AW803466 AW803402 AW803413 AW803268 AW803396 AW803334 AW803355
410835	1223785_1	AW806906 AW806915 AW866460 AW866475 AW866462 AW866448 AW866372 AW866604
411050	1230330_1	AW814902 BE156656 BE156687 BE156590 BE156441 BE156447
411088	1231500_1	BE070800 AW875226 BE149115
411093	1231970_1	BE067630 AW817053
411111	1232669_1	AW818127 AW818161 R09719
411171	1234393_1	AW820260 AW820332 R94408
411337	1239217_1	AW837349 AW837355 AW882717
411514	1248638_1	AW850178 AW850233 AW850445 AW850446
411670	1253880_1	AW856552 AW881101 AW856574 AW861099 AW881100 AW856573 AW856578 AW856562
411905	1265181_1	BE265067 BE264978 AW875420
412102	1277395_1	H56435 H56572 AW892929
412209	1283610_1	AW901456 AW901450 AW901441
412248	1285000_1	BE176480 AW903298 AW903313
413043	1346556_1	BE158768 BE081699 BE147360 BE147362 BE061666 BE081697 BE061647 BE061678
413111	1349546_1	BE065837 BE065805 BE065799 BE065818 BE065839 BE065831 BE065894 BE065789 BE065792
413189	1352723_1	BE070231 BE070229 BE070255
413221	1353887_1	BE161151 BE162495 BE161002 BE072205 BE160989 BE162482
413499	1373910_1	BE144884 H97942
413708	1384140_1	BE158791 BE158806 BE158748 BE158744 BE158740 BE158739 BE158811 BE158700 BE158741 BE158883 BE158685
414210	1426051_1	BE383592 BE261871
414596	1465004_1	BE386870 Z41986 H08501

414605	1465790_-1	BE390440
415747	155189_1	AA381209 AA381245 AA167683
416173	1574973_1	R52782 R17313 H24192 R19876
417742	1696282_1	R64719 Z44680 R12451
417974	171237_1	AA210785 T95700 H94407
418636	177402_1	AW749855 AA225995 AW750208 AW750206
419536	185688_1	AA603305 AA244095 AA244163
420854	197072_1	AW296927 AI684514 AI263188 AA281079
422156	212379_1	N34524 AA305071 AW954803 AA502335 AI433430 AI203597 AW026870 AW265323 AW850787 AA317554 AW993843 AW835572 AW385512 AI334966 W32951 H62658 H53902 R88904 AW835732
422996	223666_1	BE091089 BE091123 AA319959
423833	232451_1	AW503329 N46810 AA331571
423841	232507_1	AW753967 AA370795 AA331630 AW962550
423945	233568_1	AA410943 AW948953 AA334202 AA332882
425201	247933_1	AA352111 AW962247 AA429695
426650	270283_1	AA382814 AA402411 AA412355
426878	273265_1	BE069341 AW748403 AL044891 AI908240 AA393080
430284	315008_1	AA470519 BE303010 BE302954 BE384120
430785	323488_1	Z30201 AA486132 T72025
431676	336411_1	AI685464 AW971336 AA513587 AA525142
433687	373061_1	AA743991 AA604852 AW272737
434338	383982_1	AW754311 AA630185 AW803285
434469	387447_1	AA634606 C18732 AA729161 AA729860
435447	406400_1	AI872932 AA682306 BE220163 W88695 T81307 H91447
437152	43386_1	AL050027 BE089051
437854	44418_1	AL119723 AL119874 AI909018 U50537
439031	46798_1	AF075079 H48601 H48795
439255	470321_1	BE164500 AA832198 BE164502
444910	624951_1	AI201849 BE069007 AW946544
445432	63943_1	AV653771 BE089370
446922	69865_1	BE175605 Z43529 F06610 BE175602 AV681027
447197	711623_1	R36075 AI366546 R36187
448420	76273_1	BE623004 AA380669 BE263627 BE248433
448516	766241_1	AW898595 AW898588 AW898590 AW898683 AW898592 AI525093
450522	837264_1	AI698839 AI909260 AI909259
450736	844652_1	AW970060 AI732366 AI792313 AW839844
451024	85565_1	AA442178 AA259181
451067	85759_1	BE172188 AA059279 AA020815 AA013437
451340	86840_1	AW938273 AW340350 AA017208
452542	921410_1	AW812256 AW812257 AI906423 AI906422
452564	92227_1	AA026777 N50065 R09961 N54721
453472	968371_1	AL037925 AL037931 AL037957
454307	1106070_1	AW855717 AW382452 AW382443
454359	1130674_1	N71277 AW390784
454545	1223779_1	AW806899 AW868451 AW866393 AW866297 AW817869
454693	1229132_1	AW813428 AW813444 AW813367 AW813368 AW813429 AW813424
454714	1230493_1	AW815098 BE154843 BE154831
455047	1250536_1	AW852530 AW852527 AW852526
455092	1252971_1	BE152428 AW855572 AW855607
455097	1253130_1	AW855802 AW855794 AW855797 AW855808 AW855796 AW855808 AW855793 AW855807
455100	1253334_1	BE160198 AW935898 T11520 AW935930 AW856073 AW861034
455431	1289854_1	AW938484 BE001245 BE001190
455511	1321229_1	BE144762 AW979091
455609	1337548_1	BE011668 BE011689 BE011627 BE011679 BE011699 BE011678 BE011696 BE011675 BE011622 BE011635
455651	1348732_1	BE064952 BE064979 BE064853 BE064857 BE064856 BE064977 BE064960 BE064880 BE064815 BE064957 BE064804 BE064816 BE064850 BE064808 BE064796 BE064818 BE064975 BE064819 BE064810 BE064868 BE065059
455685	1350393_1	BE066976 BE066928 BE066927
455700	1351264_1	BE068115 BE068104 BE068102 BE068096 BE068103 BE068154 BE068198
455708	1352232_1	BE069326 BE069290 BE069352
455732	1353874_1	BE080908 BE072258 BE072190 BE072236
455838	1374605_1	BE145809 BE145807 BE181883
455935	1384144_1	BE158687 BE158688
455945	1385588_1	BE160636 BE160606 BE160703
456207	165078_-1	AA193450
456482	192289_1	AA485224 AA287308 AA258121
458094	47311_1	AF086325 W72956 W73221 AA219112
458673	678507_1	N99626 AI302701

TABLE 19B

Table 19B shows the genomic positioning for those pkeys lacking unigene ID's and accession numbers in Table 19. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400555	9801191	Minus	134694-134817
400608	9887666	Minus	96756-97558
400610	9887671	Minus	117606-117928,124040-124147
400925	7651921	Plus	38183-38391,43900-44086
401045	8117619	Plus	90044-90184,91111-91345
401049	7232177	Plus	149157-150692
401093	8518137	Minus	22335-23166
401256	9796573	Minus	45482-45620
401283	9800093	Minus	47256-47456
401326	9212516	Minus	226246-227505
401418	7452889	Minus	124865-125075
401451	6634068	Minus	119926-121272
401458	9187886	Plus	76485-77597
401497	7381770	Plus	92607-92813
401508	7534110	Minus	110778-110983
401575	7229804	Minus	76253-76364
401747	9789672	Minus	118596-118816,119119-119244,119609-119761,120422-120990,130161-130381,130468-130593,131097-131258,131866-131932,132451-132575,133580-134011
401781	7249190	Minus	83215-83435,83531-83656,83740-83901,84237-84393,84955-85037,86290-86814
401785	7249190	Minus	165776-165996,166189-166314,166408-166569,167112-167268,167387-167469,168634-168942
401793	7263888	Minus	102945-103083
401987	4406829	Minus	72893-73021,76938-77049
402077	8117414	Plus	65014-65195
402109	8131678	Minus	171722-171859,173197-173303
402184	8576001	Minus	112844-112988,113505-113638
402376	9825329	Minus	21753-22385
402421	9796341	Minus	45609-45662,46758-46811,86293-86346,89776-89829,90048-90101,102817-102924
402578	9884928	Plus	66350-66496
402606	9909429	Minus	81747-82094
402696	7328818	Minus	23600-23731
402765	9367757	Plus	109588-109726
402800	6010175	Plus	43921-44049,46181-46273
402820	6456853	Minus	82274-82443
402892	8086844	Minus	194384-194645
403133	7331427	Plus	38314-38634
403358	8569930	Plus	92839-93036
403388	9438331	Plus	112733-113001,114599-114735
403426	9719529	Minus	157156-158183
403585	8101208	Minus	131266-131769
403593	6862650	Minus	62554-62712,69449-69602
403637	8671936	Minus	142647-142771,145531-145762
403639	8671948	Plus	113234-113326,115186-115287,119649-119786
403677	7331517	Minus	55008-55083,62860-63051
403775	7770580	Minus	102247-102326,103095-103148
403943	7711864	Plus	100742-100904,101322-101503

404091	7684554	Minus	82121-83229
404097	7770701	Plus	55512-55781
404142	9856692	Minus	80316-80459
404253	9367202	Minus	55875-56055
404274	9885189	Plus	104127-104318
404285	2326514	Plus	32262-32416
404360	9858450	Minus	122873-122966,151324-151469,153093-153253
404440	7528051	Plus	80430-81581
404443	7579073	Minus	87198-87441
404552	7243881	Plus	19854-20010
404561	9795980	Minus	69039-70100
404580	6539738	Minus	240588-241589
404721	9856848	Minus	173783-174294
404826	6572184	Plus	47726-48046
404983	4432779	Minus	51178-51374,52000-52173
405037	7543748	Minus	127374-127576
405041	7547195	Plus	121230-121714
405095	8072599	Plus	138877-139056
405153	9965565	Minus	175317-175500
405196	7230083	Minus	135718-135851
405232	7249042	Plus	125904-126063
405248	7259728	Plus	637-777
405336	6094635	Plus	33267-33563
405394	6824123	Minus	31900-32373
405460	7684569	Minus	52223-52389
405494	8050952	Minus	70284-70518
405547	1054740	Plus	124361-124520,124914-125050
405609	5757553	Minus	42814-43010,43583-43783,44863-45033,46429-46554,47815-48018,49961-50153,51624-51727,51823-51959,52702-52918,55469-55601,57111-57307,58169-58266,60215-60332,61482-61727
405638	6289229	Plus	199260-199372,199826-199929
405654	4895155	Minus	53624-53759
405718	9795467	Plus	113080-113266
405822	6273498	Minus	154660-154974,155203-155379
405848	7851809	Minus	28135-28244
405873	6758747	Minus	32129-32764
405906	7705124	Minus	10835-11059
405917	7712162	Minus	106829-107213
405925	6758795	Plus	129935-130282
405953	7960374	Minus	65101-65574
406069	9117732	Plus	68880-69374
406151	7144806	Minus	94087-94285
406153	9929734	Minus	12902-13069
406182	5923650	Minus	28256-28935
406271	7534217	Plus	36179-36692
406291	5586274	Plus	9562-9887
406348	9255985	Minus	71754-71944
406414	9256407	Plus	49593-49850
406446	9454509	Minus	116424-116527,118721-118859,121187-121364
406504	7711360	Minus	107068-107277
406554	7711566	Plus	106956-107121

TABLE 20: 544 GENES UP-REGULATED IN BREAST CANCER COMPARED TO NORMAL ADULT TISSUES THAT ARE LIKELY TO ENCODE EXTRACELLULAR OR CELL-SURFACE PROTEINS

Table 20 shows 544 genes up-regulated in breast cancer compared to normal adult tissues that are likely to encode extracellular or cell-surface proteins. These were selected as for Table 19, except that the ratio was greater than or equal to 3.0, the "average" normal adult tissue level was set to the 85th percentile value amongst 144 non-malignant tissues, and the 96th percentile value amongst the 73 breast cancer specimens was greater than or equal 100 units, and the predicted protein contained a structural domain that is indicative of extracellular localization (e.g. ig, fn3, egf, 7tm domains, signal sequences, transmembrane domains). The predicted protein domains are noted.

Pkey: Unique Eos probeset Identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Pred.Prot.Domains: Predicted Protein Domains
Unigene Title: Unigene gene title
R1: Ratio of 93rd percentile of tumor to 85th percentile of normal body tissue

Pkey	ExAccn	UnigeneID	Pred.Prot.Domains	UnigeneTitle	R1
408591	AF015224	Hs.46452	SS,Uteroglobin,SS,Uteroglobin	mammaglobin 1	168.6
400291	AA401369	Hs.190721	TM	ESTs	73.2
449746	AI668594	Hs.176588	,SS,p450	ESTs, Weakly similar to CP4Y_HUMAN CYTOC	65.7
407277	AW170035	Hs.326736	TM	Homo sapiens breast cancer antigen NY-BR	57.6
400292	AA250737	Hs.72472	death,ZU5,TM,Activin_recp,pkinase,	BMP-R1B	55.9
424735	U31875	Hs.272499	,SS,TM	short-chain alcohol dehydrogenase family	53.8
426878	BE069341		TM	gb:QV3-BT0381-270100-073-c08 BT0381 Homo	50.3
428848	NM_000230	Hs.194236	SS,Leptin,SS,Leptin,	leptin (murine obesity homolog)	40.8
407178	AA195851	Hs.104106	,SS,Dihydroorotase,	ESTs	39.3
408000	L11690	Hs.620	Plectin_repeat,SH3,spectrin,SS,Plectin_r	bullous pemphigoid antigen 1 (230/240kD)	37.3
427585	D31152	Hs.179729	SS,C1q,Collagen,SS,C1q,Collagen,	collagen, type X, alpha 1 (Schmid metaph	35.2
429441	AJ224172	Hs.204096	,SS,Uteroglobin,	lipophilin B (uteroglobin family member)	30.0
450375	AA009647	Hs.8850	,SS,TM,disintegrin,Pep_M12B_propep,Repro	a disintegrin and metalloproteinase dome	25.7
420931	AF044197	Hs.100431	SS,IL8,SS	small inducible cytokine B subfamily (Cy	25.2
422109	S73265	Hs.1473	SS,Bombesin,SS	gastrin-releasing peptide	24.8
445730	AI824342	Hs.170042	,SS,TM,Cation_efflux	ESTs	24.1
451110	AI955040	Hs.265398	SS	ESTs, Weakly similar to transformation-r	24.0
400297	AI127076	Hs.334473	TM	hypothetical protein DKFZp564O1278	23.8
420813	X51501	Hs.99949	SS,SS	prolactin-induced protein	22.6
452744	AI267652	Hs.30504	,SS,TM,GNS1_SUR4,cNMP_binding,Rifa	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	22.6
424634	NM_003613	Hs.151407	ig,tsp_1,SS,AAA	cartilage intermediate layer protein, nu	21.7
420757	X78592	Hs.99915	hormone_rec,Androgen_recep,zf-C4,	androgen receptor (dihydrotestosterone r	21.7
424399	AI905687	Hs.2533	SS	aldehyde dehydrogenase 9 family, member	20.3
447350	AI375572	Hs.172634	,pkinase,	ESTs	19.2
458207	AA193450		,SS,TM,p450,p450	gb:zr40e07.r1 Soares_NhHMPu_S1 Homo sapi	18.3
431448	AL137517	Hs.334473	TM	hypothetical protein DKFZp564O1278	18.2
427217	AA399272	Hs.144341	SS	ESTs	18.2
456938	X52509	Hs.161640	,SS,TM,aminotran_1_2,Cadherin_C_term,cad	tyrosine aminotransferase	18.1
435496	AW840171	Hs.265398	SS	ESTs, Weakly similar to transformation-r	17.9
402578			SS,p450,SS,TM,p450	C1001134:g|2117372|pir||I65981 fatty ac	17.8
453160	AI263307	Hs.239884	SS	H2B histone family, member L	17.8
422505	AL120862	Hs.124165	SS	programmed cell death 9 (PDCD9)	17.7
444342	NM_014398	Hs.10887	Lamp,SS,TM,Lamp,	similar to lysosome-associated membrane	17.5

449765	N92293	Hs.206832	SS	ESTs, Moderately similar to ALU8_HUMAN A	17.3
428227	AA321649	Hs.2248	SS,IL8,	small inducible cytokine subfamily B (CX	17.0
425692	D90041	Hs.155956	,SS,Acetyltransf2,	N-acetyltransferase 1 (arylamine N-acety	16.7
424001	W67883	Hs.137476	,pkinase,	paternally expressed 10	16.5
448595	AB014544	Hs.21572	LRRCT,LRR,SS,LRRCT,serine_carbpept	KIAA0644 gene product	16.3
449448	D60730	Hs.57471	SS	ESTs	16.2
416007	M13509	Hs.83169	SS,hemopexin,Peptidase_M10,SS,Peptidase_	matrix metalloproteinase 1 (MMP1; inters	15.7
418994	AA296520	Hs.89548	SS,lectin_c,sushi,EGF,SS,EGF,lectin_c,su	selectin E (endothelial adhesion molecul	15.5
453596	AA441838	Hs.62905	SS	hypothetical protein FLJ14834	15.5
452401	NM_007115	Hs.29352	,SS,CUB,Xlink,	tumor necrosis factor, alpha-induced pro	15.0
446591	H44188	Hs.15458	PDZ,SS	PDZ domain containing 1	14.9
419296	AA236115	Hs.120785	SS	ESTs	14.8
452838	U65011	Hs.30743	SS,SS	preferentially expressed antigen in mela	14.7
422805	AA436989	Hs.121017	histone,SS,histone,histone	H2A histone family, member A	14.3
448390	AL035414	Hs.21088	SS	hypothetical protein	14.2
447342	AI199288	Hs.19322	,SS,lipocalin	Homo sapiens, Similar to RIKEN cDNA 2010	14.2
411869	W20027	Hs.23439	,SS,Peptidase_M1,	ESTs	13.9
443709	AI082692	Hs.134662	,SS,TM,SNF	ESTs	13.7
459587	AA031958		,SS,LIM,	gb:zk15e04.s1 Soares_pregnant_uterus_NbH	13.7
442580	AI733682	Hs.130239	SS	ESTs	13.5
400289	X07820	Hs.2258	hemopexin,Peptidase_M10,SS,Peptidase_M10	matrix metalloproteinase 10 (MMP10; str	13.5
411598	BE336654	Hs.70937	histone,SS,histone,histone	H3 histone family, member A	13.3
415263	AA948033	Hs.130853	,SS,histone,histone,linker_histone	ESTs	13.2
433805	AA705910	Hs.112742	,SS,Ribosomal_L7Ae,	ESTs	13.1
407275	AI951118	Hs.326736	TM	Homo sapiens breast cancer antigen NY-BR	13.1
443348	AW873596	Hs.182278	,SS,DENN	calmodulin 2 (phosphorylase kinase, delt	13.0
421037	AI584808	Hs.197653	SS	programmed cell death 9 (PDCD9)	12.9
424086	AI351010	Hs.102267	,SS,Lysyl_oxidase	lysyl oxidase	12.8
400295	W72638	Hs.2533	SS	aldehyde dehydrogenase 9 family, member	12.7
452451	N78223	Hs.108106	,SS,G9a,PHD,	transcription factor	12.5
427365	AI873274	Hs.190721	TM	ESTs	12.4
433365	AF026944	Hs.293797	,SS,TPR	ESTs	12.3
409269	AA576953	Hs.22972	SS,TM,UPF0016,SS,TM,UPF0016	hypothetical protein FLJ13352	12.0
432598	AJ224741	Hs.278481	SS,EGF,vwa,SS,TM,vwa,	matrilin 3	11.9
408771	AW732573	Hs.47584	TM,K_tetra,Ion_trans,SS,TM,K_tetra,Ion_t	potassium voltage-gated channel, delayed	11.9
432912	BE007371	Hs.200313	,SS,TM,Folate_carrier	ESTs	11.9
447033	AI357412	Hs.157601	SS	ESTs	11.8
421155	H87879	Hs.102267	SS,Lysyl_oxidase,Aldosa_epim,Epimerase,S	lysyl oxidase	11.8
424905	NM_002497	Hs.153704	pkinase,SS,TM,pkinase,polyprenyl_synt,	NIMA (never in mitosis gene a)-related k	11.7
425398	AL049689	Hs.156369	SS	hypothetical protein similar to tenascin	11.6
438167	R28363	Hs.24286	,SS,TM,7tm_1,p450,rrm	ESTs	11.5
459583	AI907673		,pkinase,	gb:IL-BT152-080399-004 BT152 Homo sapien	11.5
423945	AA410943		death,ZU5,TM,Activin_recp,pkinase,	gb:zt32h03.r1 Soares ovary tumor NbHOT H	11.4
439820	AL360204	Hs.283853	SS	Homo sapiens mRNA full length insert cDN	11.4
402606			SS	NM_024626:Homo sapiens hypothetical prot	11.3
445263	H57648	Hs.42586	,SS,Acyltransferase,	KIAA1560 protein	11.2
430217	N47883	Hs.336901	,SS,RNA_pol_A,RNA_pol_A2,Ribosomal_S24e,	ribosomal protein S24	11.1
447164	AF026941	Hs.17518	,TM,IBR	Homo sapiens clg5 mRNA, partial sequence	11.1
431385	BE178536	Hs.11090	,SS,TM	membrane-spanning 4-domains, subfamily A	11.1
423887	AL080207	Hs.134585	,SS,TM,BRCT,ank,ABC_tran,ABC_tran	DKFZP434G232 protein	10.9
415385	R17798	Hs.7535	,SS,Fork_head,	COBW-like protein	10.9
425704	U79293	Hs.159264	SS	Human clone 23948 mRNA sequence	10.7
429859	NM_007050	Hs.225952	,SS,TM,Y_phosphatase,MAM,fn3,	protein tyrosine phosphatase, receptor t	10.4
425523	AB007948	Hs.158244	,SS,laminin_B,laminin_EGF,laminin_Nterm	KIAA0479 protein	10.3
428368	BE440042	Hs.83326	SS,Peptidase_M10,hemopexin,SS,Peptidase_	matrix metalloproteinase 3 (stromelysin	10.3
418912	NM_000685	Hs.89472	SS,TM,7tm_1,SS,TM,7tm_1,	angiotensin receptor 1	10.3
422026	U80736	Hs.110826	SS	trinucleotide repeat containing 9	10.3
451952	AL120173	Hs.301663	,SS,pkinase,	ESTs	10.3
438199	AW016531	Hs.122147	,SS,ArfGap,	ESTs	10.2
400608			SS,TM,SS,TM	C10001899:g|7508633|pir||T25392 hypothe	10.1
413472	BE242870	Hs.75379	SS	solute carrier family 1 (glial high affi	10.0
432374	W56816	Hs.301885	SS	Homo sapiens cDNA FLJ11348 fis, clone PL	9.9
402408	NA		,SS,carb_anhydrase	NM_030920:Homo sapiens hypothetical pro	9.8
445537	AJ245671	Hs.12844	,SS,TM,ras	EGF-like-domain, multiple 6 (EGFL6)	9.7
451621	AI879148	Hs.26770	SS,lipocalin,lipocalin,	fatty acid binding protein 7, brain	9.6
405654	NA		BTB,SS	C12001521:g|7513934|pir||T31081 cca3 pr	9.6
434988	AI418055	Hs.161160	SS	ESTs	9.6

416220	N49776	Hs.170994	,SS,TM	hypothetical protein MGC10946	9.5
431808	M30703	Hs.270833	SS,TM,EGF,SS	amphiregulin (schwannoma-derived growth	9.5
414142	AW368397	Hs.150042	,SS,UDPGT	Homo sapiens cDNA FLJ14438 fis, clone HE	9.4
400298	AA032279	Hs.61635	TM	six transmembrane epithelial antigen of	9.4
418601	AA279490	Hs.88368	SS,TM,calreticulin,SS,TM,calreticulin,	calmegin	9.4
415539	AI733881	Hs.72472	death,ZU5,TM,Activin_recp,pkinase,	BMP-R1B	9.4
421451	AA291377	Hs.50831	TM	ESTs	9.3
429432	AI678059	Hs.202676	SS	synaptonemal complex protein 2	9.3
442441	AI820662	Hs.128598	SS	ESTs	9.1
426429	X73114	Hs.169849	,SS,TM,fn3,Ig,	myosin-binding protein C, slow-type	9.1
406687	M31126	Hs.272620	SS,Peptidase_M10,hemopexin,SS,Peptidase_	matrix metalloproteinase 11 (MMP11; stro	9.1
448693	AW004854	Hs.228320	SS	hypothetical protein FLJ23537	9.1
419948	AB041035	Hs.93847	Ferric_reduct,TM,Ferric_reduct,	NM_016931:Homo sapiens NADPH oxidase 4 (	9.1
426214	H59846	Hs.128355	SS	ESTs, Moderately similar to ALU7_HUMAN A	9.0
427718	AI798680	Hs.25933	,SS,TM,histone,Sec1,histone,sugar_tr	ESTs	8.9
414812	X72755	Hs.77367	SS,IL8,SS,IL8	monokine induced by gamma interferon	8.8
400285	NA		,TM,ABC_tran,ABC_membrane,	Eos Control	8.8
422330	D30783	Hs.115263	SS,TM,EGF,SS,TM	epiregulin	8.8
416182	NM_004354	Hs.79069	cyclin,SS	cyclin G2	8.8
420077	AW512260	Hs.87767	SS	ESTs	8.7
452281	T93500	Hs.28792	,SS,TGF-beta,TGFb_propeptide,	Homo sapiens cDNA FLJ11041 fis, clone PL	8.7
434531	AA642007	Hs.116369	SS	ESTs	8.6
408380	AF123050	Hs.44532	,SS,TM,ubiquitin,7tm_3,ANF_receptor,sush	dlubiquitin	8.6
443788	AI732643	Hs.144151	TM	ESTs	8.6
411078	AI222020	Hs.182364	SS,SS	CoccaCrisp	8.5
445495	BE622641	Hs.38489	SS,SS,ENTH,I_LWEQ,ENTH,I_LWEQ,DNA_mts_re	ESTs, Weakly similar to I38022 hypotheti	8.5
433426	H69125	Hs.133525	,SS,TM	ESTs	8.5
424871	NM_004525	Hs.153595	SS,EGF,ldl_recept_a,ldl_recept_b,SS,TM,E	low density lipoprotein-related protein	8.4
426215	AW963419	Hs.155223	SS	stanniocalcin 2	8.4
409045	AA635062	Hs.50094	TM	Homo sapiens mRNA; cDNA DKFZp434C0515 (f	8.4
435525	AI831297	Hs.123310	TM	ESTs	8.3
409203	AA780473	Hs.887	SS,p450,SS,p450	cytochrome P450, subfamily IVB, polypept	8.3
424902	NM_003856	Hs.153687	SS,SS	inositol polyphosphate-4-phosphatase, ty	8.3
431725	X65724	Hs.2839	SS,Cys_knot,SS	Norrie disease (pseudoglioma)	8.3
418092	R45154	Hs.106604	,death,ZU5,pkinase,Activin_recp,	ESTs	8.3
439840	AW449211	Hs.105445	SS	GDNF family receptor alpha 1	8.2
427811	M81057	Hs.180884	SS,Zn_carbOpept,Propep_M14,SS,Propep_M14	carboxypeptidase B1 (tissue)	8.2
420807	AA280827	Hs.57846	SS,cpn10	ESTs	8.2
426320	W47595	Hs.169300	SS,TGF-beta,TGFb_propeptide,SS	transforming growth factor, beta 2	8.2
447078	AW885727	Hs.301570	,SS,kazal,	ESTs	8.1
415788	AW419196	Hs.257924	SS	hypothetical protein FLJ13782	8.1
410102	AW248508	Hs.279727	SS	Homo sapiens cDNA FLJ14035 fis, clone HE	8.0
404347			SS	Target Exon	8.0
433687	AA743991		TM	gbtmy57g01.s1 NCI_CGAP_Pr18 Homo sapiens	8.0
421373	AA808229	Hs.167771	,SS,IMPDH_C,IMPDH_N,CBS	ESTs	8.0
422634	NM_016010	Hs.118821	SS	CGI-62 protein	7.9
453310	X70697	Hs.553	TM,SNF,SS,TM,SNF,	solute carrier family 6 (neurotransmitte	7.9
435957	N39015	Hs.190368	,SS,TM	ESTs	7.8
407771	AL138272	Hs.62713	,TM,cpn60_TCP1,Sema,	ESTs	7.8
443646	AI085198	Hs.164226	,TSPN,vwc,tsp_1,EGF,fhlored,	ESTs	7.8
446142	AI754693	Hs.145968	,TM,cadherin,Cadherin_C_term,	ESTs	7.7
444649	AW207523	Hs.197628	,SS,rrn,	ESTs	7.6
435147	AL133731	Hs.4774	,TM,SDF,UPAR_LY6,	Homo sapiens mRNA; cDNA DKFZp761C1712 (f	7.6
439138	AI742605	Hs.193698	TM	ESTs	7.6
429220	AW207206	Hs.138319	SS	ESTs	7.6
428804	AK000713	Hs.193736	,SS,UDPGT	hypothetical protein FLJ20706	7.5
453511	AL031224	Hs.33102	SS,SS	transcription factor AP-2 beta (activati	7.5
439809	R41396	Hs.101774	SS	hypothetical protein FLJ23045	7.5
414869	AA157291	Hs.21479	SS	tubinudein 1	7.5
416276	U41060	Hs.79136	SS,TM,TM	LIV-1 protein, estrogen regulated	7.5
452862	AW378065	Hs.8587	,SS,Pep_M12B_propep,Reprolysin,tsp_1,	ESTs	7.4
452926	AI742170	Hs.31297	,SS,TM	duodenal cytochrome b	7.4
453331	AI240665	Hs.8895	,SS,TM,disintegrin,Pep_M12B_propep,Repro	ESTs	7.3
420802	U22376	Hs.1334	SS,NA,myb_DNA-binding	v-myb avian myeloblastosis viral oncogen	7.3
450503	R43646	Hs.12422	SS	ESTs	7.2
422867	L32137	Hs.1584	SS,EGF,tsp_3,SS,E2F_TDP,	cartilage oligomeric matrix protein (COM	7.2
418004	U37519	Hs.87539	SS,aldedh,SS,aldedh,	aldehyde dehydrogenase 3 family, member	7.2

426451	AI908165	Hs.169946	SS,GATA,	GATA-binding protein 3 (T-cell receptor	7.1
450701	H39960	Hs.288467	,SS,LRR	Homo sapiens cDNA FLJ12280 fis, clone MA	7.1
419519	AI198719	Hs.176376	SS	ESTs	7.1
410555	U92649	Hs.64311	,TM,disintegrin,Reprolysin,	a disintegrin and metalloproteinase doma	7.1
433138	AB029496	Hs.59729	SS,Ig,Sema,SS,Sema,efhand	semaphorin sem2	7.0
411558	AA102670	Hs.70725	SS,TM,SS,TM	gamma-aminobutyric acid (GABA) A recepto	7.0
409079	W87707	Hs.82065	,TM,fn3,	interleukin 6 signal transducer (gp130,	7.0
417275	X63578	Hs.295449	SS,efhand,SS,efhand,ras	parvalbumin	7.0
432731	R31178	Hs.287820	,SS,fn3,fn1,fn2,fn2,fn1	fibronectin 1	6.9
442818	AK001741	Hs.8739	WD40,SS	hypothetical protein FLJ10879	6.8
407366	AF026942		,TM,IBR	gbtHomo sapiens clg33 mRNA, partial sequ	6.8
427427	AF077345	Hs.177938	SS,lectin_c,SS	ESTs	6.8
410785	AW803341		SS	gbtIL2-UM0079-090300-050-D03 UM0079 Homo	6.7
401045			ICE_p20,SS,ICE_p10,ICE_p20,ICE_p10,ICE_p		
	C11001883*:gi[6753278]ref[NP_033938.1] c			6.7	
418986	AI123555	Hs.81796	,SS,Reprolysin,tsp_1,	ESTs	6.7
442082	R41823	Hs.7413	,TM,EPH_lbd,pkinase,SAM,fn3,	ESTs; calsyntenin-2	6.7
442861	AA243837	Hs.57787	SS	ESTs	6.6
418836	AI655499	Hs.161712	,TM,Activin_recp,pkinase,death,ZU5,	ESTs	6.6
422060	R20893	Hs.325823	,SS,TM,CD36	ESTs, Moderately similar to ALU5_HUMAN A	6.6
444381	BE387335	Hs.283713	,SS,mito_carr	ESTs, Weakly similar to S64054 hypotheti	6.6
404091	NA		,TM,7tm_3,ANF_receptor,	Target Exon	6.6
417866	AW067903	Hs.82772	SS,Collagen,COLFI,TSPN,SS,TSPN	collagen, type XI, alpha 1	6.6
428819	AL135623	Hs.193914	SS,SS	KIAA0575 gene product	6.5
410275	U85658	Hs.81796	,SS,Ribosomal_S4e	transcription factor AP-2 gamma (activat	6.4
425236	AW067800	Hs.155223	SS	stanniocalcin 2	6.2
415669	NM_005025	Hs.78589	,SS,serpin,	serine (or cysteine) proteinase inhibito	6.2
416319	AI815601	Hs.79197	SS,TM,Ig,SS,TM	CD63 antigen (activated B lymphocytes, I	6.2
412140	AA219691	Hs.73625	,SS,kinesin,	RAB6 interacting, kinesin-like (rabkines	6.2
442942	AW167087	Hs.131562	,SS,Ig,Sema,pkinase,	ESTs	6.2
446163	AA026880	Hs.25252	,SS,TM,fn3,	prolactin receptor	6.1
443162	T49951	Hs.9029	filament,SS,filament,filament	DKFZP434G032 protein	6.1
409602	W26713	Hs.256972	,SS,TM,DAGKa,DAGKc,	ESTs	6.1
428479	Y00272	Hs.184572	,SS,pkinase,pkinase	cell division cycle 2, G1 to S and G2 to	6.1
400300	X03363		,SS,TM,pkinase,Recep_L_domain,SH2,PH,Fur	HER2 receptor tyrosine kinase (c-erb-b2,	6.1
433404	T32982	Hs.102720	SS	ESTs	6.1
410079	U94362	Hs.58589	Glyco_transf_8,SS	glycogenin 2	6.1
401781			,SS,filament,Pribosyltran,filament,Armad	Target Exon	6.1
447359	NM_012093	Hs.18268	SS,adenylatekinase,	adenylate kinase 5	6.1
402230	NA		,SS,TM,p450,	Target Exon	6.1
427674	NM_003528	Hs.2178	histone,SS,histone,	H2B histone family, member Q	6.1
428398	AI249368	Hs.98558	,SS,TM	ESTs	6.0
458098	BE550224	Hs.74170	SS	metallothionein 1E (functional)	6.0
419968	X04430	Hs.93913	SS,IL6,IL6,	interleukin 6 (interferon, beta 2)	6.0
416636	N32536	Hs.42845	,SS,TM	solute carrier family 16 (monocarboxylic	6.0
419703	AI793257	Hs.128151	,SS,zf-C2H2,	ESTs	5.8
424687	J05070	Hs.151738	SS,Peptidase_M10,fn2,hemopexin,SS,TM,Pep	matrix metalloproteinase 9 (gelatinase B	5.8
449879	AI823951	Hs.129700	SS	tolloid-like 1	5.8
421296	NM_002666	Hs.103253	SS	perilipin	5.8
442117	AW684964	Hs.128899	,SS,TM	ESTs	5.7
400303	AA242758	Hs.79136	,SS,TM	LIV-1 protein, estrogen regulated	5.7
419440	AB020689	Hs.90419	SS	KIAA0882 protein	5.7
444858	AI199738	Hs.208275	SS	ESTs, Weakly similar to ALUA_HUMAN !!!!	5.7
432239	X81334	Hs.2936	SS,Peptidase_M10,hemopexin,SS,Peptidase_	matrix metalloproteinase 13 (collagenase	5.6
440705	AA904244	Hs.153205	TM	ESTs	5.6
400286	NA		SS,TM,ABC_tran,ABC_membrane,SS	C16000922:gi[7499103]pir[T20903 hypothe	5.6
448468	H38026	Hs.308	arrestin,SS	arrestin 3, retinal (X-arrestin)	5.5
423201	NM_000163	Hs.125180	SS,TM,fn3,SS	growth hormone receptor	5.5
433043	W57554	Hs.125019	SS	lymphoid nuclear protein (LAF-4) mRNA	5.5
439509	AF086332	Hs.58314	,SS,TM,Syntaxin	ESTs	5.4
425247	NM_005940	Hs.155324	SS,Peptidase_M10,hemopexin,SS	matrix metalloproteinase 11 (MMP11; stro	5.4
409757	NM_001698	Hs.123114	,SS,cystatin,	cystatin SN	5.4
425292	NM_005824	Hs.155545	SS	37 kDa leucine-rich repeat (LRR) protein	5.4
448045	AJ297436	Hs.20166	,SS,TM	prostate stem cell antigen	5.4
452681	AF153330	Hs.30248	,SS,TM	solute carrier family 19 (thiamine trans	5.3
452243	AL355715	Hs.28555	SS	programmed cell death 9	5.3
439310	AF086120	Hs.102793	,SS,TM,UDPGT,casein_kappa	ESTs	5.2

441111	AI806867	Hs.126594	,SS,TM,Phosphodiest,	ESTs	5.2
452355	N54926	Hs.29202	TM,7tm_1,TM	G protein-coupled receptor 34	5.2
427711	M31659	Hs.180408	SS	solute carrier family 25 (mitochondrial	5.2
418636	AW749855		,SS,TM,HECT	gb:QV4-BT0534-281299-053-c05 BT0534 Homo	5.2
429353	AL117406	Hs.200102	,SS,TM,ABC_tran,ABC_membrane,	ATP-binding cassette transporter MRP8	5.1
441690	R81733	Hs.33106	,SS,HECT,zf-UBR1,PABP,14-3-3,	ESTs	5.1
430447	W17064	Hs.332848	SS	SWI/SNF related, matrix associated, acti	5.1
429698	AI685086	Hs.26339	,SS,ras,	ESTs, Weakly similar to S21348 probable	5.1
425325	X52730	Hs.1892	SS,NNMT_PNMT_TEMT,SS,NNMT_PNMT_TEMT,STAR		
	phenylethanolamine N-methyltransferase				5.1
423600	AI633559	Hs.310359	SS	ESTs	5.1
414737	AI160386	Hs.125087	SS	ESTs	5.1
403593	NA		,CIDE-N,pkinase	Target Exon	5.1
407758	D50915	Hs.38365	SS,SS	KIAA0125 gene product	5.0
445234	AW137636	Hs.146059	,SS,TM	ESTs	5.0
411165	NM_000169	Hs.69089	SS,Melibiase,BTK,PH,pkinase,SH2,SH3,Ribo	galactosidase, alpha	4.9
420833	NM_014581	Hs.274480	SS,lipocalin,SS,lipocalin	odorant-binding protein 2A	4.9
414117	W88559	Hs.1787	,TM,ion_trans,K_tetra,	proteolipid protein 1 (Pelizaeus-Merzbac	4.9
416783	AA206186	Hs.79889	SS,TM,TM	monocyte to macrophage differentiation-a	4.9
401093			TM,LRRCT,TM,LRRCT,	C12000588*:gi|6330167|db|BAA88477.1| (A	4.9
411096	U80034	Hs.68583	Peptidase_M3,	mitochondrial intermediate peptidase	4.9
457411	AW085961	Hs.130093	SS	ESTs	4.9
436007	AI247718	Hs.232168	,SS,adh_zinc,	ESTs	4.9
450506	NM_004460	Hs.418	SS,DPPIV_N_term,Peptidase_S9,SS,DPPIV_N	fibroblast activation protein, alpha	4.9
417975	AA841838	Hs.30085	,SS,trypsin	hypothetical protein FLJ23186	4.9
421072	AI215069	Hs.89113	SS	ESTs	4.8
427032	AF012023	Hs.173274	,SS,14-3-3	integrin cytoplasmic domain-associated p	4.8
447752	M73700	Hs.105938	SS,transferrin,7tm_1,transferrin,	lactotransferrin	4.8
403199	NA		SS,TM,Folate_carrier,SS,TM,Folate_carrie	NM_025243*:Homo sapiens solute carrier f	4.8
427122	AW057738	Hs.323910	,SS,TM,pkinase,Recep_L_domain,SH2,PH,Fur	HER2 receptor tyrosine kinase (c-erb-b2,	4.8
445900	AF070526	Hs.13429	,SS,Ca_channel_B,	Homo sapiens clone 24787 mRNA sequence	4.7
413048	M93221	Hs.75182	SS,TM,lectin_c,fn2,Ricin_B_lectin,SS,TM	mannose receptor, C type 1	4.7
419563	AA526235	Hs.193162	SS	Homo sapiens cDNA FLJ11983 fis, clone HE	4.7
442432	BE093589	Hs.38178	SS	hypothetical protein FLJ23468	4.6
452093	AA447453	Hs.27860	,SS,TM,7tm_1,	Homo sapiens mRNA; cDNA DKFZp586M0723 (f	4.6
442323	AW016669	Hs.29190	,SS,TM,CBS,voltage_CLC	ESTs	4.6
450606	AI688605	Hs.60380	,TM,Glyco_hydro_1	ESTs, Moderately similar to ALU6_HUMAN A	4.6
435542	AA687376	Hs.269533	,SS,pkinase,RhoGEF,ig,PH,SH3,	ESTs	4.6
417576	AA339449	Hs.82285	AIRS,formyl_transf,GARS,SS,GARS,AIRS,for	phosphoribosylglycinamide formyltransfer	4.6
446089	AI860021	Hs.270651	,pkinase	ESTs, Moderately similar to A47582 B-cel	4.6
445413	AA151342	Hs.12677	SS,UPF0099,SS,UPF0099,	CGI-147 protein	4.6
424420	BE614743	Hs.146888	,SS,TM,MAPEG,	prostaglandin E synthase	4.5
432378	AI493046	Hs.146133	,SS,TM,UDPGT	ESTs	4.5
452190	H26735	Hs.91668	,SS,TM,PH,SH2,Furin-like,pkinase,Recep_L	Homo sapiens clone PP1496 unknown mRNA	4.5
434674	AA831879	Hs.136985	,SS,Hist_deacetyl,	ESTs	4.5
419986	AI345455	Hs.78915	pkinase,OPR,	GA-binding protein transcription factor,	4.5
421582	AI910275	Hs.1406	SS,trefoil,SS,TM,ldl_recept_a,SRCR,tryps	trefoil factor 1 (pS2)	4.5
410361	BE391804	Hs.62661	SS,TM,GBP,TM,GBP	guanylate binding protein 1, interferon-	4.5
426327	W03242	Hs.44898	SS	Homo sapiens clone TCCCTA00151 mRNA sequ	4.5
406639	M97711		SS,SS,ig,	gb:Human T-cell receptor (V beta 18.1, J	4.5
452834	AI638627	Hs.105685	,SS,DEAD,Fork_head	KIAA1688 protein	4.5
427315	AA179949	Hs.175563	SS	Homo sapiens mRNA; cDNA DKFZp564N0763 (f	4.4
446733	AA883380	Hs.26040	,SS,TM,p450,	ESTs, Weakly similar to fatty acid omega	4.4
442118	AA978718	Hs.202242	,ig,Sema,	ESTs	4.4
421524	AA312082	Hs.105445	SS	GDNF family receptor alpha 1	4.4
453060	AW294092	Hs.21594	,SS,ras,Y_phosphatase,ras	hypothetical protein MGC15754	4.4
453403	BE466839	Hs.61779	,SS,HMG_box,filament,	Homo sapiens cDNA FLJ13591 fis, clone PL	4.4
444301	AK000138	Hs.10760	SS,LRR,SS	asporin (LRR class 1)	4.4
453619	H87648	Hs.33922	SS	Homo sapiens, clone MGC:9084, mRNA, comp	4.3
432656	NM_000246	Hs.3076	SS,LRR,	MHC class II transactivator	4.3
426384	AI472078	Hs.303662	,SS,ArfGap,	ESTs	4.3
431701	AW935490	Hs.14658	,SS,BIR	Human chromosome 5q13.1 clone 5G8 mRNA	4.3
416931	D45371	Hs.80485	SS,C1q,Collagen,SS,C1q,	adipose most abundant gene transcript 1	4.3
420854	AW296927		,SS,TM,Peptidase_M1,	gb:UI-H-BW0-ejc-c-07-0-UI.s1 NCI_CGAP_Su	4.3
418867	D31771	Hs.89404	SS,homeobox,homeobox,	msh (Drosophila) homeo box homolog 2	4.3
443514	BE464288	Hs.141937	,SS,TM,MIP,	ESTs	4.3
447499	AW262580	Hs.147674	,SS,TM,cadherin,cadherin	protocadherin beta 16	4.3

441560	F13386	Hs.7888	,pkinase,	Homo sapiens clone 23736 mRNA sequence	4.3
409064	AA062954	Hs.141883	,SS,CUB,	ESTs	4.3
422687	H25642	Hs.133471	,SS,TM,FMO-like	ESTs	4.3
454032	W31790	Hs.194293	,SS,TM	ESTs, Weakly similar to I54374 gene NF2	4.3
432683	AI984317	Hs.122589	TM	ESTs	4.3
401747			,SS,filament,filament	Homo sapiens keratin 17 (KRT17)	4.3
432882	NM_013257	Hs.279696	pkinase,pkinase_C,	serum/glucocorticoid regulated kinase-li	4.2
437036	AI571514	Hs.133022	,SS,TM	ESTs	4.2
447754	AW073310	Hs.183533	,pkinase,	Homo sapiens cDNA FLJ14142 fis, clone MA	4.2
443194	AI954968	Hs.279009	,SS,TM	matrix Gla protein	4.2
451871	AI821005	Hs.118599	,SS,GDNF,	ESTs	4.2
457211	AW972565	Hs.32399	WH1,WH1	ESTs, Weakly similar to S51797 vasodilat	4.2
421566	NM_000399	Hs.1395	zf-C2H2,SS	early growth response 2 (Krox-20 (Drosop	4.2
431657	AI345227	Hs.105448	,SS,TM,pkinase	ESTs, Weakly similar to B34087 hypothetl	4.1
427699	AA829286	Hs.332053	,SS,SAA_proteins,ABC_membrane,ABC_tran	serum amyloid A1	4.1
444779	AI192105	Hs.147170	SS	ESTs	4.1
442295	AI827248	Hs.224398	,COLFI,vwc,Collagen,	Homo sapiens cDNA FLJ11469 fis, clone HE	4.1
436396	AI583487	Hs.152213	,wnt,	wingless-type MMTV integration site fami	4.1
446039	AI150491	Hs.90756	,TM,Glyco_hydro_1	ESTs	4.1
422638	NM_001809	Hs.1594	,SS,TM,thiolase,	centromere protein A (17kD)	4.1
406922	S70284		SS,TM,Desaturase,SS	gb:stearoyl-CoA desaturase [human, adipo	4.1
439285	AL133916	Hs.172572	,SS,ig,pkinase,LRRNT,LRRCT,	hypothetical protein FLJ20093	4.1
424800	AL035588	Hs.153203	HLH,SS	MyoD family inhibitor	4.1
429922	Z97630	Hs.226117	,SS,TM,linker_histone,7tm_1	H1 histone family, member 0	4.1
447178	AW594641	Hs.192417	,SS,TM	ESTs	4.0
409038	T97490	Hs.50002	SS,IL8,SS,IL8	small inducible cytokine subfamily A (Cy	4.0
452747	BE153855	Hs.61460	,SS,HLH	ig superfamily receptor LNIR	4.0
420139	NM_005357	Hs.95351	,SS,TM,p450,	lipase, hormone-sensitive	4.0
408877	AA479033	Hs.130315	,SS,TM	ESTs, Weakly similar to A47582 B-cell gr	4.0
403329	NA		SS,SS	Target Exon	4.0
439926	AW014875	Hs.137007	SS	ESTs	4.0
430832	AI073913	Hs.100686	SS	ESTs, Weakly similar to JE0350 Anterior	4.0
432481	AW451645	Hs.151504	,SS,Collagen,COLFI,TSPN,	Homo sapiens cDNA FLJ11973 fis, clone HE	4.0
452410	AL133619	Hs.29383	,SS,TM,ras	Homo sapiens mRNA; cDNA DKFZp434E2321 (f	4.0
418661	NM_001949	Hs.1189	SS	E2F transcription factor 3	4.0
431958	X63629	Hs.2877	SS,TM,Cadherin_C_term,cadherin,SS,TM,cad	cadherin 3, type 1, P-cadherin (placenta	4.0
425071	NM_013989	Hs.154424	SS,T4_deiodinase,T4_deiodinase,	deiodinase, iodothyronine, type II	4.0
447197	R38075		,TM,SDF,	gb:yh88b01.s1 Soares placenta NbZHP Homo	4.0
428722	U76456	Hs.190787	,SS,TIMP,	tissue inhibitor of metalloproteinase 4	3.9
426330	L22524	Hs.2256	SS,Peptidase_M10,SS,Peptidase_M10,hemo	pematrix metalloproteinase 7 (MMP7; uterin	3.9
423242	AL039402	Hs.125783	SS	DEME-6 protein	3.9
449048	Z45051	Hs.22920	SS,SS,TM	similar to 568401 (cattle) glucose induc	3.9
414831	M31158	Hs.77439	,SS,cNMP_binding,Rita,HMG_box	protein kinase, cAMP-dependent, regulato	3.9
413589	AW452631	Hs.313803	,SS,abhydrolase	ESTs, Highly similar to AF157833 1 nonci	3.8
408875	NM_015434	Hs.48604	SS	DKFZP434B168 protein	3.8
418629	BE247550	Hs.86859	SS,SH2,PH,SS,TM,PH,SH2,Furin-like,pkinas	growth factor receptor-bound protein 7	3.8
450787	AB006190	Hs.25475	SS,TM,MIP,SS,TM,MIP,	aquaporin 7	3.8
414870	N72264	Hs.300670	SS	KIAA1204 protein	3.8
450325	AI935962	Hs.26289	SS	ESTs	3.8
407633	NM_007069	Hs.37189	TM,TM	similar to rat HREV107	3.8
426172	AA371307	Hs.125056	,SS,DENN	ESTs	3.8
442262	BE170651	Hs.8700	,SS,START,	deleted in liver cancer 1	3.8
427981	AW293165	Hs.143134	SS	ESTs	3.8
445563	AW873606	Hs.149006	,SS,WH1,WH1	ESTs	3.8
403943			p450,SS,p450	C5000355:gi|4503225|ref|NP_000765.1| cyt	3.8
408761	AA057264	Hs.238936	,SS,TM,7tm_1,	ESTs, Weakly similar to (define not eva	3.8
423279	AW959881	Hs.290943	SS	ESTs	3.8
420440	NM_002407	Hs.97644	,SS,SRCR,Uteroglobin	mammaglobin 2 (MGB2; mammaglobin B; lip	3.8
445107	AI208121	Hs.147313	,SS,TM	ESTs, Weakly similar to I38022 hypothetl	3.7
428303	AW974476	Hs.183601	SS,RGS,RGS,RGS	regulator of G-protein signalling 16	3.7
411667	BE160198		TM	gb:QV1-HT0413-010200-059-h03 HT0413 Homo	3.7
427809	M26380	Hs.180878	,SS,lipase,PLAT,Sec7,PH,	lipoprotein lipase	3.7
418203	X54942	Hs.83758	CKS,SS,CKS,	CDC28 protein kinase 2	3.7
430378	AW292053	Hs.12532	SS	chromosome 1 open reading frame 21	3.7
444190	AI878918	Hs.10526	SS	cysteine and glycine-rich protein 2	3.7
433495	AW373784	Hs.71	SS,ig,MHC_I,connexin,SCAN,SS,TM	alpha-2-glycoprotein 1, zinc	3.7
429638	AI916662	Hs.211577	SS,TM,SS	kinectin 1 (kinesin receptor)	3.7

454071	AI041783	Hs.42502	,TM,7tm_1,	ESTs	3.7
451859	H44491	Hs.252936	,SS,TM,EGF,kll_recept_a,kll_recept_b,EGF	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.7
420281	AI823693	Hs.191533	,SS,AAA,	ESTs	3.7
427691	AW194426	Hs.20726	,SS,Glycos_transf_2,	ESTs	3.7
428824	W23824	Hs.173059	SS	ESTs	3.7
424676	Y08565	Hs.151678	Glycos_transf_2,Ricin_B_lectin,SS,Glycos	UDP-N-acetyl-alpha-D-galactosamine:polyp	3.7
418026	BE379727	Hs.83213	lipocalin,SS,lipocalin,lipocalin,ferriti	fatty acid binding protein 4, adipocyte	3.7
457465	AW301344	Hs.122906	,SS,Pribosyltran,Sulfatase	DNA replication factor	3.7
417601	NM_014735	Hs.82292	PHD,pkinase,SS	KIAA0215 gene product	3.7
407999	AI126271	Hs.49433	SS	ESTs, Weakly similar to YZ28_HUMAN HYPOT	3.7
425548	AA890023	Hs.1906	SS,TM,fn3,SS,TM,fn3,	prolactin receptor	3.7
446819	AU076643	Hs.313	,SS,TM,efhand,Ion_trans	secreted phosphoprotein 1 (osteopontin,	3.7
411213	AA676939	Hs.69285	SS,TM,CUB,F5_F8_type_C,MAM,SS,TM,CUB,F5	neuropilin 1	3.6
408625	Y13647	Hs.119597	SS,TM,Desaturase,SS	stearoyl-CoA desaturase (delta-9-desatur	3.6
417511	AL049176	Hs.82223	SS	chordin-like	3.6
428769	AW207175	Hs.106771	,SS,7tm_1,SPRY,	ESTs	3.6
407137	T97307		,SS,TM,GDA1_CD39	gb:ye53h05.s1 Soares fetal liver spleen	3.6
401866			,SS,filament,	Target Exon	3.6
451195	U10492	Hs.438	SS,homeobox,Ets,SS,homeobox,	mesenchyme homeo box 1	3.6
426044	AA502490	Hs.336695	SS	ESTs	3.6
426310	NM_000909	Hs.169266	SS,TM,7tm_1,	neuropeptide Y receptor Y1	3.6
440029	AW089705	Hs.293711	SS	ESTs, Weakly similar to S64329 probable	3.6
408573	AA284775	Hs.43148	,SS,TM,PMP22_Claudin,	ESTs	3.6
431830	Y16845	Hs.271387	,SS,TM,IL8	small inducible cytokine subfamily A (Cy	3.6
444781	NM_014400	Hs.11950	,SS,PH,lactamase_B	GPI-anchored metastasis-associated prote	3.6
431493	AI791493	Hs.129873	,SS,p450,p450	ESTs, Weakly similar to A36036 cytochrom	3.6
414175	AI308876	Hs.103849	,TM,hemopexin,Peptidase_M10,hemopexin,	Pehypothetical protein DKFZp761D112	3.6
411789	AF245505	Hs.72157	lg,LRRCT,	DKFZP564I1922 protein	3.6
418851	AI417828	Hs.192435	,SS,TM	ESTs	3.5
453968	AA847843	Hs.62711	,SS,HMG_box,	Homo sapiens, clone IMAGE:3351295, mRNA	3.5
407104	S57296	Hs.323910	,SS,TM,SH2,PH,pkinase,Recep_L_domain,	Furv-erb-b2 avian erythroblastic leukemia v	3.5
449051	AW981400	Hs.333526	SS	HER2 receptor tyrosine kinase (c-erb-b2,	3.5
434398	AA121098	Hs.3838	pkinase,POLO_box,SS,pkinase,POLO_box,	serum-inducible kinase	3.5
454042	H22570	Hs.172572	,SS,lg,pkinase,LRRNT,LRRCT,	hypothetical protein FLJ20093	3.5
459496	AA808940	Hs.274450	,SS,TM,KRAB,SCAN,zf-C2H2,lg	EST	3.5
414998	NM_002543	Hs.77729	,S5,TM	oxidised low density lipoprotein (lectin	3.5
407756	AA116021	Hs.38260	S8,UCH-1,UCH-2,SS,TM,G_glu_transpept	ubiquitin specific protease 18	3.5
442101	AI651930	Hs.135884	SS	ESTs	3.5
449722	BE280074	Hs.23960	cyclin,SS,TM,cyclin,	cyclin B1	3.5
452554	AW452434	Hs.58006	SS	ESTs, Weakly similar to ALU5_HUMAN ALU S	3.5
421991	NM_014918	Hs.110488	SS	KIAA0990 protein	3.4
420058	AK001423	Hs.94694	SS	Homo sapiens cDNA FLJ10581 fis, clone NT	3.4
425776	U25128	Hs.159499	SS,TM,7tm_2,SS,TM,7tm_2	parathyroid hormone receptor 2	3.4
407846	AA426202	Hs.40403	,TM,ABC_membrane,ABC_tran,Ribosomal_S4	sCbp/p300-interacting transactivator, wit	3.4
406925	L34041	Hs.9739	,SS,TM,transport_prot,SWIB,RhoGAP,DAG_P	Eglycerol-3-phosphate dehydrogenase 1 (so	3.4
445873	AA250970	Hs.251946	,SS,rrm,PABP,pkinase,14-3-3,rrm	poly(A)-binding protein, cytoplasmic 1-l	3.4
418054	NM_002318	Hs.83354	,SS,TM,mito_carr,Lysyl_oxidase	lysyl oxidase-like 2	3.4
414921	BE390551	Hs.77628	SS,START,SS,START,NNMT_PNMT_TEMT,	steroidogenic acute regulatory protein r	3.4
452268	NM_003512	Hs.28777	SS,histone,Calc_CGRP_IAPP,lg,MHC_I,SPRY,	H2A histone family, member L	3.4
428852	NM_000346	Hs.2316	SS,HMG_box,	SRY (sex determining region Y)-box 9 (ca	3.4
412520	AA442324	Hs.795	histone,SS,histone,BolA	H2A histone family, member O	3.4
410530	M25809	Hs.64173	ATP-synt_ab,SS,7tm_1,ATP-synt_ab	ATPase, H transporting, lysosomal (vacuo	3.4
401780			filament,SS,filament,filament	NM_005557*:Homo sapiens keratin 16 (foca	3.4
447131	NM_004585	Hs.17466	TM	retinoic acid receptor responder (tazaro	3.4
418334	AA319233	Hs.5521	,SS,TM,Ribosomal_L27e,	ESTs	3.4
415138	C18356	Hs.295944	,Kunitz_BPTI,	tissue factor pathway inhibitor 2	3.4
421166	AF182277	Hs.330780	SS,p450,SS	cytochrome P450, subfamily IIB (phenobar	3.4
431473	AA825686	Hs.321176	SS	ESTs, Weakly similar to S65824 reverse t	3.4
421379	Y15221	Hs.103982	SS,IL8,	small inducible cytokine subfamily B (Cy	3.4
411984	NM_005419	Hs.72988	SH2,STAT,SS,STAT	signal transducer and activator of trans	3.4
408101	AW958504	Hs.123073	,pkinase,	CDC2-related protein kinase 7	3.4
405368			RhoGEF,PH,SS,RhoGEF,PH,	NM_003371*:Homo sapiens vav 2 oncogene (	3.4
414612	BE274552	Hs.76578	SAP,SS,FG-GAP,vwa	protein inhibitor of activated STAT3	3.4
411393	AW797437	Hs.69771	SS,sushi,trypsin,vwa,rrm,fibrinogen_C,fn	B-factor, properdin	3.3
435787	H73505	Hs.117874	,SS,Peptidase_S8,P,Peptidase_S8,P	ESTs	3.3
416406	D86961	Hs.79299	,SS,TM	lipoma HMGIC fusion partner-like 2	3.3
433068	NM_006458	Hs.288215	,SS,Pribosyltran,	sialyltransferase	3.3

445462	AA378776	Hs.288649	SS,SS	hypothetical protein MGC3077	3.3
439452	AA918317	Hs.57987	SS,SS	B-cell CLL/lymphoma 11B (zinc finger pro	3.3
452017	AF109302	Hs.27495	SS	prostate cancer associated protein 7	3.3
409099	AK000725	Hs.50579	SS	hypothetical protein FLJ20718	3.3
452106	AI141031	Hs.21342	SS	ESTs	3.3
447519	U46258	Hs.339685	SS	ESTs	3.3
426926	AF037062	Hs.172914	,SS,adh_short,TGF-beta,TGFb_propeptide	retinol dehydrogenase 5 (11-cis and 9-ci	3.3
438825	BE327427	Hs.79953	,SS,TM,histone,ANF_receptor,guanylate_cy	ESTs	3.3
414575	H11257	Hs.22968	,SS,pkinase,lg,	Homo sapiens clone IMAGE:451939, mRNA se	3.3
417837	AL079905	Hs.1103	SS,TGFb_propeptide,TGF-beta,SS	transforming growth factor, beta 1	3.3
422128	AW881145		SS	gb:QV0-OT0033-010400-182-a07 OT0033 Homo	3.3
445941	AI267371	Hs.172636	SS,SS,lipoxygenase,PLAT	ESTs	3.3
429973	AI423317	Hs.164680	,SS,T-box,UDPGT	ESTs	3.3
444542	AI161293	Hs.280380	SS,SS,Peptidase_M1,EGF,lg,lectin_c,sushi	aminopeptidase	3.3
459561	AI547306	Hs.134981	SS	ESTs	3.3
425741	AF052152	Hs.159412	,pkinase,	Homo sapiens clone 24628 mRNA sequence	3.3
426501	AW043782	Hs.293816	SS	ESTs	3.3
455508	AA502764	Hs.123469	SS	ESTs, Weakly similar to AF208855 1 BM-01	3.3
434228	Z42047	Hs.283978	,SS,TM,7tm_1	Homo sapiens PRO2751 mRNA, complete cds	3.3
415752	BE314524	Hs.78776	TM	putative transmembrane protein	3.3
400419	AF084545		,SS,Peptidase_M1,	Target	3.3
439750	AL359053	Hs.57664	,TM,Integrin_B,Ricin_B_lectin,rrm	Homo sapiens mRNA full length insert cDN	3.3
423858	AL137328	Hs.133483	,SS,TM	Homo sapiens mRNA; cDNA DKFZp434B0650 (f	3.3
428514	AW238861	Hs.193139	,SS,START,NNMT_PNMT_TEMT,	ESTs	3.3
428698	AA852773	Hs.334838	SS	KIAA1866 protein	3.3
448988	Y09763	Hs.22785	SS,TM,TM	gamma-aminobutyric acid (GABA) A recepto	3.3
432072	N62937	Hs.269109	,Sema,lg,	ESTs	3.3
417433	BE270266	Hs.82128	SS,TM,LRRCT,LRRNT,LRR,TM,LRRCT,	5T4 oncofetal trophoblast glycoprotein	3.3
452194	AI594413	Hs.332649	,SS,TM,7tm_3,ANF_receptor,sushi	olfactory receptor, family 2, subfamily	3.2
444051	N48373	Hs.10247	,SS,lg,	activated leucocyte cell adhesion molecu	3.2
420042	AW015140	Hs.181723	,SS,CUB,	ESTs	3.2
457292	AI921270	Hs.334882	SS,TM,SS,TM,G-patch	hypothetical protein FLJ14251	3.2
421458	NM_003654	Hs.104576	SS	carbohydrate (keratan sulfate Gal-6) sul	3.2
431104	AW970859	Hs.313503	,Sema,lg,	ESTs	3.2
443767	BE562136	Hs.9736	,SS,PCI,RasGEF,hormone_rec,zf-C4,	proteasome (prosome, macropain) 26S subu	3.2
419589	AW973708	Hs.201925	,FGF,	Homo sapiens cDNA FLJ13446 fis, clone PL	3.2
415447	Z97171	Hs.78454	SS,OLF,OLF,OLF,Ribosomal_L4	myoclin, trabecular meshwork inducible	3.2
443484	BE548446	Hs.5167	SS,TM,SSF,SS,TM	Homo sapiens mRNA; cDNA DKFZp434F152 (fr	3.2
423431	AA326082		,SS,p450,p450	gb:EST29171 Cerebellum II Homo sapiens c	3.2
413278	BE563085	Hs.833	,SS,TM,ubiquitin,laminin_G,laminin_EGF,k	interferon-stimulated protein, 15 kDa	3.2
458451	AW297181	Hs.195922	,SS,Ribosomal_L14	ESTs	3.2
440449	AA855430	Hs.201925	,FGF,	Homo sapiens cDNA FLJ13446 fis, clone PL	3.2
413753	U17760	Hs.75517	SS,laminin_EGF,laminin_Nterm,adh_short,S	laminin, beta 3 (nicein (125kD), kalinin	3.2
434876	AF160477	Hs.61460	,S8,HLH	Ig superfamily receptor LNIR	3.2
435575	AF213457	Hs.44234	SS,lg,SS,TM	triggering receptor expressed on myeloid	3.2
415773	R21651	Hs.324725	,SS,TM,Ribosomal_S3Ae,G-gamma	ESTs, Moderately similar to A47582 B-cel	3.2
446440	AV658411	Hs.42658	SS	KIAA1681 protein	3.2
450847	NM_003155	Hs.25590	,SS,homeobox,	stanniocalcin 1	3.2
426075	AW513691	Hs.270149	,SS,fn3,	ESTs, Weakly similar to 2109260A B cell	3.2
452110	T47667	Hs.28005	,SS,TM,Activin_recp,pkinase	Homo sapiens cDNA FLJ11309 fis, clone PL	3.2
439963	AW247529	Hs.6793	,TM,p450,Ets	platelet-activating factor acetylhydrola	3.2
402837	NA		SS	ENSP00000241312*:DJ947L8.1.8 (novel Sush	3.2
439451	AF088270	Hs.278554	,SS,Chromo_shadow,chromo,	heterochromatin-like protein 1	3.1
406684	L34041	Hs.9739	,SS,TM,transport_prot,SWIB,RhoGAP,DAG_P	Eglycerol-3-phosphate dehydrogenase 1 (so	3.1
417315	AI080042	Hs.336901	,SS,RNA_pol_A,RNA_pol_A2,Ribosomal_S24e,	ribosomal protein S24	3.1
413011	AW068115	Hs.821	SS,LRR,LRRNT,SS,LRRNT,LRR,	biglycan	3.1
414987	AA524394	Hs.294022	,SS,connexin,hormone_rec,zf-C4,connexin	hypothetical protein FLJ14950	3.1
429197	H24471	Hs.26930	,SS,Gelsolin,	ESTs, Weakly similar to T20272 hypotheti	3.1
448030	N30714	Hs.325960	SS,TM	membrane-spanning 4-domains, subfamily A	3.1
407604	AW191962	Hs.249239	,SS,TM,C1q,	collagen, type VIII, alpha 2	3.1
419092	J05581	Hs.89603	SS,TM,SEA,	mucin 1, transmembrane	3.1
456672	AK002016	Hs.114727	,SS,PK,PK	Homo sapiens, clone MGC:16327, mRNA, com	3.1
443171	BE281128	Hs.9030	SS,TM,7tm_1,rrm,SS	TONDU	3.1
452256	AK000933	Hs.28661	,TM,GDI,7tm_1,	Homo sapiens cDNA FLJ10071 fis, clone HE	3.1
432201	AI538613	Hs.298241	SS,TM,trypsin,SS,TM,trefoil,trypsin,traf	Transmembrane protease, serine 3	3.1
406642	AJ245210		SS	gb:Homo sapiens mRNA for immunoglobulin	3.1
400903	NA		SS	Target Exon	3.1

434408	AI031771	Hs.132586	,SS,Glyco_hydro_2	ESTs	3.1
452994	AW982597	Hs.31305	SS,WD40,SS,WD40,	KIAA1547 protein	3.1
445903	AI347487	Hs.132781	fn3,SS,TM,EF1BD	class I cytokine receptor	3.1
424364	AW383226	Hs.201189	SS	ESTs, Weakly similar to G01763 atrophin-	3.1
410196	AI936442	Hs.59838	UBACT_repeat,SS,UBACT_repeat,ThiF_family	hypothetical protein FLJ10808	3.1
419150	T29618	Hs.89640	,TM,pkinase,fn3,	TEK tyrosine kinase, endothelial (venous	3.1
433417	AA587773	Hs.8859	,SS,SRCR,	Homo sapiens, Similar to RIKEN cDNA 5830	3.1
418624	AI734080	Hs.104211	,Sema,Ig,	ESTs	3.1
436291	BE568452	Hs.5101	,SS,abhydrolase,	protein regulator of cytokinesis 1	3.1
411000	N40449	Hs.201619	SS	ESTs, Weakly similar to S38383 SEB4B pro	3.1
412519	AA196241	Hs.73980	SS,Troponin,Hemagglutinin,SS,TM,C2,Tropo	troponin T1, skeletal, slow	3.1
450223	AA418204	Hs.241493	,SS,pro_isomerase,	natural killer-tumor recognition sequenc	3.1
422790	AA809875	Hs.25933	,TM,histone,Sec1,histone,sugar_tr	ESTs	3.1
424269	AW137691	Hs.199754	,SS,TM,7tm_2,GPS	ESTs	3.1
435854	AJ278120	Hs.4996	,SS,WD40	putative ankyrin-repeat containing prote	3.1
447388	AW630534	Hs.76277	,SS,TM,rrm,oxidored_q6,oxidored_q6	Homo sapiens, clone MGC:9381, mRNA, comp	3.1
451631	R00868		SS	gb:ye79c02.s1 Soares fetal liver spleen	3.0
448105	AW591433	Hs.288241	,SS,TM,trefoil,trypsin,trefoil	Transmembrane protease, serine 3	3.0
438637	BE500941	Hs.126730	,TM,PH,	ESTs, Weakly similar to KIAA1214 protein	3.0
423024	AA593731	Hs.325823	,SS,TM,CD36	ESTs, Moderately similar to ALU5_HUMAN A	3.0
456592	R91600		,SS,Ran_BP1,LIM,Ran_BP1,GRIP,TPR,LIM	gb:yq10c02.r1 Soares fetal liver spleen	3.0
425920	AL049977	Hs.162209	SS,TM,SS,TM,PMP22_Claudin,PMP22_Claudin	claudin 6	3.0
444670	H58373	Hs.332938	,SS,TM	hypothetical protein MGC5370	3.0
401197			arf,arf,	ENSP00000229263:HSPC213.	3.0
437755	AW204256	Hs.291887	,wnt,	ESTs	3.0
452560	BE077084	Hs.336432	,SS,rrm,zf-RanBP,pkinase,C2,pkinase_C,DA	ESTs	3.0
410274	AA381807	Hs.61762	SS,SS	hypoxia-inducible protein 2	3.0
450098	W27249	Hs.8109	SS	hypothetical protein FLJ21080	3.0
404826			,SS,TM	Target Exon	3.0
458389	H70284	Hs.160152	,SS,RA	ESTs, Weakly similar to FPHU alpha-fetop	3.0
408196	AL034548	Hs.43627	HMG_box,pkinase,zf-CCHC,SS,TM,HMG_box,	SRY (sex determining region Y)-box 22	3.0
433675	AW977653	Hs.75319	,SS,ribonuc_red_sm,	ribonucleotide reductase M2 polypeptide	3.0
418848	AI820961	Hs.193465	,death,ZU5,pkinase,Activin_recp,	ESTs	3.0
422095	AI868872	Hs.282804	SS,Cu-oxidase,SS,Cu-oxidase,Cu-oxidase	hypothetical protein FLJ22704	3.0
415992	C05837	Hs.145807	,SS,TM	hypothetical protein FLJ13593	3.0
424631	AA688021	Hs.179808	SS	ESTs	3.0
409956	AW103364	Hs.727	SS,TGF-beta,TGFb_propeptide,SS,TGF-beta,	inhibin, beta A (activin A, activin AB a	3.0
419687	AU077005	Hs.92208	SS,disintegrin,Reprolysin,Pep_M12B_prope	a disintegrin and metalloproteinase doma	3.0
450946	AA374569	Hs.127698	SS	ESTs, Moderately similar to 2109260A B c	3.0
447770	AB032417	Hs.19545	Frizzled,Fz,SS,TM,Frizzled,Fz,	frizzled (Drosophila) homolog 4	3.0
423826	U20325	Hs.1707	SS,SS	cocaine- and amphetamine-regulated trans	3.0
418838	AW385224	Hs.35198	,SS,TM,Phosphodiest,	ectonucleotide pyrophosphatase/phosphodi	3.0
442804	AW300118	Hs.131257	,SS,TM,G-gamma	ESTs	3.0
432284	AA532807	Hs.105822	,SS,TM,pkinase,	ESTs	3.0

TABLE 20A

Table 20A shows the accession numbers for those pkeys lacking unigeneID's for Table 20. For each probeset, we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT number	Accessions
410785	1221055_1	AW803341 AW803265 AW803403 AW803466 AW803402 AW803413 AW803268 AW803396 AW803334 AW803355
411667	1253334_1	BE160196 AW935898 T11520 AW935930 AW856073 AW861034
418636	177402_1	AW749855 AA225995 AW750208 AW750206
420854	197072_1	AW296927 AI684514 AI263158 AA281079
422128	211994_1	AW881145 AA490718 M85637 AA304575 T06067 AA331991
423431	228182_1	AA326082 AA325758 AW962182
423945	233568_1	AA410943 AW948953 AA334202 AA332882
426878	273285_1	BE069341 AW748403 AL044891 AI908240 AA393080
433687	373061_1	AA743991 AA604852 AW272737
447197	711623_1	R36075 AI368546 R36167
451631	878098_1	R00868 R01523 AI808815
455207	165078_1	AA193450
456592	202684_1	R91600 T67079 AA291455

TABLE 20B

Table 20B shows the genomic positioning for those pkeys lacking unigene ID's and accession numbers in Table 20. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400608	9887666	Minus	96756-97556
400903	2911732	Plus	59112-59228
401045	8117619	Plus	90044-90184,91111-91345
401093	8516137	Minus	22335-23166
401197	9719705	Plus	176341-176452
401747	9789672	Minus	118596-118816,119119-119244,119609-119761,120422-120990,130181-130381,130468-130593,131097-131258,131866-131932,132451-132575,133560-134011
401780	7249190	Minus	28397-28617,28920-29045,29135-29296,29411-29567,29705-29787,30224-30573
401781	7249190	Minus	83215-83435,83531-83656,83740-83901,84237-84393,84955-85037,86290-86814
401868	8016106	Plus	73126-73823
402230	9966312	Minus	29782-29932
402408	9796239	Minus	110326-110491
402578	9884928	Plus	66350-66496
402606	9909429	Minus	81747-82094
402837	9369121	Minus	2013-2166,9570-9758,11136-11309,19429-19677,21210-21455,23368-23562,24342-24527,29132-29320
403199	9958183	Minus	58895-59036,66618-66789
403329	8516120	Plus	95450-96598
403593	6862650	Minus	62554-62712,69449-69602
403943	7711864	Plus	100742-100904,101322-101503
404091	7684554	Minus	82121-83229
404347	9838195	Plus	74493-74829
404826	6572184	Plus	47726-48046
405366	2182280	Plus	22478-22632
405654	4895155	Minus	53824-53759

TABLE 21: 210 GENES UP-REGULATED IN BREAST CANCER COMPARED TO NORMAL ADULT TISSUES THAT ARE LIKELY TO ENCODE EITHER ENZYMES OR PROTEINS AMENABLE TO MODULATION BY SMALL MOLECULES

Table 21 shows 210 genes up-regulated in breast cancer compared to normal adult tissues that are likely to encode either enzymes or proteins amenable to modulation by small molecules. These were selected as for Table 19, except that the ratio was greater than or equal to 3.0, the "average" normal adult tissue level was set to the 85th percentile value amongst 144 non-malignant tissues, and the 96th percentile value amongst 73 breast cancers was greater than or equal 80 units, and the predicted protein contained a structural domain that is indicative of enzymatic function or of being modulatable by small molecules (e.g. pkinase, peptidase, phosphatase, ATPase, or ion_transporter domains). The predicted protein domains are noted.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of 93rd percentile tumor to 85th percentile of normal body tissue

Pkey	ExAccn	UnigeneID	Predicted Protein Domains	UnigeneTitle	R1
449746	AI668594	Hs.176588	SS,p450	ESTs, Weakly similar to CP4Y_HUMAN CYTOC	65.7
400292	AA250737	Hs.72472	death,ZU5,TM,Activin_recp,pkinase,	BMP-R1B	55.9
424735	U31875	Hs.272499	SS,TM	short-chain alcohol dehydrogenase family	53.8
407178	AA195651	Hs.104106	SS,Dihydroorotase,	ESTs	39.3
408045	AW138959	Hs.245123	Phosphodiest,Somatomedin_B,	ESTs	34.9
450375	AA009647	Hs.8850	SS,TM,disintegrin,Pep_M12B_propep,Reprol	a disintegrin and metalloproteinase doma	25.7
429170	NM_001394	Hs.2359	DSPc,Rhodanese,	dual specificity phosphatase 4	24.9
445730	AI624342	Hs.170042	SS,TM,Cation_efflux	ESTs	24.1
424634	NM_003613	Hs.151407	Ig,tsp_1,SS,AAA	cartilage intermediate layer protein, nu	21.7
420757	X76592	Hs.99915	hormone_rec,Androgen_recep,zf-C4,	androgen receptor (dihydrotestosterone r	21.7
424399	AI905687	Hs.2533	SS	aldehyde dehydrogenase 9 family, member	20.3
447350	AI375572	Hs.172634	pkinase,	ESTs	19.2
456207	AA193450		SS,TM,p450,p450	gb:zr40e07.r1 Soares_NhHMPu_S1 Homo sapi	18.3
456938	X52509	Hs.161640	SS,TM,aminotran_1_2,Cadherin_C_term,cadhtyrosine aminotransferase		18.1
402578			SS,p450,SS,TM,p450	C1001134:gi[2117372]pir[i]i55081 fatty ac	17.8
425692	D80041	Hs.155956	SS,Acetyltransf2,	N-acetyltransferase 1 (arylamine N-acety	16.7
424001	W67883	Hs.137476	pkinase,	paternally expressed 10	16.5
418007	M13509	Hs.83169	SS,hemopexin,Peptidase_M10,SS,Peptidase_	matrix metalloproteinase 1 (MMP1; inters	15.7
421727	Y13153	Hs.107318		kynurenine 3-monooxygenase (kynurenine 3	15.3
411869	W20027	Hs.23439	SS,Peptidase_M1,	ESTs	13.9
400289	X07820	Hs.2258	hemopexin,Peptidase_M10,SS,Peptidase_M10	matrix metalloproteinase 10 (MMP10; str	13.5
443348	AW873596	Hs.182278	SS,DENN	calmodulin 2 (phosphorylase kinase, delt	13.0
424088	AI351010	Hs.102267	SS,Lysyl_oxidase	lysyl oxidase	12.8
400295	W72838	Hs.2533	SS	aldehyde dehydrogenase 9 family, member	12.7
408771	AW732573	Hs.47584	TM,K_tetra,Ion_trans,SS,TM,K_tetra,Ion_t	potassium voltage-gated channel, delayed	11.9
421155	H87879	Hs.102267	SS,Lysyl_oxidase,Aldose_epim,Epimerase,S	lysyl oxidase	11.8
424905	NM_002497	Hs.153704	pkinase,SS,TM,pkinase,polyprenyl_synt,	NIMA (never in mitosis gene a)-related k	11.7
438167	R28363	Hs.24266	SS,TM,7tm_1,p450,rrm	ESTs	11.5
459583	AI907673		pkinase,	gb:IL-BT152-080399-004 BT152 Homo sapien	11.5
423945	AA410943		death,ZU5,TM,Activin_recp,pkinase,	gb:zt32h03.r1 Soares ovary tumor NbHOT H	11.4
445263	H57646	Hs.42586	SS,Acyltransferase,	KIAA1560 protein	11.2

423887	AL080207	Hs.134585	SS,TM,BRCT,ank,ABC_tran,ABC_tran	DKFZP434G232 protein	10.9
429859	NM_007050	Hs.225952	SS,TM,Y_phosphatase,MAM,fn3,	protein tyrosine phosphatase, receptor t	10.4
428368	BE440042	Hs.83326	SS,Peptidase_M10,hemopexin,SS,Peptidase_	matrix metalloproteinase 3 (stromelysin	10.3
418912	NM_000685	Hs.89472	SS,TM,7tm_1,SS,TM,7tm_1,	angiotensin receptor 1	10.3
451952	AL120173	Hs.301663	SS,pkinase,	ESTs	10.3
402408	NA		SS,carb_anhydrase	NM_030920*:Homo sapiens hypothetical pro	9.8
415539	AI733881	Hs.72472	death,ZU5,TM,Activin_recp,pkinase,	BMP-R1B	9.4
406687	M31126	Hs.272620	SS,Peptidase_M10,hemopexin,SS,Peptidase_	matrix metalloproteinase 11 (MMP11; stro	9.1
419948	AB041035	Hs.93847	Ferric_reduct,TM,Ferric_reduct,	NM_016931:Homo sapiens NADPH oxidase 4 (	9.1
400285	NA		TM,ABC_tran,ABC_membrane,	Eos Control	8.8
408380	AF120050	Hs.44532	SS,TM,ubiquitin,7tm_3,ANF_receptor,sushi	ubiquitin	8.6
409203	AA780473	Hs.687	SS,p450,SS,p450	cytochrome P450, subfamily IVB, polypept	8.3
424902	NM_003866	Hs.153687	SS,SS	inositol polyphosphate-4-phosphatase, ty	8.3
431725	X65724	Hs.2839	SS,Cys_knot,SS	Norrie disease (pseudoglioma)	8.3
418092	R45154	Hs.106604	death,ZU5,pkinase,Activin_recp,	ESTs	8.3
427811	M81057	Hs.180884	SS,Zn_carbOpept,Propep_M14,SS,Propep_M14	carboxypeptidase B1 (tissue)	8.2
423554	M90516	Hs.1674	GATase_2,SIS,	glutamine-fructose-6-phosphate transamin	8.1
426261	AW242243	Hs.168670	SS,TM,WD40,ubiquitin,E1-E2_ATPase,Cation	peroxisomal farnesylated protein	7.8
413374	NM_001034	Hs.75319	SS	ribonucleotide reductase M2 polypeptide	7.6
432677	NM_004482	Hs.278611	SS,TM,Glycos_transf_2,Ricin_B_lectin,DPP	UDP-N-acetyl-alpha-D-galactosamine:polyp	7.6
456988	D38299	Hs.170917	SS,TM,7tm_1,	prostaglandin E receptor 3 (subtype EP3)	7.5
453331	AI240665	Hs.8895	SS,TM,disintegrin,Pep_M12B_propep,Reprol	ESTs	7.3
407721	Y12735	Hs.38018	pkinase,	dual-specificity tyrosine-(Y)-phosphoryl	7.2
418004	U37519	Hs.87539	SS,aldedh,SS,aldedh,	aldehyde dehydrogenase 3 family, member	7.2
410555	U92649	Hs.64311	TM,disintegrin,Reprolysin,	a disintegrin and metalloproteinase doma	7.1
443695	AW204099	Hs.337720		ESTs, Weakly similar to AF126760 1 retin	6.9
423545	AP000892	Hs.129781	GAF,PDEase	chromosome 21 open reading frame 5	6.8
401045			ICE_p20,SS,ICE_p10,ICE_p20,ICE_p10,ICE_p		
	C11001883*:gi|8753278|ref|NP_033938.1| c			6.7	
442082	R41823	Hs.7413	TM,EPH_lbd,pkinase,SAM,fn3,	ESTs; calsyntenin-2	6.7
418836	AI655499	Hs.161712	TM,Activin_recp,pkinase,death,ZU5,	ESTs	6.6
404091	NA		TM,7tm_3,ANF_receptor,	Target Exon	6.6
450865	AI248013	Hs.106532	zf-C2H2	ESTs, Weakly similar to I38568 reverse t	6.5
424085	NM_002914	Hs.139226	SS,AAA,Viral_helicase1,rrm,	replication factor C (activator 1) 2 (40	6.5
449650	AF055575	Hs.23838	TM,Ion_trans,SS,TM,Ion_trans,	calcium channel, voltage-dependent, L ty	6.4
432304	AA932186	Hs.69297	TM,7tm_1,	ESTs	6.2
415669	NM_005025	Hs.78589	SS,serpin,	serine (or cysteine) proteinase inhibito	6.2
442942	AW167087	Hs.131562	SS,Ig,Sema,pkinase,	ESTs	6.2
428795	R45503	Hs.97469	SS,TM	ESTs, Highly similar to A39769 N-acetyl	6.1
428479	Y00272	Hs.184572	SS,pkinase,pkinase	cell division cycle 2, G1 to S and G2 to	6.1
400300	X03363		SS,TM,pkinase,Recep_L_domain,SH2,PH,Furi	HER2 receptor tyrosine kinase (c-erb-b2,	6.1
447359	NM_012093	Hs.18268	SS,adenylatekinase,	adenylate kinase 5	6.1
402230	NA		SS,TM,p450,	Target Exon	6.1
424687	J05070	Hs.151738	SS,Peptidase_M10,fn2,hemopexin,SS,TM,Pep	matrix metalloproteinase 9 (gelatinase B	5.8
432328	AI572739	Hs.195471	6PF2K,PGAM,	6-phosphofructo-2-kinase/fructose-2,6-bi	5.8
432239	X81334	Hs.2936	SS,Peptidase_M10,hemopexin,SS,Peptidase_	matrix metalloproteinase 13 (collagenase	5.6
400286	NA		SS,TM,ABC_tran,ABC_membrane,SS	C16000922:gi|7499103|pir||T20903 hypothe	5.6
425247	NM_005940	Hs.155324	SS,Peptidase_M10,hemopexin,SS	matrix metalloproteinase 11 (MMP11; stro	5.4
434737	AA828246	Hs.291884	UCH-1,pkinase,OPR,Rhodanese,AMP-binding,	ESTs	5.4
439310	AF086120	Hs.102793	SS,TM,UDPGT,casein_kappa	ESTs	5.2
441111	AI806867	Hs.126594	SS,TM,Phosphodiest,	ESTs	5.2
452355	N54926	Hs.29202	TM,7tm_1,TM	G protein-coupled receptor 34	5.2
427711	M31659	Hs.180408	SS	solute carrier family 25 (mitochondrial	5.2
429353	AL117406	Hs.200102	SS,TM,ABC_tran,ABC_membrane,	ATP-binding cassette transporter MRP8	5.1
425325	X52730	Hs.1892	SS,NNMT_PNMT_TEMT,SS,NNMT_PNMT_TEMT,STAR		
	phenylethanolamine N-methyltransferase			5.1	
448706	AW291095	Hs.21814	SS,TM,pkinase,	interleukin 20 receptor, alpha	5.1
403593	NA		CIDE-N,pkinase	Target Exon	5.1
432777	AA564991	Hs.269477	alpha-amylase,	ESTs	5.0
446232	AI281848	Hs.194691	SS,TM,7tm_3,Ribosomal_L13	retinoic acid induced 3	4.9
411165	NM_000169	Hs.69089	SS,Melibiase,BTK,PH,pkinase,SH2,SH3,Ribo	galactosidase, alpha	4.9
414117	W88559	Hs.1787	TM,Ion_trans,K_tetra,	protacalpid protein 1 (Pelizaeus-Merzbac	4.9
411096	U80034	Hs.68583	Peptidase_M3,	mitochondrial intermediate peptidase	4.9
450506	NM_004460	Hs.418	SS,DPPIV_N_term,Peptidase_S9,SS,DPPIV_N_	fibroblast activation protein, alpha	4.9
417975	AA641838	Hs.30085	SS,trypsin	hypothetical protein FLJ23186	4.9
447752	M73700	Hs.105938	SS,transferrin,7tm_1,transferrin,	lactotransferrin	4.8
427122	AW057736	Hs.323910	SS,TM,pkinase,Recep_L_domain,SH2,PH,Furi	HER2 receptor tyrosine kinase (c-erb-b2,	4.8

400181	NA		SS,TM,3Beta_HSD,	ENSP00000171555:cDNA FLJ10727 fis, clone	4.6
452093	AA447453	Hs.27860	SS,TM,7tm_1,	Homo sapiens mRNA; cDNA DKFZp586M0723 (f	4.6
435542	AA687376	Hs.269533	SS,pkinase,RhoGEF,Ig,PH,SH3,	ESTs	4.6
417576	AA339449	Hs.82285	AIRS,formyl_transf,GARS,SS,GARS,AIRS,for	phosphoribosylglycinamide formyltransfer	4.6
446089	AI850021	Hs.270651	pkinase	ESTs, Moderately similar to A47582 B-cel	4.6
424420	BE614743	Hs.146688	SS,TM,MAPEG,	prostaglandin E synthase	4.5
452190	H26735	Hs.91668	SS,TM,PH,SH2,Furin-like,pkinase,Recep_L_	Homo sapiens clone PP1498 unknown mRNA	4.5
419986	AI345455	Hs.78915	pkinase,OPR,	GA-binding protein transcription factor,	4.5
421582	AI910275	Hs.1406	SS,trefoil,SS,TM,ldl_recept_a,SRCR,tryps	trefoil factor 1 (pS2)	4.5
448733	AA863360	Hs.26040	SS,TM,p450,	ESTs, Weakly similar to fatty acid omega	4.4
453060	AW294092	Hs.21594	SS,ras,Y_phosphatase,ras	hypothetical protein MGC15754	4.4
400205	NA			NM_006265*:Homo sapiens RAD21 (S. pombo)	4.4
420854	AW296927		SS,TM,Peptidase_M1,	gb:UI-H-BW0-ajc-c-07-0-UI.s1 NCI_CGAP_Su	4.3
432690	AF181490	Hs.278627	SS,pyr_redox,SS,Ribosomal_L39	prenylcysteine lyase	4.3
441560	F13388	Hs.7888	pkinase,	Homo sapiens clone 23736 mRNA sequence	4.3
416445	AL043004	Hs.79337	SS,pkinase,	KIAA0135 protein	4.3
439024	R96696	Hs.35598	SS,TM,trypsin,vwd,Ig	ESTs	4.3
432882	NM_013257	Hs.279696	pkinase,pkinase_C,	serum/glucocorticoid regulated kinase-li	4.2
447754	AW073310	Hs.163533	pkinase,	Homo sapiens cDNA FLJ14142 fis, clone MA	4.2
453775	NM_002916	Hs.35120	SS,AAA,PI3_P14_kinase,PI3Ka,PI3K_rbd,PI3	replication factor C (activator 1) 4 (37	4.2
431657	AI345227	Hs.105448	SS,TM,pkinase	ESTs, Weakly similar to B34087 hypotheti	4.1
427899	AA829266	Hs.332053	SS,SAA_proteins,ABC_membrane,ABC_tran,	serum amyloid A1	4.1
422938	NM_001809	Hs.1594	SS,TM,thiolase,	centromere protein A (17kD)	4.1
418478	U38945	Hs.1174	ank,ank	cyclin-dependent kinase inhibitor 2A (me	4.1
406922	S70264		SS,TM,Desaturase,SS	gb:stearoyl-CoA desaturase [human, adipo	4.1
439285	AL133916	Hs.172572	SS,Ig,pkinase,LRRNT,LRRCT,	hypothetical protein FLJ20093	4.1
429922	Z97630	Hs.226117	SS,TM,linker_histone,7tm_1	H1 histone family, member 0	4.1
420139	NM_005357	Hs.95351	SS,TM,p450,	lipase, hormone-sensitive	4.0
425071	NM_013989	Hs.154424	SS,T4_deiodinase,T4_deiodinase,	deiodinase, iodothyronine, type II	4.0
424511	BE300512	Hs.193557	SS,Y_phosphatase,Band_41	ESTs, Moderately similar to ALU7_HUMAN A	4.0
428722	U76456	Hs.190787	SS,TIMP,	tissue inhibitor of metalloproteinase 4	3.9
428330	L22524	Hs.2256	SS,Peptidase_M10,SS,Peptidase_M10,hemope	matrix metalloproteinase 7 (MMP7; uterin	3.9
414831	M31158	Hs.77439	SS,cNMP_binding,Rtia,HMG_box	protein kinase, cAMP-dependent, regulato	3.9
413589	AW452631	Hs.313803	SS,abhydrolase	ESTs, Highly similar to AF157833 1 nonci	3.8
418629	BE247550	Hs.86859	SS,SH2,PH,SS,TM,PH,SH2,Furin-like,pkinas	growth factor receptor-bound protein 7	3.8
413453	AA129640	Hs.128065	SS,Peptidase_C1,gpdh	ESTs	3.8
403943			p450,SS,p450	C5000355:gi|4503225|ref|NP_000765.1| cyt	3.8
444618	AV653785	Hs.173334		ELL-RELATED RNA POLYMERASE II, ELONGATIO	3.8
408761	AA057264	Hs.238938	SS,TM,7tm_1,	ESTs, Weakly similar to (define not ava	3.8
427809	M26380	Hs.180878	SS,tRNA,PLAT,Sec7,PH,	lipoprotein lipase	3.7
418203	X54942	Hs.83758	CK8,SS,CK8,	CDC28 protein kinase 2	3.7
454071	AI041793	Hs.42502	TM,7tm_1,	ESTs	3.7
424676	Y08565	Hs.151678	Glycos_transf_2,Ricin_B_lectin,SS,Glycos	UDP-N-acetyl-alpha-D-galactosamine:polyp	3.7
457465	AW301344	Hs.122908	SS,Ribosyltran,Sufatase	DNA replication factor	3.7
417601	NM_014735	Hs.82292	PHD,pkinase,SS	KIAA0215 gene product	3.7
446819	AU076643	Hs.313	SS,TM,ethanol_ion_trans	secreted phosphoprotein 1 (osteopontin,	3.7
406625	Y13647	Hs.119597	SS,TM,Desaturase,SS	stearoyl-CoA desaturase (delta-9-desatur	3.6
428769	AW207175	Hs.106771	SS,7tm_1,SPRY,	ESTs	3.6
426310	NM_000909	Hs.169266	SS,TM,7tm_1,	neuropeptide Y receptor Y1	3.6
417531	NM_003157	Hs.1087	SS,pkinase,wwa,wwa,Glyco_transf_8	serine/threonine kinase 2	3.6
444781	NM_014400	Hs.11950	SS,PH,lactamase_B	GPI-anchored metastasis-associated prote	3.6
431493	AI791493	Hs.129873	SS,p450,p450	ESTs, Weakly similar to A36038 cytochrom	3.6
428966	AF059214	Hs.194687		cholesterol 25-hydroxylase	3.6
414175	AI308876	Hs.103849	TM,hemopexin,Peptidase_M10,hemopexin,Pep	hypothetical protein DKFZp761D112	3.6
455325	AW895719		TM,Ion_trans,K_tetra,	gb:QV4-NN0039-290300-154-f08 NN0039 Homo	3.6
429597	NM_003816	Hs.2442		a disintegrin and metalloproteinase doma	3.6
425320	U29344	Hs.83190	Acyl_transf,adh_zinc,ketoacyl-synt,pp-bi	fatty acid synthase	3.5
431854	AA383550	Hs.271699	IMS,SS	polymerase (DNA directed) iota	3.5
407104	S57296	Hs.323910	SS,TM,SH2,PH,pkinase,Recep_L_domain,Furi	v-erb-b2 avian erythroblastic leukemia v	3.5
449051	AW961400	Hs.333526	SS	HER2 receptor tyrosine kinase (c-erb-b2,	3.5
434398	AA121098	Hs.3638	pkinase,POLO_box,SS,pkinase,POLO_box,	serum-inducible kinase	3.5
454042	H22570	Hs.172572	SS,Ig,pkinase,LRRNT,LRRCT,	hypothetical protein FLJ20093	3.5
407758	AA116021	Hs.38260	SS,UCH-1,UCH-2,SS,TM,G_glu_transpept	ubiquitin specific protease 18	3.5
401464	AF039241	Hs.9028	Peptidase_M24,	histone deacetylase 5	3.5
412970	AB026436	Hs.177534	DSPc,Myosin_tail,	dual specificity phosphatase 10	3.5
412049	N53437	Hs.18268	SS,adenylatekinase,	adenylate kinase 5	3.5
425776	U25128	Hs.159499	SS,TM,7tm_2,SS,TM,7tm_2	parathyroid hormone receptor 2	3.4

407846	AA426202	Hs.40403	TM,ABC_membrane,ABC_tran,Ribosomal_S4eCbp/p300-interacting transactivator, wit		3.4
406925	L34041	Hs.8739	SS,TM,transport_prot,SWIB,RhoGAP,DAG_PE-glycerol-3-phosphate dehydrogenase 1 (so		3.4
445873	AA250970	Hs.251946	SS,rrm,PABP,pkinase,14-3-3,rrm	poly(A)-binding protein, cytoplasmic 1-l	3.4
418054	NM_002318	Hs.83354	SS,TM,mito_carr,Lysyl_oxidase	lysyl oxidase-like 2	3.4
406815	AA833930	Hs.288036	SS,IPPT,	tRNA isopentenylpyrophosphate transferas	3.4
410530	M25809	Hs.64173	ATP-synt_ab,SS,7tm_1,ATP-synt_ab	ATPase, H transporting, lysosomal (vacuo	3.4
407021	U52077			gb:Human mariner1 transposase gene, comp	3.4
421168	AF182277	Hs.330780	SS,p450,SS	cytochrome P450, subfamily IIB (phenobar	3.4
431473	AA825688	Hs.321176	SS	ESTs, Weakly similar to S65824 reverse t	3.4
408101	AW968504	Hs.123073	pkinase,	CDC2-related protein kinase 7	3.4
422083	NM_001141	Hs.111256	lipoxygenase,PLAT,	arachidonate 15-lipoxygenase, second typ	3.3
411393	AW797437	Hs.69771	SS,sushi,trypsin,vwa,rrm,fibrinogen_C,fn	B-factor, properdin	3.3
435767	H73505	Hs.117874	SS,Peptidase_S8,P,Peptidase_S8,P	ESTs	3.3
433068	NM_006456	Hs.288215	SS,Pribosyltran,	alalytransferase	3.3
426928	AF037062	Hs.172914	SS,adh_short,TGF-beta,TGFb_propeptide	retinol dehydrogenase 5 (11-cis and 9-ci	3.3
414575	H11257	Hs.22968	SS,pkinase,Ig,	Homo sapiens clone IMAGE:451939, mRNA se	3.3
445941	AI267371	Hs.172636	SS,SS,lipoxygenase,PLAT	ESTs	3.3
444542	AI161293	Hs.280380	SS,SS,Peptidase_M1,EGF,Ig,lectin_c,sushi	aminopeptidase	3.3
425741	AF052152	Hs.159412	pkinase,	Homo sapiens clone 24628 mRNA sequence	3.3
434228	Z42047	Hs.283978	SS,TM,7tm_1	Homo sapiens PRO2751 mRNA, complete cds	3.3
433264	D85782	Hs.3229		cysteine dioxygenase, type I	3.3
400419	AF084545		SS,Peptidase_M1,	Target	3.3
439750	AL359053	Hs.57664	TM,Integrin_B,Ricin_B_lectin,rrm	Homo sapiens mRNA full length insert cDN	3.3
417757	R19897	Hs.106604	death,ZU5,pkinase,Activin_recp,	ESTs	3.3
452194	AI694413	Hs.332649	SS,TM,7tm_3,ANF_receptor,sushi	olfactory receptor, family 2, subfamily	3.2
421458	NM_003654	Hs.104576	SS	carbohydrate (keratan sulfate Gal-6) sul	3.2
443767	BE562136	Hs.9736	SS,PCI,RasGEF,hormone_rec,zf-C4,	proteasome (prosome, macropain) 26S subu	3.2
422648	D86983	Hs.118893	peroxidase,LRRCT,	Melanoma associated gene	3.2
423431	AA326062		SS,p450,p450	gb:EST29171 Cerebellum II Homo sapiens c	3.2
451264	AI768235		SS,Trehalase	gb:wg82g08.x1 Soares_NSF_F8_9W_OT_PA_P_S	3.2
452110	T47667	Hs.28005	SS,TM,Activin_recp,pkinase	Homo sapiens cDNA FLJ11309 fis, clone PL	3.2
439963	AW247529	Hs.6793	TM,p450,Ets	platelet-activating factor acetylhydrola	3.2
453941	U39817	Hs.36820	SS,DEAD,HRDC,helicase_C,	Bloom syndrome	3.1
406664	L34041	Hs.9739	SS,TM,transport_prot,SWIB,RhoGAP,DAG_PE-		glycerol-3-
phosphate dehydrogenase 1 (so			3.1		
453487	R31770	Hs.23540	TM,7tm_1,	ESTs	3.1
420911	U77413	Hs.100293		O-linked N-acetylglucosamine (GlcNAc) tr	3.1
443171	BE281128	Hs.9030	SS,TM,7tm_1,rrm,SS	TONDU	3.1
452256	AK000933	Hs.28661	TM,GDI,7tm_1,	Homo sapiens cDNA FLJ10071 fis, clone HE	3.1
432201	AI538613	Hs.298241	SS,TM,trypsin,SS,TM,trefoil,trypsin,tref	Transmembrane protease, serine 3	3.1
419150	T29618	Hs.89640	TM,pkinase,fn3,	TEK tyrosine kinase, endothelial (venous	3.1
444443	AI149286	Hs.55099	SS	rab6 GTPase activating protein (GAP and	3.1
426283	NM_003937	Hs.169139		kynureninase (L-kynurenine hydrolase)	3.1
436291	BE568452	Hs.5101	SS,abhydrolase,	protein regulator of cytokinesis 1	3.1
450223	AA418204	Hs.241493	SS,pro_isomerase,	natural killer-tumor recognition sequenc	3.1
424269	AW137691	Hs.199754	SS,TM,7tm_2,GPS	ESTs	3.1
448105	AW591433	Hs.298241	SS,TM,trefoil,trypsin,trefoil	Transmembrane protease, serine 3	3.0
452560	BE077084	Hs.336432	SS,rrm,zf-RanBP,pkinase,C2,pkinase_C,DAG	ESTs	3.0

TABLE 21A

Table 21 A shows the accession numbers for those pkeys lacking unigeneID's for Table 21. For each probeset, we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT number	Accessions
420854	197072_1	AW296927 AI684514 AI263168 AA281079
423431	228162_1	AA326062 AA325758 AW962182
423945	233566_1	AA410943 AW948953 AA334202 AA332882
451264	663988_1	AI768235 R31400 H29082 H23107
455325	1279475_1	AW895719 N31451 N41451
456207	165078_-1	AA193450

TABLE 21B

Table 21B shows the genomic positioning for those pkeys lacking unigene ID's and accession numbers in Table 21. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique number corresponding to an Ecs probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
401045	8117619	Plus	90044-90184,91111-91345
402230	9966312	Minus	29782-29932
402408	9796239	Minus	110326-110491
402578	9884928	Plus	66350-66498
403593	6862650	Minus	62554-62712,69449-69602
403943	7711864	Plus	100742-100904,101322-101503
404091	7684554	Minus	82121-83229

TABLE 22: 739 GENES UP-REGULATED IN BREAST CANCER COMPARED TO NORMAL ADULT BREAST

Table 22 shows 739 genes up-regulated in breast cancer compared to normal adult breast. These were selected as for Table 19, except that the ratio was greater than or equal to 3.0, the denominator was the 85th percentile value for 12 non-malignant breast specimens, and the 96th percentile value amongst the 73 breast cancers was greater than or equal 100 units.

Pkey: Unique Ecs probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of 90th percentile tumor to 85th percentile normal breast tissue

Pkey	ExAccn	UnigeneID	UnigeneTitle	R1
400292	AA250737	Hs.72472	BMP-R1B	51.5
424735	U31875	Hs.272499	short-chain alcohol dehydrogenase family	38.3
400297	AI127076	Hs.334473	hypothetical protein DKFZp564O1278	29.9
431448	AL137517	Hs.334473	hypothetical protein DKFZp564O1278	26.9
451110	AI955040	Hs.265398	ESTs, Weakly similar to transformation-r	25.8
431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	23.2
418203	X54942	Hs.83758	CDC28 protein kinase 2	22.6
407980	AA048309		gb:zf12f01.s1 Soares_fetal_heart_NbHH19W	19.8
414646	AA353776	Hs.901	CD48 antigen (B-cell membrane protein)	18.9
446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	18.0
409041	AB033025	Hs.50081	KIAA1199 protein	17.6
412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	17.6
407824	AA147884	Hs.9812	Homo sapiens cDNA FLJ14388 fis, clone HE	17.1
453160	AI263307	Hs.239884	H2B histone family, member L	17.0
407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	16.1
426692	D90041	Hs.155856	N-acetyltransferase 1 (arylamine N-acety	16.1
438533	AI440266	Hs.170673	ESTs, Weakly similar to T24832 hypotheti	16.0
426227	AA321649	Hs.2248	small inducible cytokine subfamily B (CX	15.5
444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	15.1
422505	AL120862	Hs.124165	programmed cell death 9 (PDCD9)	14.9
430515	AA746503	Hs.283313	ESTs	14.7
417308	H60720	Hs.81892	KIAA0101 gene product	14.4
452744	AI267652	Hs.30504	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	14.4
412446	AI768015	Hs.92127	ESTs	14.2
415539	AI733881	Hs.72472	BMP-R1B	14.1
435496	AW840171	Hs.265398	ESTs, Weakly similar to transformation-r	13.8
438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear transl	13.8
400205	NA		NM_006265*:Homo sapiens RAD21 (S. pombe)	13.5
430965	AA489732	Hs.154918	ESTs	13.4
415263	AA948033	Hs.130853	ESTs	13.3
451952	AL120173	Hs.301683	ESTs	13.2
449722	BE280074	Hs.23960	cyclin B1	13.2
406685	M18728		gb:Human nonspecific crossreacting antig	13.0
406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	12.8
429925	NM_000786	Hs.226213	cytochrome P450, 51 (lanosterol 14-alpha	12.8
416498	U33632	Hs.78351	potassium channel, subfamily K, member 1	12.7
432378	AI493046	Hs.146133	ESTs	12.5
441377	BE218239	Hs.202656	ESTs	12.5
456207	AA193450		gb:zr40e07.r1 Soares_NhHMPu_S1 Homo sapi	12.4
422805	AA436989	Hs.121017	H2A histone family, member A	12.2
407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	12.2
407178	AA195651	Hs.104106	ESTs	12.2

420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	12.1
421727	Y13153	Hs.107318	kynurenine 3-monooxygenase (kynurenine 3	12.0
434408	AI031771	Hs.132586	ESTs	12.0
446591	H44186	Hs.15456	PDZ domain containing 1	11.9
431385	BE178536	Hs.11090	membrane-spanning 4-domains, subfamily A	11.8
443348	AW873596	Hs.182278	calmodulin 2 (phosphorylase kinase, delt	11.7
416602	NM_006159	Hs.79389	nel (chicken)-like 2	11.7
433365	AF026944	Hs.293787	ESTs	11.6
437866	AA156781	Hs.74170	metallothionein 1E (functional)	11.5
412472	AW975398	Hs.293836	ESTs	11.4
416030	H15261	Hs.21948	ESTs	11.3
439979	AW600291	Hs.6823	hypothetical protein FLJ10430	11.3
420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	11.3
411598	BE336654	Hs.70937	H3 histone family, member A	11.2
423600	AI633559	Hs.310359	ESTs	11.2
430770	AA765694	Hs.123296	ESTs	11.0
421037	AI684808	Hs.197653	programmed cell death 9 (PDCD9)	10.9
452461	N78223	Hs.108106	transcription factor	10.7
409269	AA576953	Hs.22972	hypothetical protein FLJ13352	10.6
417791	AW965339	Hs.111471	ESTs	10.6
447268	AI370413	Hs.36563	hypothetical protein FLJ22416	10.4
424001	W67883	Hs.137476	paternally expressed 10	10.4
447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	10.4
424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	10.1
453619	H87648	Hs.33922	Homo sapiens, clone MGC:9084, mRNA, comp	10.1
442942	AW167087	Hs.131562	ESTs	10.1
434377	AW137148	Hs.306593	Homo sapiens cDNA FLJ11382 fis, clone HE	10.1
427217	AA399272	Hs.144341	ESTs	10.1
445730	AI624342	Hs.170042	ESTs	10.0
432887	AI926047	Hs.162859	ESTs	10.0
452243	AL355715	Hs.28555	programmed cell death 9	9.9
424590	AW966399	Hs.46821	hypothetical protein FLJ20086	9.9
432169	Y00971	Hs.2910	phosphoribosyl pyrophosphate synthetase	9.9
438950	H23789	Hs.144530	EST	9.9
418836	AI655499	Hs.161712	ESTs	9.8
430291	AV660345	Hs.238126	CGI-49 protein	9.8
444665	BE613126	Hs.47783	B aggressive lymphoma gene	9.7
407377	C16391		gb:C16391 Clontech human aorta polyA mRN	9.7
445413	AA151342	Hs.12677	CGI-147 protein	9.7
443462	AI064690	Hs.171176	ESTs	9.7
442145	AI022650	Hs.8117	erbb2-interacting protein ERBIN	9.7
435570	AF212222	Hs.177812	uncharacterized bone marrow protein BM04	9.7
439820	AL360204	Hs.283853	Homo sapiens mRNA full length insert cDN	9.6
428968	AF059214	Hs.194687	cholesterol 25-hydroxylase	9.6
449448	D60730	Hs.57471	ESTs	9.6
433929	AI375499	Hs.27379	ESTs	9.5
432731	R31178	Hs.287820	fibronectin 1	9.3
411815	AA156679	Hs.125790	leucine-rich repeat-containing 2	9.3
415385	R17798	Hs.7535	COBW-like protein	9.3
422026	U80736	Hs.110826	trinucleotide repeat containing 9	9.2
432596	AJ224741	Hs.278461	matrilin 3	9.2
439451	AF086270	Hs.278554	heterochromatin-like protein 1	9.2
423945	AA410943		gb:zt32h03.r1 Soares ovary tumor NbHOT H	9.1
442432	BE093589	Hs.38178	hypothetical protein FLJ23468	9.1
446715	AI337735	Hs.173919	ESTs, Moderately similar to ZN91_HUMAN Z	9.0
408771	AW732573	Hs.47584	potassium voltage-gated channel, delayed	9.0
437021	AI076089	Hs.292239	ESTs	9.0
428479	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to	8.9
428839	AI767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	8.9
402408	NA		NM_030920:Homo sapiens hypothetical pro	8.9
418601	AA279490	Hs.86368	calnegin	8.8
426327	W03242	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	8.8
419519	AI198719	Hs.176376	ESTs	8.8
440821	AW296024	Hs.150434	ESTs	8.8
446142	AI754693	Hs.145968	ESTs	8.8
418196	AI745849	Hs.26549	KIAA1706 protein	8.7
447178	AW594641	Hs.192417	ESTs	8.7

427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	8.6
415857	AA868115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	8.6
435061	AI651474	Hs.163944	ESTs	8.6
431374	BE258532	Hs.251871	CTP synthase	8.4
417866	AW087903	Hs.82772	collagen, type XI, alpha 1	8.4
437211	AA382207	Hs.5509	ecotropic viral integration site 2B	8.3
437751	AA767373	Hs.35669	ESTs, Moderately similar to ALU1_HUMAN A	8.3
423887	AL080207	Hs.134585	DKFZP434G232 protein	8.2
440941	BE268362	Hs.7535	COBW-like protein	8.2
429859	NM_007050	Hs.225952	protein tyrosine phosphatase, receptor t	8.2
410193	AJ132592	Hs.59757	zinc finger protein 281	8.2
431725	X65724	Hs.2839	Norrie disease (pseudoglioma)	8.1
446258	AI283476	Hs.263478	ESTs	8.1
416747	AW876523	Hs.15929	hypothetical protein FLJ12910	8.1
434424	AI811202	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	8.1
421650	AA781795	Hs.122587	ESTs	8.0
429534	AW976987	Hs.163327	ESTs, Weakly similar to 2109260A B cell	8.0
457465	AW301344	Hs.122906	DNA replication factor	8.0
427961	AW293165	Hs.143134	ESTs	8.0
436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	8.0
418216	AA662240	Hs.283099	AF15q14 protein	8.0
418250	U29926	Hs.83918	adenosine monophosphate deaminase (isofo	7.9
400285	NA		Eos Control	7.9
401464	AF039241	Hs.9028	histone deacetylase 5	7.9
407242	M18728		gb:Human nonspecific crossreacting antig	7.8
422232	D43945	Hs.113274	transcription factor EC	7.8
454024	AA993527	Hs.293907	hypothetical protein FLJ23403	7.8
444542	AI161293	Hs.280380	aminopeptidase	7.8
436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	7.7
437204	AL110216	Hs.12285	ESTs, Weakly similar to I55214 salivary	7.6
408805	H69912	Hs.48269	vaccinia related kinase 1	7.6
437207	T27503	Hs.15929	hypothetical protein FLJ12910	7.6
442818	AK001741	Hs.8739	hypothetical protein FLJ10879	7.6
426283	NM_003937	Hs.169139	kynureninase (L-kynurenine hydrolase)	7.5
424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	7.5
448315	NM_016293	Hs.14770	bridging integrator 2	7.5
433426	H69125	Hs.133525	ESTs	7.5
406639	M97711		gb:Human T-cell receptor (V beta 18.1, J	7.5
420077	AW512260	Hs.87767	ESTs	7.4
457332	AA961694	Hs.105187	kinesin protein 9 gene	7.4
422938	NM_001809	Hs.1594	centromere protein A (17kD)	7.4
447555	AI391662	Hs.160983	Homo sapiens, clone MGC:12318, mRNA, com	7.4
444618	AV653785	Hs.173334	ELL-RELATED RNA POLYMERASE II, ELONGATIO	7.3
410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-	7.3
400268	NA		NM_003292:Homo sapiens translocated prom	7.3
439609	AF086332	Hs.58314	ESTs	7.3
407771	AL138272	Hs.62713	ESTs	7.3
407202	N58172	Hs.109370	ESTs	7.3
433096	AU076803	Hs.282975	carboxylesterase 2 (intestine, liver)	7.2
422094	AF129535	Hs.272027	F-box only protein 5	7.1
430832	AI073913	Hs.100686	ESTs, Weakly similar to JE0350 Anterior	7.1
430287	AW182459	Hs.125759	ESTs, Weakly similar to LEU5_HUMAN LEUKE	7.0
423739	AA398155	Hs.97600	ESTs	7.0
448212	AI475858		gb:tc67d07.x1 NCI_CGAP_CLL1 Homo sapiens	7.0
407277	AW170035	Hs.326736	Homo sapiens breast cancer antigen NY-BR	7.0
454440	BE062906	Hs.28338	KIAA1546 protein	7.0
444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	7.0
421373	AA808229	Hs.167771	ESTs	6.9
431960	AW241821	Hs.301927	c6.1A	6.9
424704	AI263293	Hs.152098	cytochrome P450, subfamily IIJ (arachido	6.8
449517	AW500106	Hs.23643	serine/threonine protein kinase MASK	6.8
439840	AW449211	Hs.105445	GDNF family receptor alpha 1	6.8
414080	AA135257	Hs.47783	B aggressive lymphoma gene	6.8
441243	AI767056	Hs.193002	ESTs	6.7
408380	AF123050	Hs.44532	dlubiquitin	6.7
422956	BE545072	Hs.122579	hypothetical protein FLJ10461	6.7
446651	AA393907	Hs.97179	ESTs	6.7

	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	6.7
	437740	AA810265	Hs.122915	ESTs	6.7
	421582	AI910275	Hs.1406	trefoil factor 1 (pS2)	6.7
	427356	AW023482	Hs.97849	ESTs	6.6
5	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase dome	6.6
	422634	NM_016010	Hs.118821	CGI-62 protein	6.6
	421072	AI215069	Hs.89113	ESTs	6.5
	427718	AI798880	Hs.25933	ESTs	6.5
	411000	N40449	Hs.201819	ESTs, Weakly similar to S38383 SEB4B pro	6.5
10	449343	AI151418	Hs.272458	protein phosphatase 3 (formerly 2B), cat	6.4
	409757	NM_001898	Hs.123114	cystatin SN	6.4
	447164	AF026941	Hs.17518	Homo sapiens clg5 mRNA, partial sequence	6.4
	456938	X52509	Hs.161640	tyrosine aminotransferase	6.4
	418848	AI820961	Hs.193465	ESTs	6.4
15	424902	NM_003866	Hs.153687	inositol polyphosphate-4-phosphatase, ty	6.4
	452838	U65011	Hs.30743	preferentially expressed antigen in mela	6.4
	439452	AA918317	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	6.4
	407266	AJ235664		gb:Homo sapiens mRNA for immunoglobulin	6.3
	411078	AI222020	Hs.182384	CocoaCrisp	6.3
20	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	6.3
	434340	AI193043	Hs.128585	ESTs, Weakly similar to T17226 hypothetl	6.2
	429503	AA394183	Hs.26873	ESTs	6.2
	402578			C1001134:gi|2117372|pir||I65981 fatty ac	6.2
	409646	AW161391	Hs.709	deoxycytidine kinase	6.1
25	430447	W17064	Hs.332848	SWI/SNF related, matrix associated, acti	6.1
	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	6.1
	443709	AI082692	Hs.134682	ESTs	6.1
	420929	AI694143	Hs.296251	programmed cell death 4	6.1
	428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin	6.1
30	428248	AI126772	Hs.40479	ESTs	6.0
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	6.0
	453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11	6.0
	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	6.0
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (MMP1; inters	6.0
35	428585	AB007863	Hs.185140	KIAA0403 protein	6.0
	437608	AA761605	Hs.292308	ESTs, Weakly similar to ALU1_HUMAN ALU S	6.0
	427408	AA583206	Hs.2156	RAR-related orphan receptor A	6.0
	406687	M31126	Hs.272820	matrix metalloproteinase 11 (MMP11; stro	6.0
	418092	R45154	Hs.106604	ESTs	6.0
40	447051	AW139130	Hs.160951	ESTs, Weakly similar to Con1 [H.sapiens]	6.0
	441233	AA972965	Hs.135568	ESTs	6.0
	432239	X81334	Hs.2936	matrix metalloproteinase 13 (collagenase	6.0
	435106	AA100847	Hs.193380	ESTs, Highly similar to AF174600 1 F-box	5.9
	435525	AI831297	Hs.123310	ESTs	5.9
45	458809	AW972512	Hs.20985	sin3-associated polypeptide, 30kD	5.9
	410785	AW803341		gb:IL2-UM0079-090300-050-D03 UM0079 Homo	5.9
	422578	BE548555	Hs.118554	CGI-83 protein	5.9
	451398	AI793124	Hs.144479	ESTs	5.9
	441881	AW968904	Hs.179566	hypothetical protein FLJ22624	5.8
50	412022	AI005043	Hs.24143	Wiskott-Aldrich syndrome protein interac	5.8
	416636	N32536	Hs.42645	solute carrier family 16 (monocarboxylic	5.8
	447350	AI375572	Hs.172634	ESTs	5.8
	434094	AA305599	Hs.238205	hypothetical protein PRO2013	5.8
	409151	AA306105	Hs.50785	SEC22, vesicle trafficking protein (S. c	5.8
55	448807	AI571940	Hs.7549	ESTs	5.8
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	5.8
	421281	AI299139	Hs.17517	ESTs	5.8
	430361	AK033965	Hs.239926	sterol-C4-methyl oxidase-like	5.8
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (MMP10; str	5.7
60	440527	AV657117	Hs.184164	ESTs, Moderately similar to S65657 alpha	5.7
	434874	AA831879	Hs.136985	ESTs	5.7
	426320	W47595	Hs.169300	transforming growth factor, beta 2	5.7
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	5.7
	448683	BE614599	Hs.106823	hypothetical protein MGC14797	5.7
65	438189	AW016531	Hs.122147	ESTs	5.7
	446203	Z47553	Hs.14288	flavin containing monooxygenase 5	5.7
	428338	AA503115	Hs.183752	microseminoprotein, beta-	5.6

	430379	AF134149	Hs.240395	potassium channel, subfamily K, member 6	5.6
	422835	BE218705	Hs.121378	metallothionein-like 5, testis-specific	5.6
	444758	AL044878	Hs.11899	3-hydroxy-3-methylglutaryl-Coenzyme A re	5.6
	443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	5.6
5	400301	X03635	Hs.1857	estrogen receptor 1	5.6
	447078	AW885727	Hs.301570	ESTs	5.6
	432015	AL157504	Hs.159115	Homo sapiens mRNA; cDNA DKFZp586O0724 (f	5.5
	438691	AA906288	Hs.212184	ESTs	5.5
	439809	R41396	Hs.101774	hypothetical protein FLJ23045	5.5
10	415788	AW419198	Hs.257924	hypothetical protein FLJ13782	5.5
	456373	BE247706	Hs.89751	membrane-spanning 4-domains, subfamily A	5.5
	401845	NA		C18001440*:gi|12330704|gb|AAG52890.1|AF	5.5
	437987	BE277414	Hs.5947	mel transforming oncogene (derived from	5.5
	445885	AI734009	Hs.127699	KIAA1603 protein	5.4
15	439138	AI742605	Hs.193698	ESTs	5.4
	440270	NM_015986	Hs.7120	cytokine receptor-like molecule 9	5.4
	437536	X91221	Hs.144465	ESTs	5.4
	438167	R28363	Hs.24286	ESTs	5.4
	452741	BE392914	Hs.30503	Homo sapiens cDNA FLJ11344 fis, clone PL	5.4
20	426214	H59846	Hs.128355	ESTs, Moderately similar to ALU7_HUMAN A	5.4
	413554	AA319148	Hs.75426	secretogranin II (chromogranin C)	5.4
	422887	L32137	Hs.1584	cartilage oligomeric matrix protein (COM	5.4
	434263	N34895	Hs.44848	ESTs	5.4
	446382	AW205168	Hs.150823	ESTs	5.4
25	422406	AF025441	Hs.116206	Opa-interacting protein 5	5.3
	438321	AA576835	Hs.6153	CGI-48 protein	5.3
	418310	AA814100	Hs.86693	ESTs	5.3
	419625	U91616	Hs.91640	nuclear factor of kappa light polypeptid	5.3
	450701	H39960	Hs.288467	Homo sapiens cDNA FLJ12280 fis, clone MA	5.3
30	445900	AF070526	Hs.13429	Homo sapiens clone 24787 mRNA sequence	5.2
	449051	AW961400	Hs.333526	HER2 receptor tyrosine kinase (c-erb-b2,	5.2
	418758	AW959311	Hs.172012	hypothetical protein DKFZp434J037	5.2
	431070	AW408164	Hs.249184	transcription factor 19 (SC1)	5.2
	417079	U65590	Hs.81134	interleukin 1 receptor antagonist	5.2
35	421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	5.2
	428804	AK000713	Hs.193736	hypothetical protein FLJ20706	5.2
	427427	AF077345	Hs.177936	ESTs	5.2
	403485			C3001813*:gi|12737279|ref|XP_012163.1| k	5.2
	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias	5.1
40	421937	AI878857	Hs.109706	hematological and neurological expressed	5.1
	428752	X69490	Hs.172004	titin	5.1
	453310	X70697	Hs.553	solute carrier family 6 (neurotransmitte	5.1
	423198	M81933	Hs.1634	cell division cycle 25A	5.1
	412281	AI810054	Hs.14119	ESTs	5.1
45	447513	AW955778	Hs.313500	ESTs, Moderately similar to ALU7_HUMAN A	5.1
	453931	AL121278	Hs.25144	ESTs	5.1
	404347			Target Exon	5.1
	431608	M30703	Hs.270833	amphiregulin (schwannoma-derived growth	5.1
	429113	D28235	Hs.198384	prostaglandin-endoperoxide synthase 2 (p	5.1
50	436291	BE568452	Hs.5101	protein regulator of cytokinesis 1	5.1
	450603	R43848	Hs.12422	ESTs	5.1
	434725	AK000796	Hs.4104	hypothetical protein	5.0
	435981	H74319	Hs.188620	ESTs	5.0
	407376	AA993138	Hs.142287	ESTs, Weakly similar to ALUF_HUMAN !!!!	5.0
55	431689	AA305688	Hs.267695	UDP-Gal:betaGlcNAc beta 1,3-galactosyltr	5.0
	405348	NA		C7001684:gi|12698061|db|BAB21849.1| (AB	5.0
	436196	AK001084	Hs.333498	Homo sapiens cDNA FLJ10222 fis, clone HE	5.0
	437065	AL038450	Hs.103238	ESTs	5.0
	410186	AI936442	Hs.59838	hypothetical protein FLJ10808	5.0
60	429412	NM_006235	Hs.2407	POU domain, class 2, associating factor	5.0
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	4.9
	403329	NA		Target Exon	4.9
	442875	BE623003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequ	4.9
	442441	AI820662	Hs.129598	ESTs	4.9
65	430375	AW371048	Hs.93758	H4 histone family, member H	4.9
	424128	AW966163		gb:EST378236 MAGE resequences, MAGI Homo	4.9
	408873	AL046017	Hs.182276	calmodulin 2 (phosphorylase kinase, delt	4.9

407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	4.9
432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	4.9
453204	R10799	Hs.191990	ESTs	4.8
452020	AA722012	Hs.255757	ESTs, Weakly similar to AT2A_HUMAN POTEN	4.8
449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	4.8
408369	R38438	Hs.182575	solute carrier family 15 (H??? transport	4.8
431845	AF078849	Hs.266483	dynein light chain-A	4.8
423575	C18863	Hs.163443	Homo sapiens cDNA FLJ11576 fis, clone HE	4.8
444248	H93281	Hs.10710	hypothetical protein FLJ20417	4.8
421524	AA312082	Hs.105445	GDNF family receptor alpha 1	4.8
452827	AI571835	Hs.55468	ESTs	4.8
414222	AL135173	Hs.878	sorbitol dehydrogenase	4.8
456086	AL161999	Hs.77324	eukaryotic translation termination facto	4.8
419078	M93119	Hs.89584	insulinoma-associated 1	4.8
418973	AA233056	Hs.191518	ESTs	4.8
447033	AI357412	Hs.157601	ESTs	4.8
451621	AI879148	Hs.26770	fatty acid binding protein 7, brain	4.7
419968	X04430	Hs.93913	interleukin 6 (interferon, beta 2)	4.7
424326	NM_014479	Hs.145296	disintegrin protease	4.7
431585	BE242803	Hs.262823	hypothetical protein FLJ10326	4.7
429294	AA095971	Hs.198793	Homo sapiens cDNA: FLJ22463 fis, clone H	4.7
416814	AW192307	Hs.80042	dolichyl-P-Glc:Man9GlcNAc2-PP-dolichylgl	4.7
439897	NM_015310	Hs.6763	KIAA0942 protein	4.7
429687	AI675749	Hs.211608	nucleoporin 153kD	4.7
422880	AF226704	Hs.121524	glutathione reductase	4.7
405801			NM_000390:Homo sapiens choroideremia (Ra	4.6
432435	BE218888	Hs.282070	ESTs	4.6
439544	W26354	Hs.26891	hypothetical protein FLJ11360; artemis p	4.6
425354	U62027	Hs.155935	complement component 3a receptor 1	4.6
436027	AI864053	Hs.39972	ESTs, Weakly similar to I38588 reverse t	4.6
424623	AW963062	Hs.337404	ESTs	4.6
403366	NA		Target Exon	4.6
402542			Target Exon	4.6
450193	AI916071	Hs.15607	Homo sapiens Fanconi anemia complementat	4.6
411678	AI907114	Hs.71465	squalene epoxidase	4.6
456844	AI264155	Hs.152981	CDP-diacylglycerol synthase (phosphatida	4.6
448072	AI459306	Hs.24908	ESTs	4.5
408045	AW138959	Hs.245123	ESTs	4.5
423782	AI472209	Hs.323117	ESTs	4.5
447388	AW630534	Hs.76277	Homo sapiens, clone MGC:9381, mRNA, comp	4.5
448140	AF146761	Hs.20450	BCM-like membrane protein precursor	4.5
452561	AI692181	Hs.49169	KIAA1634 protein	4.5
425331	AW862128		gb:EST374201 MAGE resequences, MAGG Homo	4.5
428801	AW277121	Hs.254881	ESTs	4.5
428500	AI815395	Hs.184841	fatty acid desaturase 2	4.5
426075	AW513691	Hs.270149	ESTs, Weakly similar to 2109260A B cell	4.4
437259	AI377755	Hs.120695	ESTs	4.4
400409	AF153341	Hs.283954	Homo sapiens winged helix/forkhead trans	4.4
412683	AA121673	Hs.59757	zinc finger protein 281	4.4
426989	AI815206	Hs.99395	ESTs	4.4
401856			Target Exon	4.4
418819	AA226776	Hs.191721	ESTs	4.4
406348			Target Exon	4.4
412138	AW895387		gb:QV4-NN0038-300300-157-c10 NN0038 Homo	4.4
428550	AW297880	Hs.98661	ESTs	4.4
411743	AW862214		gb:QV4-CT0361-301299-074-b05 CT0361 Homo	4.4
429958	BE081342	Hs.283037	HSPC039 protein	4.4
423281	NM_004129	Hs.126590	guanylate cyclase 1, soluble, beta 2	4.4
423458	AL110151	Hs.128797	DKFZP586D0824 protein	4.4
452190	H26735	Hs.91668	Homo sapiens clone PP1498 unknown mRNA	4.4
424871	NM_004525	Hs.153595	low density lipoprotein-related protein	4.3
428575	AA706003	Hs.89387	ESTs	4.3
429922	Z97630	Hs.226117	H1 histone family, member 0	4.3
421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	4.3
400300	X03363		HER2 receptor tyrosine kinase (c-erb-b2,	4.3
437258	AL041243	Hs.174104	ESTs	4.3
446595	T57448	Hs.15467	hypothetical protein FLJ20725	4.3

403011	NA		ENSP00000215330*:Probable serine/threonl	4.3
419055	AI365384	Hs.11571	Homo sapiens cDNA FLJ11570 fis, clone HE	4.3
418681	NM_001949	Hs.1189	E2F transcription factor 3	4.3
407788	AA687538	Hs.38972	tetraspan 1	4.3
429183	AB014604	Hs.197955	KIAA0704 protein	4.3
442914	AW188551	Hs.99519	hypothetical protein FLJ14007	4.3
441029	AI091795	Hs.179246	ESTs	4.3
452194	AI694413	Hs.332649	olfactory receptor, family 2, subfamily	4.3
414821	M63835	Hs.77424	Fc fragment of IgG, high affinity Ia, re	4.2
410102	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035 fis, clone HE	4.2
452110	T47667	Hs.28005	Homo sapiens cDNA FLJ11309 fis, clone PL	4.2
442007	AA301116	Hs.142838	nucleolar phosphoprotein Nopp34	4.2
417318	AW953937	Hs.12691	ESTs	4.2
431818	AW510444	Hs.191705	ESTs, Weakly similar to T47184 hypotheti	4.2
443846	AI085198	Hs.164226	ESTs	4.2
419169	AW851980	Hs.262346	ESTs, Weakly similar to S72482 hypotheti	4.2
446839	BE091926	Hs.16244	mitotic spindle coiled-coil related prot	4.2
423242	AL039402	Hs.125783	DEME-6 protein	4.2
432116	AA902953	Hs.308538	ESTs	4.2
409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	4.2
445625	BE246743	Hs.288529	hypothetical protein FLJ22635	4.2
425139	AW630488	Hs.325820	protease, serine, 23	4.2
447397	BE247876	Hs.18442	E-1 enzyme	4.2
410166	AK001376	Hs.59346	hypothetical protein FLJ10514	4.1
437295	AW779318	Hs.88417	ESTs	4.1
430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	4.1
441790	AW294909	Hs.132208	ESTs	4.1
410129	BE244074	Hs.58831	regulator of Fas-induced apoptosis	4.1
427521	AW973352	Hs.290585	ESTs	4.1
425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (MMP11; stro	4.1
412886	AF041163	Hs.74847	Human T-cell receptor active alpha-chain	4.1
441153	BE562826		gb:601336534F1 NIH_MGC_44 Homo sapiens c	4.1
444301	AK000138	Hs.10760	asporin (LRR class 1)	4.1
428711	AA383471	Hs.180669	conserved gene amplified in osteosarcoma	4.1
405850	NA		Target Exon	4.1
440283	AI732892	Hs.190489	ESTs	4.0
432441	AW292425	Hs.163484	ESTs	4.0
400284	NA		estrogen receptor 1	4.0
417341	N91453	Hs.102987	ESTs	4.0
429732	U20158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 doma	4.0
411393	AW797437	Hs.69771	B-factor, properdin	4.0
425704	U79293	Hs.159264	Human clone 23948 mRNA sequence	4.0
419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	4.0
419092	J05581	Hs.89603	mucin 1, transmembrane	4.0
443147	AI034351	Hs.19030	ESTs	4.0
408633	AW963372	Hs.46677	PRO2000 protein	4.0
433404	T32882	Hs.102720	ESTs	4.0
421506	BE302796	Hs.105097	thymidine kinase 1, soluble	4.0
417900	BE250127	Hs.82906	CDC20 (cell division cycle 20, S. cerevi	3.9
414802	AW630068	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (3	3.9
413762	AW411479	Hs.848	FK506-binding protein 4 (59kD)	3.9
404580			NM_014112*:Homo sapiens trichorhinophala	3.9
452046	AB018345	Hs.27657	KIAA0802 protein	3.9
459587	AA031956		gb:zk15e04.s1 Soares_pregnant_uterus_NbH	3.9
416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	3.9
426847	AA243484	Hs.294101	pre-B-cell leukemia transcription factor	3.9
429353	AL117406	Hs.200102	ATP-binding cassette transporter MRP8	3.9
419038	AW134924	Hs.190325	ESTs	3.9
418916	X07871	Hs.89476	CD2 antigen (p50), sheep red blood cell	3.9
421977	W94197	Hs.110165	ribosomal protein L26 homolog	3.9
442567	AI201183	Hs.130251	ESTs	3.9
421168	AF182277	Hs.330780	cytochrome P450, subfamily IIB (phenobar	3.9
431701	AW935490	Hs.14658	Human chromosome 5q13.1 clone 5G8 mRNA	3.9
418526	BE019020	Hs.85838	solute carrier family 16 (monocarboxylic	3.9
414998	NM_002543	Hs.77729	oxidised low density lipoprotein (lectin	3.9
422790	AA809875	Hs.25933	ESTs	3.9
419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	3.9

430017	AA263172	Hs.35	protein tyrosine phosphatase, non-recept	3.9	
458814	AI498957	Hs.170881	ESTs, Weakly similar to Z195_HUMAN ZINC	3.8	
428514	AW236861	Hs.193139	ESTs	3.8	
434521	NM_002267	Hs.3886	karyopherin alpha 3 (importin alpha 4)	3.8	
409425	U40462	Hs.54452	zinc finger protein, subfamily 1A, 1 (Ik	3.8	
439560	BE565647	Hs.74899	hypothetical protein FLJ12820	3.8	
424028	AF055084	Hs.153692	Homo sapiens cDNA FLJ14354 fis, clone Y7	3.8	
400021			AFFX control - HUMISGF3A/M97935_MA	3.8	
453403	BE466839	Hs.61779	Homo sapiens cDNA FLJ13591 fis, clone PL	3.8	
445941	AI267371	Hs.172636	ESTs	3.8	
434378	AA631739	Hs.335440	EST	3.8	
429220	AW207206	Hs.136319	ESTs	3.8	
439176	AI446444	Hs.190394	ESTs, Weakly similar to B28096 line-1 pr	3.8	
401045			C11001883*:gi|6753278|ref|NP_033938.1| c	3.8	
430178	AW449612	Hs.152475	ESTs	3.8	
423397	NM_001838	Hs.1652	chemokine (C-C motif) receptor 7	3.8	
447630	AI660149	Hs.44865	lymphoid enhancer-binding factor 1	3.8	
436391	AJ227892	Hs.146274	ESTs	3.8	
413011	AW068115	Hs.821	biglycan	3.8	
422121	AI767949	Hs.178833	ESTs	3.8	
452268	NM_003512	Hs.28777	H2A histone family, member L	3.8	
427811	M81057	Hs.180884	carboxypeptidase B1 (tissue)	3.8	
415579	AA165232	Hs.222069	ESTs	3.8	
437330	AL353944	Hs.50115	Homo sapiens mRNA; cDNA DKFZp761J1112 (f	3.8	
427122	AW057736	Hs.323910	HER2 receptor tyrosine kinase (c-erb-b2,	3.7	
400286	NA		C16000922:gi|7499103|pir||T20903 hypothe	3.7	
420281	AI623693	Hs.191533	ESTs	3.7	
419926	AW900992	Hs.93796	DKFZP586D2223 protein	3.7	
417541	AI992191	Hs.180040	hypothetical protein FLJ22439	3.7	
426172	AA371307	Hs.125056	ESTs	3.7	
429638	AI916662	Hs.211577	kinectin 1 (kinesin receptor)	3.7	
457001	J03258	Hs.2062	vitamin D (1,25- dihydroxyvitamin D3) re	3.7	
424109	AW406878		gb:UI-HF-BL0-adg-g-06-0-UI.r1 NIH_MGC_37	3.7	
417022	NM_014737	Hs.80905	Ras association (RalGDS/AF-6) domain fam	3.7	
436222	AI208737	Hs.122810	Homo sapiens cDNA FLJ11489 fis, clone HE	3.7	
430448	AI633553	Hs.13303	Homo sapiens cDNA: FLJ21784 fis, clone H	3.7	
432729	AK000292	Hs.278732	hypothetical protein FLJ20285	3.7	
413918	N49813	Hs.75615	apolipoprotein C-II	3.7	
421662	NM_014141	Hs.106552	cell recognition molecule Caspr2	3.7	
441633	AW958544	Hs.112242	normal mucosa of esophagus specific 1	3.7	
408761	AA057264	Hs.238936	ESTs, Weakly similar to (defline not ava	3.7	
406153			Target Exon	3.7	
445563	AW873606	Hs.149008	ESTs	3.7	
453464	AI884911	Hs.32989	receptor (calcitonin) activity modifying	3.7	
448918	AB011152	Hs.22572	KIAA0580 protein	3.7	
413936	AF113676	Hs.297681	serine (or cysteine) proteinase inhibito	3.6	
448069	U76248	Hs.20191	seven in absentia (Drosophila) homolog 2	3.6	
453313	BE005771	Hs.153745	hypothetical protein FLJ22490	3.6	
425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypotheti	3.6	
419941	X98654	Hs.93837	phosphatidylinositol transfer protein, m	3.6	
402397	AF188625	Hs.169507	phospholipase A2, group IID	3.6	
430378	Z29572	Hs.2556	tumor necrosis factor receptor superfami	3.6	
448106	AI800470	Hs.171941	ESTs	3.6	
428431	NM_000458	Hs.169853	transcription factor 2, hepatic; LF-B3;	3.6	
431843	AA518420	Hs.183526	ESTs, Weakly similar to I38022 hypotheti	3.6	
426878	BE059341		gb:QV3-BT0381-270100-073-c08 BT0381 Homo	3.6	
434081	AW024973	Hs.283675	NPD009 protein	3.6	
445292	AV653264	Hs.13982	Homo sapiens cDNA FLJ14666 fis, clone NT	3.6	
452101	T60298	Hs.10844	Homo sapiens cDNA FLJ14478 fis, clone MA	3.6	
427581	NM_014788	Hs.179703	KIAA0129 gene product	3.6	
409047	AW961434	Hs.31539	ESTs	3.6	
416820	NM_000402	Hs.80206	glucose-6-phosphate dehydrogenase	3.6	
410386	W26187	Hs.3327	Homo sapiens cDNA: FLJ22219 fis, clone H	3.6	
440518	S42303	Hs.161	cadherin 2, type 1, N-cadherin (neuronal	3.6	
434350	AW015415	Hs.127780	ESTs	3.6	
428970	BE276891	Hs.194891	retinoic acid induced 3	3.6	
415079	R43179	Hs.22895	hypothetical protein FLJ23548	3.6	

409619	AK001015	Hs.55220	BCL2-associated athanogene 2	3.6	
430044	AA464510	Hs.152812	ESTs	3.6	
430829	AW451999	Hs.194024	ESTs	3.6	
434224	AA380731	Hs.84	interleukin 2 receptor, gamma (severe co	3.6	
439247	AF088020	Hs.46767	EST	3.6	
431542	H63010	Hs.5740	ESTs	3.5	
430713	AA351647	Hs.2642	eukaryotic translation elongation factor	3.5	
434988	AI418055	Hs.161160	ESTs	3.5	
437748	AF234882	Hs.5814	suppression of tumorigenicity 7	3.5	
418322	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	3.5	
439569	AW602166	Hs.222399	CEGP1 protein	3.5	
459583	AI907673		gb:IL-BT152-080399-004 BT152 Homo sapien	3.5	
403212			NM_019595:Homo sapiens intersectin 2 (IT	3.5	
409099	AK000725	Hs.50579	hypothetical protein FLJ20718	3.5	
453968	AA847843	Hs.62711	Homo sapiens, clone IMAGE:3351295, mRNA	3.5	
436338	W92147	Hs.118394	ESTs	3.5	
422890	Z43784	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)	3.5	
442295	AI827248	Hs.224398	Homo sapiens cDNA FLJ11469 fis, clone HE	3.5	
417975	AA641836	Hs.30085	hypothetical protein FLJ23186	3.5	
433730	AK002135	Hs.3542	hypothetical protein FLJ11273	3.5	
439926	AW014875	Hs.137007	ESTs	3.5	
445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-l	3.4	
410153	BE311926	Hs.15830	hypothetical protein FLJ12691	3.4	
422128	AW881145		gb:QV0-OT0033-010400-182-e07 OT0033 Homo	3.4	
414921	BE390551	Hs.77626	steroidogenic acute regulatory protein r	3.4	
441134	W29092	Hs.7678	cellular retinoic acid-binding protein 1	3.4	
444564	AI167877	Hs.143718	ESTs	3.4	
402470	NA		Target Exon	3.4	
418120	AA213437	Hs.192249	ESTs	3.4	
422414	AW875237	Hs.13701	ESTs	3.4	
433345	AI681545	Hs.152982	hypothetical protein FLJ13117	3.4	
409213	U81412	Hs.51133	PTK6 protein tyrosine kinase 6	3.4	
422611	AA158177	Hs.118722	fucosyltransferase 8 (alpha (1,6) fucosy	3.4	
423554	M90516	Hs.1874	glutamine-fructose-6-phosphate transamin	3.4	
442619	AA447492	Hs.20183	ESTs, Weakly similar to AF164783 1 prote	3.4	
402359	NA		C19001991*:gi|12656111|gb|AAK00751.1|AF23	3.4	
439398	AA284267	Hs.221504	ESTs	3.4	
415208	F01020	Hs.172004	titin	3.4	
452853	AA812633	Hs.10845	ESTs	3.4	
429345	R11141	Hs.199695	hypothetical protein	3.4	
449027	AJ271216	Hs.22880	dipeptidylpeptidase III	3.4	
412115	AK001763	Hs.73239	hypothetical protein FLJ10901	3.4	
432180	Y18418	Hs.272822	RuvB (E coli homolog)-like 1	3.4	
428977	AK001404	Hs.194698	cyclin B2	3.4	
431611	U58766	Hs.284428	tissue specific transplantation antigen	3.4	
418288	AA622528	Hs.319825	Homo sapiens, clone IMAGE:3616574, mRNA	3.4	
436895	AF037335	Hs.5338	carbonic anhydrase XII (tumor antigen H	3.4	
443378	AW392550	Hs.9280	proteasome (prosome, macropain) subunit,	3.4	
428450	NM_014791	Hs.184339	KIAA0175 gene product	3.3	
449571	AW016812	Hs.200266	ESTs	3.3	
412777	AI335773	Hs.270123	ESTs	3.3	
420542	NM_000505	Hs.1321	coagulation factor XII (Hageman factor)	3.3	
412754	AW160375	Hs.74565	amyloid beta (A4) precursor-like protein	3.3	
418327	U70370	Hs.84136	paired-like homeodomain transcription fa	3.3	
449065	AI627393	Hs.258998	ESTs, Weakly similar to high mobility gr	3.3	
425999	AW513051	Hs.332981	ESTs, Weakly similar to I38022 hypotheti	3.3	
430280	AA361258	Hs.237868	interleukin 7 receptor	3.3	
407777	AA161071	Hs.71465	squalene epoxidase	3.3	
426516	BE262660	Hs.170197	glutamic-oxaloacetic transaminase 2, mit	3.3	
414361	AI088138	Hs.204044	ESTs	3.3	
427080	AW068287	Hs.173466	ras-related C3 botulinum toxin substrate	3.3	
426429	X73114	Hs.169849	myosin-binding protein C, slow-type	3.3	
446183	AA026880	Hs.25252	prolactin receptor	3.3	
428568	U41763	Hs.184916	clathrin, heavy polypeptide-like 1	3.3	
418641	BE243136	Hs.86947	a disintegrin and metalloproteinase dome	3.3	
436293	AI601188	Hs.120910	ESTs	3.3	
411257	AA628967	Hs.115274	ESTs, Highly similar to IHH_HUMAN INDIAN	3.3	

430253	AK001514	Hs.236844	hypothetical protein FLJ10652	3.3
430066	AI929659	Hs.237825	signal recognition particle 72kD	3.3
436469	AK001455	Hs.5198	Down syndrome critical region gene 2	3.3
437786	BE142681	Hs.155573	polymerase (DNA directed), eta	3.3
444079	H09048	Hs.23608	ESTs	3.3
457183	H91882	Hs.118569	Dvl-binding protein IDAX (inhibition of	3.3
431215	AA496078	Hs.121554	Human DNA sequence from clone RP11-218C13	3.3
424563	AA446932	Hs.151428	ret finger protein 2	3.3
450828	AW270655	Hs.193804	ESTs	3.3
408652	R43409	Hs.6829	Homo sapiens mRNA for KIAA1644 protein,	3.3
445142	AW978484	Hs.93842	Homo sapiens cDNA: FLJ22554 fis, clone H	3.3
426761	AI015709	Hs.172089	Homo sapiens mRNA; cDNA DKFZp586I2022 (f	3.3
439237	AW408158	Hs.318893	ESTs, Weakly similar to A47582 B-cell gr	3.3
422616	BE300330	Hs.118725	selenophosphate synthetase 2	3.3
443247	BE614387	Hs.333893	c-Myc target JPO1	3.3
406663	U24883	Hs.302083	immunoglobulin heavy constant mu	3.3
434137	AA907734	Hs.124895	ESTs	3.3
408877	AA479033	Hs.130315	ESTs, Weakly similar to A47582 B-cell gr	3.3
439101	C01765	Hs.38750	hypothetical protein FLJ11526	3.3
408221	AA912183	Hs.47447	ESTs	3.3
447519	U46258	Hs.339665	ESTs	3.3
404755	NA		Target Exon	3.3
451871	AI821005	Hs.118599	ESTs	3.2
420319	AW406289	Hs.96583	hypothetical protein	3.2
430580	AA806105	Hs.300697	immunoglobulin heavy constant gamma 3 (G	3.2
400202	NA		NM_002795*:Homo sapiens proteasome (pros	3.2
400222	NA		NM_002082*:Homo sapiens G protein-couple	3.2
425988	BE045897	Hs.274454	ESTs, Weakly similar to I38022 hypotheti	3.2
458098	BE550224	Hs.74170	metallothionein 1E (functional)	3.2
430589	AJ002744	Hs.246315	UDP-N-acetyl-alpha-D-galactosamine:polyp	3.2
431563	AI027643	Hs.120912	ESTs	3.2
442353	BE379594	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN A	3.2
422309	U79745	Hs.114924	solute carrier family 16 (monocarboxylic	3.2
419703	AI793257	Hs.128151	ESTs	3.2
420380	AA640891	Hs.102406	ESTs	3.2
410853	H04588	Hs.30469	ESTs	3.2
454417	AI244459	Hs.110826	trinucleotide repeat containing 9	3.2
432745	AI821926		gb:nt78l05.x5 NCI_CGAP_Pr3 Homo sapiens	3.2
422032	AA476966	Hs.110857	polymerase (RNA) III (DNA directed) poly	3.2
415339	NM_015156	Hs.78398	KIAA0071 protein	3.2
426384	AI472078	Hs.303662	ESTs	3.2
448030	N30714	Hs.325960	membrane-spanning 4-domains, subfamily A	3.2
418739	AA310984	Hs.88012	SHP2 interacting transmembrane adaptor	3.2
442053	R35343	Hs.24968	Human DNA sequence from clone RP1-233G16	3.2
434747	AA837085	Hs.220585	ESTs	3.2
427297	AW292593	Hs.334907	Homo sapiens, clone MGC:17333, mRNA, com	3.2
412228	AW503785	Hs.73792	complement component (3d/Epstein Barr vi	3.2
452304	AA025388	Hs.61311	ESTs, Weakly similar to S10590 cysteine	3.2
453953	AW406337	Hs.36972	CD7 antigen (p41)	3.2
407758	D50915	Hs.38365	KIAA0125 gene product	3.2
451149	AL047586	Hs.10283	RNA binding motif protein 8B	3.2
430015	AW768399	Hs.112157	ESTs	3.2
433313	W20128	Hs.296039	ESTs	3.2
418334	AA319233	Hs.5521	ESTs	3.2
450223	AA418204	Hs.241493	natural killer-tumor recognition sequenc	3.2
454355	AW966728	Hs.54642	methionine adenosyltransferase II, beta	3.2
451128	AL118668		gb:DKFZp761I0310_r1 761 (synonym: hamy2)	3.2
417793	AW405434	Hs.82575	small nuclear ribonucleoprotein polypept	3.2
428027	U22029	Hs.334345	cytochrome P450, subfamily IIA (phenobar	3.2
441197	BE244638	Hs.166	sterol regulatory element binding transc	3.2
424634	NM_003813	Hs.151407	cartilage intermediate layer protein, nu	3.2
419986	AI345455	Hs.78915	GA-binding protein transcription factor,	3.2
416714	AF283770	Hs.79630	CD79A antigen (immunoglobulin-associated	3.2
449465	NM_004380	Hs.23598	CREB binding protein (Rubinstein-Taybi s	3.2
422166	W72424	Hs.112405	S100 calcium-binding protein A9 (calgran	3.2
409079	W87707	Hs.82065	interleukin 6 signal transducer (gp130,	3.2
423551	AA327598	Hs.233785	ESTs	3.2

453553	AA036849	Hs.61829	Homo sapiens cDNA FLJ12763 fis, clone NT	3.2
442580	AI733682	Hs.130239	ESTs	3.2
458079	AI796870	Hs.54277	DNA segment on chromosome X (unique) 9923	3.2
425700	AF076292	Hs.159251	forkhead box H1	3.2
417124	BE122762	Hs.25338	ESTs	3.2
407104	S57296	Hs.323910	v-erb-b2 avian erythroblastic leukemia v	3.2
442215	AI703172	Hs.129005	ESTs, Weakly similar to 2109260A B cell	3.1
430271	T06199	Hs.237506	DnaJ (Hsp40) homolog, subfamily B, membe	3.1
425317	AW205118	Hs.210548	interleukin 21 receptor	3.1
426095	AI278023	Hs.89986	ESTs	3.1
442313	BE388898	Hs.8215	hypothetical protein FLJ11307	3.1
424709	AL137589	Hs.152149	hypothetical protein DKFZp434K0410	3.1
429671	BE379335	Hs.211594	proteasome (prosome, macropain) 26S subu	3.1
432715	AA247152	Hs.200483	ESTs, Weakly similar to KIAA1074 protein	3.1
431574	AW572659	Hs.261373	hypothetical protein dJ434O14.3	3.1
436876	AI124756	Hs.5337	isocitrate dehydrogenase 2 (NADP), mitoc	3.1
405017	NA		Target Exon	3.1
433805	AA706910	Hs.112742	ESTs	3.1
437352	AL353957	Hs.284181	hypothetical protein DKFZp434P0531	3.1
430105	X70297	Hs.2540	cholinergic receptor, nicotinic, alpha p	3.1
422083	NM_001141	Hs.111256	arachidonate 15-lipoxygenase, second typ	3.1
413507	BE145360	Hs.190064	ESTs, Weakly similar to I38022 hypotheti	3.1
415989	AI267700	Hs.317584	ESTs	3.1
422907	AI879263	Hs.6986	Human glucose transporter pseudogene	3.1
425548	AA890023	Hs.1906	prolactin receptor	3.1
422599	BE387202	Hs.118638	non-metastatic cells 1, protein (NM23A)	3.1
439963	AW247529	Hs.8793	platelet-activating factor acetylhydrola	3.1
453883	AI638516	Hs.22630	cofactor required for Sp1 transcriptiona	3.1
458021	AI885190	Hs.156089	ESTs, Weakly similar to repressor protei	3.1
418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	3.1
400814	NA		Target Exon	3.1
402327			Target Exon	3.1
416935	AA190712		gb:zp67f09.r1 Stratagene HeLa cell s3 93	3.1
439838	AL355722	Hs.106875	Homo sapiens EST from clone 35214, full	3.1
437036	AI571514	Hs.133022	ESTs	3.1
449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	3.1
406642	AJ245210		gb:Homo sapiens mRNA for immunoglobulin	3.1
406824	AF052782		gb:Homo sapiens clone csneg8-1 immunoglo	3.1
421924	BE514514	Hs.109606	coronin, actin-binding protein, 1A	3.1
414523	AU076633	Hs.76353	serine (or cysteine) proteinase inhibito	3.1
416379	N39857	Hs.203933	ESTs	3.1
422823	D89974	Hs.121102	vanin 2	3.1
433904	AI399958	Hs.208956	ESTs	3.1
421904	BE143533	Hs.109309	hypothetical protein FLJ20035	3.1
428834	AW899713	Hs.339315	ESTs	3.1
436043	AW963838	Hs.168830	Homo sapiens cDNA FLJ12136 fis, clone MA	3.1
452823	AB012124	Hs.30696	transcription factor-like 5 (basic helix	3.1
405381	NA		Target Exon	3.1
428746	AW503820	Hs.192861	Sp1-B transcription factor (Sp1-/PU.1 r	3.1
435147	AL133731	Hs.4774	Homo sapiens mRNA; cDNA DKFZp761C1712 (f	3.1
425782	U66468	Hs.159525	cell growth regulatory with EF-hand doma	3.1
423306	W88562	Hs.108198	ESTs	3.1
419123	AA234276	Hs.88253	ESTs	3.1
438581	AW977766	Hs.292133	ESTs, Moderately similar to I78885 serin	3.1
417105	X60992	Hs.81226	CD6 antigen	3.0
426361	NM_015905	Hs.183658	transcriptional intermediary factor 1	3.0
417880	BE241595	Hs.82848	selectin L (lymphocyte adhesion molecule	3.0
402606			NM_024626:Homo sapiens hypothetical prot	3.0
401451			NM_004496*:Homo sapiens hepatocyte nucle	3.0
421878	AA289652	Hs.111496	Homo sapiens cDNA FLJ11643 fis, clone HE	3.0
409518	BE384836	Hs.3454	KIAA1821 protein	3.0
416933	BE561850	Hs.80506	small nuclear ribonucleoprotein polypept	3.0
414324	Y14768	Hs.890	lymphotoxin beta (TNF superfamily, membe	3.0
425081	X74794	Hs.154443	minichromosome maintenance deficient (S.	3.0
401519			C15000476*:gi|12737279|ref|XP_012163.1|	3.0
411704	AI499220	Hs.71573	hypothetical protein FLJ10074	3.0
428819	AL135823	Hs.193914	KIAA0575 gene product	3.0

428423	AU076517	Hs.184276	solute carrier family 9 (sodium/hydrogen	3.0
413835	AI272727	Hs.249163	fatty acid hydroxylase	3.0
412600	L28824	Hs.74101	spleen tyrosine kinase	3.0
410491	AA465131	Hs.64001	Homo sapiens clone 25218 mRNA sequence	3.0
433658	L03678	Hs.156110	immunoglobulin kappa constant	3.0
427666	AI791495	Hs.180142	calmodulin-like skin protein	3.0
452514	AI904898		gb:RC-BT068-130399-085 BT068 Homo sapien	3.0
429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotactin)	3.0
432485	N90868	Hs.276770	CDW52 antigen (CAMPATH-1 antigen)	3.0
437400	AB011542	Hs.5599	EGF-like-domain, multiple 5	3.0
452234	AW084176	Hs.223296	ESTs, Weakly similar to I38022 hypotheti	3.0
413269	BE167526		gb:CM4-HT0509-080300-107-g07 HT0509 Homo	3.0
453216	AL137566	Hs.32405	Homo sapiens mRNA; cDNA DKFZp586G0321 (f	3.0
400929			ENSP00000252232*:Sterol regulatory eleme	3.0
445145	AI961702	Hs.147434	ESTs	3.0
432815	AA557191	Hs.55028	ESTs, Weakly similar to I54374 gene NF2	3.0
423279	AW959861	Hs.290943	ESTs	3.0
429392	AL109712	Hs.296506	Homo sapiens mRNA full length insert cDN	3.0
408548	AA055449	Hs.63187	ESTs, Weakly similar to ALUC_HUMAN !!!!	3.0
451346	NM_006338	Hs.26312	glioma amplified on chromosome 1 protein	3.0
413109	AW389845	Hs.110855	ESTs	3.0
401714	NA		ENSP00000241802*:CDNA FLJ11007 FIS, CLON	3.0
421462	AF016495	Hs.104624	aquaporin 9	3.0
421750	AK000768	Hs.107872	hypothetical protein FLJ20761	3.0
453293	AA382267	Hs.10653	ESTs	3.0
457085	AA412446	Hs.98138	ESTs	3.0
438930	AW843633	Hs.306163	hypothetical protein AL110115	3.0

TABLE 22A

Table 22A shows the accession numbers for those pkeys lacking unigeneID's for Table 22. For each probeset, we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT number	Accessions
407980	103087_1	AA046309 AI263500 AA046397
410785	1221055_1	AW803341 AW803265 AW803403 AW803466 AW803402 AW803413 AW803268 AW803396 AW803334 AW803355
411743	1256098_1	AW862214 AW859811 AW862215
412138	1279172_1	AW895387 AW895547 AW895564 AW895323 AW895405 AW895539 AW895538
413269	1356981_1	BE167526 BE167851 BE078401 R24654
416935	163179_1	AA190712 AA190665 AA252564
422128	211994_1	AW881145 AA490718 M85537 AA304575 T06067 AA331991
423945	233566_1	AA410943 AW948953 AA334202 AA332882
424109	235506_1	AW406878 AW966560 AW966151 AW966496 AA336174 AA335376 AA335537
424128	235728_1	AW966163 AA335983 AA336011 AA335668 AA335973
425331	250199_1	AW962128 AA355353 AA427363
426878	273265_1	BE069341 AW748403 AL044891 AI908240 AA393080
432745	353673_1	AI821926 AA658826 AA564492 AA635129 AI791191
441153	51084_2	BE562826 BE378727
448212	755099_1	AI475858 AW969013
451128	859865_1	AL118668 D78823 AI762178
452514	920172_1	AI904898 AI904849 AI904899
456207	165078_-1	AA193450

TABLE 22B

Table 22B shows the genomic positioning for those pkeys lacking unigene ID's and accession numbers in Table 22. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400814	8569925	Minus	72840-72924,74761-74849
400929	7651921	Minus	122033-122241,123483-124026
401045	8117619	Plus	90044-90184,91111-91345
401451	6834068	Minus	119926-121272
401519	6649315	Plus	157315-157950
401645	7657839	Minus	34986-35133
401714	6715702	Plus	96484-96681
401858	8018108	Plus	73126-73623
402327	7656695	Minus	108675-108770,109801-109910
402359	9211204	Minus	40403-41961
402408	9796239	Minus	110326-110491
402470	9797107	Plus	185129-185776
402542	9801558	Minus	67078-67594
402578	9884928	Plus	68350-68496
402606	9909429	Minus	81747-82094
403011	6693597	Minus	3468-3623
403212	7630897	Minus	156037-156210
403329	8516120	Plus	96450-96598
403366	8783692	Minus	49323-49652
403485	9966528	Plus	2888-3001,3198-3532,3655-4117
404347	9838195	Plus	74493-74829
404580	6539738	Minus	240588-241589
404755	7706327	Minus	53729-53846
405017	6532084	Plus	35551-35690
405348	2914717	Minus	43310-43462
405381	6006920	Minus	7636-8054
405801	2924321	Plus	63469-63694
405850	6164995	Plus	13871-14110
406153	9929734	Minus	12902-13069
406348	9255985	Minus	71754-71944

TABLE 23: 320 GENES DOWN-REGULATED IN BREAST CANCER COMPARED TO NORMAL ADULT BREAST

Table 23 shows 320 genes down-regulated in breast cancer compared to normal adult breast. These were selected as for Table 22, except that the numerator was set to the median value for 12 non-malignant breast specimens, the denominator was set to the median value amongst the 73 breast cancers, the 90th percentile value amongst the12 non-malignant breast specimens was greater than or equal 80 units, and the ratio was greater than or equal to 4.0 (*i.e.* 4-fold down-regulated in tumor vs. normal breast).

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of 50th percentile normal body tissue to 75th percentile tumor

Pkey	ExAccn	UnigeneID	UnigeneTitle	Ratio
428722	U76456	Hs.190787	tissue inhibitor of metalloproteinase 4	22.4
428848	NM_000230	Hs.194236	leptin (murine obesity homolog)	17.4
445263	H57646	Hs.42586	KIAA1560 protein	15.4
418935	T28499	Hs.89485	carbonic anhydrase IV	15.0
407228	M25079	Hs.155376	hemoglobin, beta	14.6
417511	AL049176	Hs.82223	chordin-like	14.6
439285	AL133916	Hs.172572	hypothetical protein FLJ20093	14.3
412442	AI983730	Hs.26530	serum deprivation response (phosphatidyl	13.6
410544	AI446543	Hs.95511	ESTs	12.6
412047	AA934589	Hs.49696	ESTs	12.2
422667	H25642	Hs.133471	ESTs	12.0
406664	L34041	Hs.9739	glycerol-3-phosphate dehydrogenase 1 (so	12.0
423201	NM_000163	Hs.125180	growth hormone receptor	11.7
422163	AF027208	Hs.112360	prominin (mouse)-like 1	10.8
428769	AW207175	Hs.106771	ESTs	10.6
407049	X72632		NM_021724*:Homo sapiens nuclear receptor	10.1
412295	AW088826	Hs.117176	poly(A)-binding protein, nuclear 1	9.8
425126	N32759	Hs.172944	chorionic gonadotropin, beta polypeptide	9.8
406791	AI220684	Hs.272572	hemoglobin, alpha 2	9.5
447471	AF039843	Hs.18676	sprouty (Drosophila) homolog 2	9.5
451533	NM_004657	Hs.26530	serum deprivation response (phosphatidyl	9.4
419407	AW410377	Hs.41502	hypothetical protein FLJ21276	9.0
411939	AI365585	Hs.146246	ESTs	9.0
410532	T53088	Hs.155376	hemoglobin, beta	8.9
425707	AF115402	Hs.11713	E74-like factor 5 (ets domain transcript	8.8
416585	X54162	Hs.79388	telomodin 1 (smooth muscle)	8.7
443060	D78874	Hs.8944	procollagen C-endopeptidase enhancer 2	8.6
435265	AA779956	Hs.165932	ESTs	8.5
422511	AU078442	Hs.117938	collagen, type XVII, alpha 1	8.4
433138	AB029496	Hs.59729	semaphorin sem2	8.3
402195			NM_004497*:Homo sapiens hepatocyte nucle	8.1
429350	AI754634	Hs.131987	ESTs	8.1
445107	AI208121	Hs.147313	ESTs, Weakly similar to I38022 hypothet	8.1
406643	N77976	Hs.272572	hemoglobin, alpha 2	8.0
410199	AW377424	Hs.205128	Homo sapiens cDNA: FLJ22567 fis, clone H	8.0
417225	AA815048	Hs.24078	hypothetical protein FLJ12649	7.8
437569	AA760849	Hs.294052	ESTs	7.5
436062	AK000027	Hs.98633	ESTs	7.5
425078	NM_002599	Hs.154437	phosphodiesterase 2A, cGMP-stimulated	7.5
430327	AW973636	Hs.55931	ESTs	7.4

447577	AI393693	Hs.183297	DKFZP566F2124 protein	7.4
445039	AI150491	Hs.90756	ESTs	7.2
422060	R20893	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	7.2
424455	AA452006	Hs.333199	ESTs	7.1
424343	AW956360	Hs.4748	adenylate cyclase activating polypeptide	7.1
442792	AI352340	Hs.131194	ESTs	7.0
406714	AI219304	Hs.283106	hemoglobin, gamma G	6.9
407571	AI446183	Hs.9572	ESTs, Highly similar to CYA5_HUMAN ADENY	6.8
429580	AA346839	Hs.209100	DKFZP434C171 protein	6.7
453500	AI478427	Hs.43125	esophageal cancer related gene 4 protein	6.7
422233	AB002058	Hs.113275	purinergic receptor P2X-like 1, orphan r	6.7
420205	AA256395	Hs.88156	ESTs	6.6
404368	NA		ENSP00000241075*:TRRAP PROTEIN.	6.6
447261	NM_006691	Hs.17917	extracellular link domain-containing 1	6.5
417090	AA193282	Hs.85863	ESTs, Weakly similar to B34612 zinc fing	6.5
410677	NM_003278	Hs.85424	tetranectin (plasminogen-binding protein	6.5
427283	AL119796	Hs.174185	ectonucleotide pyrophosphatase/phosphodi	6.5
415011	AW963085		gb:EST375158 MAGE resequences, MAGH Homo	6.4
412068	S72043	Hs.73133	metallothionein 3 (growth inhibitory fac	6.4
416253	BE250659	Hs.15463	Homo sapiens, clone IMAGE:2959994, mRNA	6.4
435865	AA701483	Hs.36341	ESTs	6.3
402779	NA		Target Exon	6.3
418138	AA213626	Hs.136204	EST	6.3
439335	AA742697	Hs.62492	ESTs, Weakly similar to B39066 proline-r	6.3
427019	AA001732	Hs.173233	hypothetical protein FLJ10970	6.2
411478	BE143068		gb:MR0-HT0158-030200-003-b09 HT0158 Homo	6.2
452654	BE004783		gb:MR2-BN0114-270400-004-e11 BN0114 Homo	6.1
447359	NM_012093	Hs.18268	adenylate kinase 5	6.1
414323	NM_014759	Hs.334688	KIAA0273 gene product	6.1
441266	H15968	Hs.293845	Homo sapiens, clone IMAGE:3502329, mRNA,	6.1
417011	F08212	Hs.234898	ESTs, Weakly similar to 2109260A B cell	6.0
400089	NA		Eos Control	6.0
433614	W07475	Hs.277101	cytochrome c oxidase subunit IV isoform	5.9
440439	N92818	Hs.64754	ESTs, Weakly similar to potential CDS [H	5.9
454404	BE067414		gb:MR4-BT0355-200100-201-e05 BT0355 Homo	5.9
436704	AA062610	Hs.148050	EST	5.9
406563	NA		Target Exon	5.9
433490	AW451023	Hs.65848	hypothetical protein DKFZp761O132	5.9
419313	AA843387	Hs.87279	ESTs	5.9
409196	NM_001874	Hs.334873	carboxypeptidase M	5.8
410882	AW809163		gb:MR4-ST0118-261099-012-e03 ST0118 Homo	5.8
453469	AB014533	Hs.33010	KIAA0633 protein	5.8
441899	AI372588	Hs.8022	TU3A protein	5.8
426210	AA372052	Hs.334559	Homo sapiens cDNA FLJ14458 fis, clone HE	5.8
413065	BE063555		gb:CM1-BT0283-061199-033-d09 BT0283 Homo	5.8
454192	AW876813	Hs.3343	phosphoglycerate dehydrogenase	5.7
425187	AW014486	Hs.22509	ESTs	5.7
429757	AW452355	Hs.256037	ESTs	5.7
420202	AL036557	Hs.95910	putative lymphocyte G0/G1 switch gene	5.7
416284	AI695473	Hs.298006	ESTs	5.7
428553	AA181641	Hs.184907	G protein-coupled receptor 1	5.6
404689	NA		Target Exon	5.6
438887	R68857	Hs.265499	ESTs	5.6
406082	S47833	Hs.82927	adenosine monophosphate deaminase 2 (iso	5.6
449748	H23953	Hs.32043	ESTs	5.6
431048	R50253	Hs.249129	cell death-inducing DFFA-like effector a	5.5
452205	C15819		gb:C15819 Clontech human aorta polyA mRN	5.5
434040	AW444613	Hs.288809	hypothetical protein FLJ20159	5.5
407744	AB020629	Hs.38095	ATP-binding cassette, sub-family A (ABC1	5.5
450606	AI568505	Hs.60380	ESTs, Moderately similar to ALU6_HUMAN A	5.5
414629	AA345824	Hs.76688	carboxylesterase 1 (monocyte/macrophage	5.5
401665			C11000703:gi|10048448|ref|NP_065258.1|g	5.5
436107	T99079	Hs.191194	ESTs	5.5
444432	AI161428	Hs.75916	splicing factor 3b, subunit 2, 145kD	5.5
434715	BE005346	Hs.116410	ESTs	5.5
447205	BE617015	Hs.11006	ESTs, Moderately similar to T17372 plasm	5.5
408122	AI432652	Hs.42824	hypothetical protein FLJ10718	5.5

454018	AW016806	Hs.233108	ESTs	5.5
414913	R25821		gb:yh45f06.r1 Soares placenta Nb2HP Homo	5.4
459033	AA017590	Hs.129907	ESTs	5.4
441003	BE172240	Hs.126379	ESTs, Weakly similar to I38022 hypothet	5.4
450637	N49826	Hs.18602	ESTs	5.4
442398	AA994520		gb:ou42g09.s1 Soares_NFL_T_GBC_S1 Homo s	5.4
403812	NA		Target Exon	5.3
407102	AA007629	Hs.9739	glycerol-3-phosphate dehydrogenase 1 (so	5.3
410057	R66634	Hs.268107	multimerin	5.3
428232	BE272452	Hs.183109	monoamine oxidase A	5.3
432769	AA620814	Hs.144959	ESTs	5.3
431344	R99530	Hs.272572	hemoglobin, alpha 2	5.3
427032	AF012023	Hs.173274	integrin cytoplasmic domain-associated p	5.3
406305	BE261320	Hs.158196	transcriptional adaptor 3 (ADA3, yeast h	5.3
437411	AW613948	Hs.194915	ESTs	5.3
442800	AI809481	Hs.131227	ESTs	5.3
402054	NA		Target Exon	5.3
432085	AF212829	Hs.272406	potassium channel, subfamily K, member 9	5.3
415313	R59638	Hs.6181	ESTs	5.2
459159	AI904646		gb:QV-BT065-020399-103 BT065 Homo sapien	5.2
427184	AB037721	Hs.173871	KIAA1300 protein	5.2
441391	BE467930	Hs.170361	ESTs	5.2
458959	AI285901	Hs.181297	ESTs	5.2
402698	NA		ENSP00000251335*:DJ1003J2.1 (sodium and	5.2
401810	NA		Target Exon	5.2
438879	AA827674	Hs.189073	ESTs	5.2
414657	AA424074	Hs.76780	protein phosphatase 1, regulatory (inhib	5.2
427809	M26380	Hs.180878	lipoprotein lipase	5.1
456063	NM_006744	Hs.76461	retinol-binding protein 4, interstitial	5.1
451186	AW023469	Hs.65256	ESTs, Weakly similar to leucine-rich gli	5.1
451882	AI821324	Hs.100445	ESTs	5.1
402583	NA		NM_021620:Homo sapiens PR domain contain	5.1
431130	NM_006103	Hs.2719	HE4; WFDC2; putative ovarian carcinoma m	5.1
458218	AI435179	Hs.126820	ESTs	5.1
416083	R53467	Hs.269122	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.1
455282	BE143867		gb:MR0-HT0164-070100-013-h02 HT0164 Homo	5.1
426488	X03350	Hs.4	alcohol dehydrogenase 1B (class I), beta	5.1
426156	BE244537	Hs.167382	natriuretic peptide receptor A/guanylate	5.1
407891	AA486620	Hs.41135	endomucin-2	5.0
408610	AW026692	Hs.224829	ESTs	5.0
445967	D59597	Hs.118821	CGI-62 protein	5.0
434813	AI524307	Hs.162870	ESTs	5.0
437526	AI076012	Hs.121388	ESTs, Weakly similar to MDHC_HUMAN MALAT	5.0
454775	BE160229		gb:QV1-HT0413-090200-062-e12 HT0413 Homo	5.0
409451	AF012626	Hs.54472	fragile X mental retardation 2	5.0
409853	AW502327		gb:UI-HF-BR0p-aka-e-07-0-UI.r1 NIH_MGC_5	5.0
405062			Target Exon	5.0
446490	AK000706	Hs.15125	hypothetical protein FLJ20699	5.0
417622	AW298163	Hs.82318	WAS protein family, member 3	5.0
421976	AJ243662	Hs.110196	NICE-1 protein	5.0
440338	R62431	Hs.12758	ESTs	5.0
415421	R35009	Hs.24903	ESTs	5.0
417574	R00348		gb:ye69e06.r1 Soares fetal liver spleen	5.0
409882	AJ243191	Hs.56874	heat shock 27kD protein family, member 7	5.0
447996	AI768289	Hs.304389	ESTs	4.9
445613	BE550889	Hs.158491	ESTs	4.9
443074	AW341470	Hs.144907	ESTs	4.9
451324	AI783600	Hs.208052	ESTs	4.9
432433	AW014734	Hs.157969	ESTs	4.9
449654	AI989812	Hs.199850	ESTs	4.9
414519	N94587	Hs.55063	ESTs	4.9
457531	AW973716	Hs.13913	KIAA1577 protein	4.9
433200	AA682722	Hs.192725	ESTs	4.9
430782	AF026263	Hs.247920	cholinergic receptor, muscarinic 5	4.8
427555	AW137094	Hs.97990	ESTs	4.8
433545	AA868510	Hs.112496	ESTs	4.8
420334	AI349351	Hs.118944	hypothetical protein FLJ22477	4.8

421795	X63094	Hs.283822	Rhesus blood group, D antigen	4.8
427138	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	4.8
413072	BE063965		gb:QV3-BT0296-140200-085-h01 BT0296 Homo	4.8
443721	AW450451	Hs.268355	ESTs	4.8
408053	AW139474	Hs.246862	ESTs	4.8
427067	AA843716	Hs.177927	ESTs	4.7
442969	AI025499	Hs.132238	ESTs	4.7
426220	AI383475	Hs.171697	ESTs, Weakly similar to T13924 sdk prote	4.7
414593	BE386764		gb:601273249F1 NIH_MGC_20 Homo sapiens c	4.7
426893	AA398716	Hs.97418	ESTs	4.7
434046	AW292618	Hs.113011	ESTs	4.7
401590	NA		Target Exon	4.7
457971	AW134679	Hs.242849	ESTs	4.7
427722	AK000123	Hs.180479	hypothetical protein FLJ20116	4.6
443793	AA045290	Hs.25930	ESTs, Weakly similar to 2109260A B cell	4.6
407737	R49187	Hs.6659	ESTs	4.6
441955	AA972327	Hs.142903	ESTs	4.6
441499	AW298235	Hs.101689	ESTs	4.6
447517	AI382726	Hs.182434	ESTs	4.6
403017			Target Exon	4.6
450580	N40087	Hs.15248	ESTs	4.6
404611	H58589	Hs.35156	Homo sapiens cDNA FLJ11027 fis, clone PL	4.6
414831	M31158	Hs.77439	protein kinase, cAMP-dependent, regulato	4.6
459290	NM_001546	Hs.34853	inhibitor of DNA binding 4, dominant neg	4.6
444341	AI142027	Hs.146650	ESTs	4.6
408614	AL137698	Hs.46531	Homo sapiens mRNA; cDNA DKFZp434C1915 (f	4.6
449638	AW204277	Hs.250723	hypothetical protein MGC2747	4.6
434418	AF134707	Hs.278679	a disintegrin and metalloproteinase doma	4.6
447360	AI375984	Hs.167216	ESTs	4.6
419583	F00312		gb:HSBB0D101 STRATAGENE Human skeletal	m4.6
440698	AI348455	Hs.147492	Homo sapiens cDNA FLJ11777 fis, clone HE	4.6
451199	AI290653	Hs.124758	ESTs	4.6
438338	NM_014861	Hs.6168	KIAA0703 gene product	4.6
433756	AW015933	Hs.112654	Homo sapiens, clone MGC:9764, mRNA, comp	4.5
423301	S67580	Hs.1645	cytochrome P450, subfamily IVA, polypept	4.5
417237	H88385	Hs.81737	palmitoyl-protein thioesterase 2	4.5
439745	AL389981	Hs.149219	Homo sapiens mRNA full length insert cDN	4.5
424137	AA335769	Hs.16262	ESTs	4.5
449338	H73444	Hs.394	adrenomedullin	4.5
434744	N94835	Hs.283828	Homo sapiens genomic DNA, chromosome 21q	4.5
407402	AF035303		gb:Homo sapiens clone 23943 mRNA sequenc	4.5
443510	NM_012190	Hs.9520	formyltetrahydrofolate dehydrogenase	4.5
415754	AA169114	Hs.12247	hypothetical protein FLJ11413	4.5
415986	Z43819		gb:HSC1GE121 normalized infant brain cDN	4.5
457416	BE142052	Hs.62654	kringle-containing transmembrane protein	4.5
418064	BE387287	Hs.83384	S100 calcium-binding protein, beta (neur	4.4
437120	AI356125	Hs.157767	ESTs, Weakly similar to HXA2_HUMAN HOMEO	4.4
453950	AA156998	Hs.211568	eukaryotic translation initiation factor	4.4
401093			C12000586*:gi|6330167|db|BAA86477.1| (A	4.4
436935	AW206494	Hs.253560	ESTs	4.4
457974	AW842353	Hs.321717	ESTs, Weakly similar to S22765 heterogen	4.4
428222	AL133112	Hs.183085	Homo sapiens mRNA; cDNA DKFZp434K098 (fr	4.4
442705	AI264634	Hs.131127	ESTs	4.4
437409	AL359599	Hs.283850	Homo sapiens mRNA; cDNA DKFZp547C126 (fr	4.4
458494	AI380906	Hs.158436	ESTs	4.4
410490	H03589		gb:yj42d08.r1 Soares placenta Nb2HP Homo	4.4
416069	R37101	Hs.20982	ESTs	4.4
438463	AA807958	Hs.314232	ESTs	4.4
444043	AI499723	Hs.135089	ESTs	4.4
438327	H87407	Hs.172944	chorionic gonadotropin, beta polypeptide	4.4
457711	AF147401	Hs.23917	ESTs	4.3
400870			C11000905:gi|11692565|gb|AAG39879.1|AF28	4.3
441425	AA933590	Hs.28937	homeobox protein from AL590526	4.3
416267	H45384		gb:yn99c10.r1 Soares adult brain N2b5HB5	4.3
407262	M12873		gb:Human Ig rearranged H-chain mRNA VDJ4	4.3
444567	AV654020	Hs.184261	ESTs, Weakly similar to T26686 hypothetl	4.3
403263	NA		Target Exon	4.3

410034	BE067414		gb:MR4-BT0355-200100-201-e05 BT0355 Homo	4.3
456804	AI421645	Hs.139851	caveolin 2	4.3
448427	BE395260	Hs.309438	EST	4.3
416931	D45371	Hs.80485	adipose most abundant gene transcript 1	4.3
421296	NM_002666	Hs.103253	perilipin	4.3
400973	NA		ENSP00000236867*:Mucin 5B (Fragment),	4.3
452602	AW366194	Hs.55962	ESTs	4.3
412330	NM_005100	Hs.788	A kinase (PRKA) anchor protein (gravin)	4.3
405016			CY000171*:gi|9280405|gb|AAF86402.1|AF245	4.3
435104	AI475671	Hs.88607	ESTs, Highly similar to F-box protein FB	4.3
406118			ENSP00000246632:CDNA FLJ20261 fis, clone	4.3
418556	T02850		gb:FB12A9 Fetal brain, Stratagene Homo s	4.3
429745	AA480818	Hs.221736	ESTs	4.3
433088	AW451206	Hs.115899	ESTs	4.3
444445	AA342329	Hs.115920	Homo sapiens cDNA: FLJ22816 fis, clone K	4.3
453880	AI803166	Hs.28462	ESTs, Weakly similar to I38022 hypothetl	4.3
447384	AI377221	Hs.40528	ESTs	4.2
414541	BE293116	Hs.76392	aldehyde dehydrogenase 1 family, member	4.2
444975	AV652165	Hs.182482	ESTs, Weakly similar to T00362 hypothetl	4.2
403921	NA		C5000212*:gi|10047237|db|BAB13407.1| (A	4.2
451477	AI798425	Hs.42710	ESTs	4.2
406344			C5001660:gi|11611537|db|BAB18935.1| (AB	4.2
416970	AA191201	Hs.35861	DKFZP586E1621 protein	4.2
413662	BE155866	Hs.25522	KIAA1808 protein	4.2
458504	AW070634	Hs.144794	ESTs	4.2
404682	NA		C9001188*:gi|12738842|ref|NP_073725.1| p	4.2
418089	N69913	Hs.6858	ESTs, Weakly similar to I78885 serine/th	4.2
403433			NM_001622:Homo sapiens alpha-2-HS-glycop	4.2
446532	AW975460	Hs.143583	ESTs	4.2
414217	AI309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	4.2
418425	AI871247	Hs.6262	hypothetical protein MGC8407	4.2
419589	AW973708	Hs.201925	Homo sapiens cDNA FLJ13446 fis, clone PL	4.2
457029	AA397789	Hs.161803	ESTs	4.2
447860	AF193807	Hs.131835	Rhesus blood group, B glycoprotein	4.2
448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	4.2
440810	AI733098	Hs.130800	ESTs	4.2
439590	AF086410		gb:Homo sapiens full length insert cDNA	4.2
427240	AA399975	Hs.274151	ligatin	4.2
408932	AW594172	Hs.278513	TP53TG3 protein	4.2
436112	T77545	Hs.187559	ESTs	4.2
444382	AI144152	Hs.58248	ESTs	4.2
456716	AA318060	Hs.135121	hypothetical protein FLJ22415	4.2
419846	NM_015977	Hs.285681	Williams-Beuren syndrome chromosome regi	4.2
410036	R57171	Hs.57975	calsequestrin 2 (cardiac muscle)	4.1
400545	NA		Target Exon	4.1
403051	NA		Target Exon	4.1
420139	NM_005357	Hs.95351	lipase, hormone-sensitive	4.1
450244	AA007534	Hs.125082	ESTs	4.1
453261	AA034116	Hs.118494	ESTs	4.1
440246	W52010	Hs.191379	ESTs	4.1
414516	AI307802	Hs.135560	ESTs, Weakly similar to T43458 hypothetl	4.1
438232	AI150595	Hs.122226	ESTs	4.1
410233	AA082947		gb:zn10g07.s1 Stratagene hNT neuron (937	4.1
412179	BE270758	Hs.69428	hypothetical protein MGC3020	4.1
441871	AI306150	Hs.153450	ESTs, Weakly similar to 1909123A Na gluc	4.1
426411	AK000708	Hs.169784	hypothetical protein FLJ20701	4.1
453692	AL110416		gb:DKFZp434K0431_r1 434 (synonym: htes3)	4.1
448640	AW817177	Hs.102558	Homo sapiens, clone MGC:5352, mRNA, comp	4.1
417481	AA203281	Hs.21798	ESTs	4.1
412912	AW118878	Hs.110835	ESTs	4.1
454183	AW807116		gb:MR4-ST0062-040100-024-b12 ST0062 Homo	4.1
426328	AW631286		gb:hh83c09.y1 NCI_CGAP_GU1 Homo sapiens	4.1
435942	R06285	Hs.191215	ESTs	4.1
417629	T76945		gb:yc92c07.r1 Soares infant brain 1NIB H	4.1
403593	NA		Target Exon	4.0
402690			Target Exon	4.0
418190	R49591	Hs.270425	ESTs	4.0

408641	AW245207	Hs.5555	hypothetical protein MGC5347	4.0
427899	AA829286	Hs.332053	serum amyloid A1	4.0
445975	AI811536	Hs.145734	ESTs	4.0
438831	BE263273	Hs.6439	synapsin II	4.0
455578	BE006350	Hs.14355	Homo sapiens cDNA FLJ13207 fis, clone NT	4.0
401840	NA		Target Exon	4.0
413753	U17760	Hs.75517	laminin, beta 3 (nicein (125kD), kalinin	4.0
445030	AI205925	Hs.147238	ESTs, Highly similar to AAC3_HUMAN ALPHA	4.0
433873	AW156913	Hs.150478	ESTs, Weakly similar to A Chain A, Cryst	4.0
456736	AW248217	Hs.1619	achaete-scute complex (Drosophila) homol	4.0
450112	BE047734	Hs.5473	ESTs, Moderately similar to ALU5_HUMAN A	4.0
448906	AI589567	Hs.309719	ESTs	4.0

TABLE 23A

Table 23A shows the accession numbers for those pkeys lacking unigeneID's for Table 23. For each probeset, we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT number	Accessions
409853	1156228_1	AW502327 AW502488 AW501829 AW502625 AW502687
410034	1170594_1	BE067414 BE067958 BE067419 BE067963 AW577127 AW601412
410233	118656_1	AA082947 AA083036
410490	1205347_1	H03589 AW750687 AW750688
410882	1225686_1	AW809183 AW809247 AW809177 AW809190 AW809225
411478	1247073_1	BE143068 AW849143 AW848705 AW848569 AW848071 AW848475 AW848092 AW848005
413065	1347960_1	BE063555 BE151321 BE151319 BE151657 BE151655 BE063556 BE151322
413072	1348183_1	BE063965 BE063968 BE064034 BE064028 BE063874 BE063966 BE063869 BE064043 BE064033 BE063884
414593	1484909_1	BE386764 BE387560
414913	1506721_1	R25621 C03959 C04010
415011	151328_1	AW963085 AA159005 AW963073
415986	1564410_1	Z43619 R61274 H12206 R12883
416287	1583547_1	H45384 H49125 H41699
417574	1687770_1	R00348 R09593
417629	1690392_1	T76945 R20210 R05755
418556	1767866_-1	T02850
419583	186198_1	F00312 AA247490 F31427 AA383663 F22045
426328	264901_1	AW631296 AA375484
439590	47413_1	AF086410 W94386 W74609
442398	541271_1	AA994520 AW393574
452205	90415_1	C15819 AA024741 AA024742
452654	925931_1	BE004783 BE004947 AI911790
453692	977825_1	AL110416 AW876759
454183	1049636_1	AW807116 AW807569 AW807415 AW807338 AW807288 AW807263 AW807316 AW177402 AW807413 AW807068 BE141561 BE141569 AW807401 AW807310 BE141565 AW807318 AW807119 AW807299 AW807241 AW807225 AW807204 AW807345 AW807103 BE141615 AW807431 AW807393 AW807337 AW807406 AW807259 AW807375 AW845890 AW807220 AW807399 AW807064 AW807376 AW807024 BE141595 AW807238 AW807027 AW807112 AW807378 AW807202 BE141593 AW807216 AW807138 AW807244 AW807221 AW807297 AW807050 AW807248 AW807404 AW807075 AW807237 AW807212 AW807308 AW807110 AW807104 BE140912 AW807301 AW807382 AW807294 AW807028 AW807020 AW807108 AW807025 AW807433 AW807124 AW807419 AW807031 AW807264 AW807032 AW807029 AW807052 AW807391 AW807207 AW807215 AW807019 AW807238 AW807201 BE141590 AW807302 AW807323 AW807380 AW807109 BE141588 AW845877 AW807418 AW807407 AW807309 BE141614 AW845861 AW807398 AW807300 AW807348 AW807311 AW807214 AW807132 AW807402 AW807350 AW807028 AW807298 AW807291 AW807305 AW807217 AW807312 AW807261 AW807268 AW807260 AW807266 AW807198 AW807346 AW807315 BE140940 AW807351 AW807122 AW807235 AW807076 AW807314 AW807213 AW807143 AW807131 AW800079 AW807068 AW807077 AW845923 AW807421 BE141619 BE140943 AW807420 AW807381 BE141621 AW845921 BE141629 BE141625 BE141624 BE141636 BE141630 AW807405 AW807290 AW807353
454404	1170594_1	BE067414 BE067958 BE067419 BE067963 AW577127 AW601412
454775	1234106_1	BE160229 AW819879 AW820179 AW819882 AW819876 AW820169 BE153201 AW993736 BE152911
455282	1273020_1	BE143867 AW935060 AW886684
459159	919998_1	AI904846 BE179494 BE179421

TABLE 23B

Table 23B shows the genomic positioning for those pkeys lacking unigene ID's and accession numbers in Table 23. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I, et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I, et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400545	9800107	Minus	124618-124881
400870	9838306	Minus	34081-35027
400973	7960452	Minus	98119-98253
401093	8516137	Minus	22335-23166
401590	9966320	Minus	33547-33649
401665	7145001	Plus	121591-122537
401810	7342191	Plus	129063-129476
401840	7684597	Plus	56283-56439
402054	8083691	Minus	8268-8806
402195	7689778	Minus	147901-148884
402583	7684486	Plus	94883-95003
402690	8348058	Plus	13368-13998
402698	8570304	Minus	108641-108903
402779	9588555	Minus	38173-39210
403017	6693623	Plus	78630-79367
403051	4827080	Minus	5269-5411
403263	7770677	Plus	52431-52737
403433	9719611	Minus	72225-72437
403593	6862650	Minus	62554-62712,69449-69602
403612	8469060	Minus	94723-94859
403921	7711590	Minus	3297-3536
404368	7630956	Minus	102053-102199
404682	9797231	Minus	40977-41150
404689	7534100	Plus	119461-119717
405016	6524300	Plus	51997-53308
405062	7657730	Plus	101283-101432
406118	9143818	Plus	53997-54629
406344	9255974	Plus	20254-20374,20526-20659,20835-21097
406563	7711604	Plus	34401-34538

TABLE 24:

Table 24 depicts Seq ID No., UnigeneID, UnigeneTitle, Pkey, Pred.Cell.Loc., and ExAccn for all of the sequences in Table 25. The information in Table 24 is linked by Seq ID No. to Table 25.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
Pred.Cell.Loc.: Predicted Cellular Localization
Seq.ID.No.: Sequence Identification Number found in Table 25

Pkey	ExAccn	UnigeneID	Unigene Title	Pred.Cell.Loc.	Seq. ID. No.
449746	AI668594	Hs.176588	ESTs, Weakly similar to CP4Y_HUMAN CYTOC		Seq ID 1 & 2
407276	AI951118	Hs.326736	Homo sapiens breast cancer antigen NY-BR		Seq ID 3 & 4
415539	AI733881	Hs.72472	BMP-R1B		Seq ID 5 & 6
400297	AI127076	Hs.334473	hypothetical protein DKFZp564O1278		Seq ID 7 & 8
450375	AA009647	Hs.8850	a disintegrin and metalloproteinase doma		Seq ID 9 & 10
102457	NM_001394	Hs.2359	dual specificity phosphatase 4	nuclear	Seq ID 11 & 12
429170	NM_001394	Hs.2359	dual specificity phosphatase 4	nuclear	Seq ID 11 & 12
424399	AI905687	Hs.2533	aldehyde dehydrogenase 9 family, member	cytoplasm	Seq ID 13 & 14
422505	AL120882	Hs.124165	ESTs		Seq ID 15 & 16
449765	N92293	Hs.206832	ESTs, Moderately similar to ALU8_HUMAN A		Seq ID 17 & 18
425692	D90041	Hs.155956	N-acetyltransferase 1 (arylamine N-acety		Seq ID 19 & 20
426215	AW963419	Hs.155223	stanniocalcin 2		Seq ID 21 & 22
439840	AW449211	Hs.105445	GDNF family receptor alpha 1		Seq ID 23 & 24
410102	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035 fis, clone HE		Seq ID 25 & 26
429220	AW207206	Hs.136319	ESTs		Seq ID 27 & 28
416276	U41060	Hs.79136	LIV-1 protein, estrogen regulated		Seq ID 29 & 30
409079	W87707	Hs.82065	interleukin 6 signal transducer (gp130,		Seq ID 31 & 32
442818	AK001741	Hs.8739	hypothetical protein FLJ10879		Seq ID 33 & 34
442082	R41823	Hs.7413	ESTs		Seq ID 35 & 36
444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypothet		Seq ID 37 & 38
446163	AA026880	Hs.25252	Homo sapiens cDNA FLJ13603 fis, clone PL		Seq ID 39 & 40
416636	N32536	Hs.42645	solute carrier family 16 (monocarboxylic		Seq ID 41 & 42
442117	AW664964	Hs.128899	ESTs		Seq ID 43 & 44
433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA		Seq ID 45 & 46
429353	AL117406	Hs.200102	ATP-binding cassette transporter MRP8		Seq ID 47 & 48
452190	H26735	Hs.91668	Homo sapiens clone PP1498 unknown mRNA		Seq ID 49 & 50
446733	AA863360	Hs.26040	ESTs, Weakly similar to fatty acid omega		Seq ID 51 & 52
452747	BE153855	Hs.61460	Ig superfamily receptor LNIR		Seq ID 53 & 54
423242	AL039402	Hs.125783	DEME-6 protein		Seq ID 55 & 56
417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein		Seq ID 57 & 58
432201	AI538613	Hs.298241	Transmembrane protease, serine 3		Seq ID 59 & 60
423961	D13666	Hs.136348	osteoblast specific factor 2 (fasciclin		Seq ID 61 & 62
439569	AW602166	Hs.222309	CEGP1 protein		Seq ID 63 & 64
114480	BE066778	Hs.151678	UDP-N-acetyl-alpha-D-galactosamine:polyp		Seq ID 65 & 66
404581			NM_014112*:Homo sapiens trichorhinophala	mitochodria	Seq ID 67 & 68
325372	NA		Phase 2 & 3 Exons	nuclear	Seq ID 69 & 70
112287	AB033084	Hs.334806	KIAA1238 protein		Seq ID 71 & 72
335824	NA		ENSP00000249072*:DJ222E13.1 (N-TERMINAL		Seq ID 73 & 74
424735	U31875	Hs.272499	short-chain alcohol dehydrogenase family		Seq ID 75 & 76
400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin		Seq ID 77 & 78
427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph		Seq ID 79 & 80
429925	NM_000786	Hs.226213	cytochrome P450, 51 (lanosterol 14-alpha	ER	Seq ID 81 & 82
429441	AJ224172	Hs.204096	lipophilin B (uteroglobin family member)		Seq ID 83 & 84
421155	H87879	Hs.102267	lysyl oxidase	extracellular	Seq ID 85 & 86
420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy		Seq ID 87 & 88
420813	X51501	Hs.99949	prolactin-induced protein	nuclear	Seq ID 89 & 90
452744	AI267652	Hs.30504	Homo sapiens mRNA; cDNA DKFZp434E082 (fr		Seq ID 91 & 92

420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	cytoplasm	Seq ID 93 & 94
424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	nuclear	Seq ID 95 & 96
429859	NM_007050	Hs.225952	protein tyrosine phosphatase, receptor t		Seq ID 97 & 98
446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	extracellular	Seq ID 99 & 100
445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6		Seq ID 101 & 102
428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	extracellular	Seq ID 103 & 104
424001	W67883	Hs.137476	paternally expressed 10		Seq ID 105 & 106
421727	Y13153	Hs.107318	kynurenine 3-monooxygenase (kynurenine 3		Seq ID 107 & 108
452838	U65011	Hs.30743	preferentially expressed antigen in mela	nuclear	Seq ID 109 & 110
419667	AU077005	Hs.92208	a disintegrin and metalloproteinase doma		Seq ID 111 & 112
414812	X72755	Hs.77367	monokine induced by gamma interferon	extracellular	Seq ID 113 & 114
426320	W47595	Hs.169300	transforming growth factor, beta 2	extracellular	Seq ID 115 & 116
422887	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	extracellular	Seq ID 117 & 118
411558	AA102670	Hs.70725	gamma-aminobutyric acid (GABA) A recepto		Seq ID 119 & 120
417866	AW067903	Hs.82772	collagen, type XI, alpha 1		Seq ID 121 & 122
428398	AI249368	Hs.98558	ESTs		Seq ID 123 & 124
431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	plasma membrane	Seq ID 125 & 126
428722	U76456	Hs.190787	tissue inhibitor of metalloproteinase 4		Seq ID 127 & 128
412970	AB026436	Hs.177534	dual specificity phosphatase 10		Seq ID 129 & 130
421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	extracellular	Seq ID 131 & 132
415752	BE314524	Hs.78776	putative transmembrane protein		Seq ID 133 & 134
444051	N48373	Hs.10247	activated leucocyte cell adhesion molecu		Seq ID 135 & 136
451110	AI955040	Hs.265398	ESTs, Weakly similar to transformation-r		Seq ID 137 & 138

TABLE 24A

Table 24A shows the accession numbers for those pkeys lacking unigeneID's for Table 24. For each probeset, we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT number	Accession
335924	CH22_3197FG_619_11_LINK_E	
325372	c12_hs	

TABLE 24B

Table 24B shows the genomic positioning for those pkeys lacking unigene ID's and accession numbers in Table 24. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
404561	9795980	Minus	69039-70100

Table 25

The 69 gene sequences identified to be overexpressed in breast cancer may be used to identify coding regions from the public DNA databases (nr and htgs in Genbank). The sequences may be used to either identify genes that encode known proteins, or they may be used to predict the coding regions from genomic DNA using exon prediction algorithms, such as FGENESH (Salamov and Solovyev, 2000, Genome Res. 10:516-522)

Seq ID NO: 1 DNA sequence
Nucleic Acid Accession #: FGENESH predicted ORF
Coding sequence: 1-1518 (underlined sequences correspond to start and stop codons)

```
1     11    21    31    41    51
|     |     |     |     |     |
ATGGAGCCCT CCTGGCTTCA GGAACTCATG GCTCACCCCT TCTTGCTGCT GATCCTCCTC   60
TGCATGTCTC TGCTGCTGTT TCAGGTAATC AGGTTGTACC AGAGGAGGAG ATGGATGATC  120
AGAGCCCTGC ACCTGTTTCC TGCACCCCCT GCCCACTGGT TCTATGGCCA CAAGGAGTTT  180
TACCCAGTAA AGGAGTTTGA GGTGTATCAT AAGCTGATGG AAAAATACCC ATGTGCTGTT  240
CCCTTGTGGG TTGGACCCTT TACGATGTTC TTCAGTGTCC ATGACCCAGA CTATGCCAAG  300
ATTCTCCTGA AAAGACAAGA TCCCAAAAGT GCTGTTAGCC ACAAAATCCT TGAATCCTGG  360
GTTGGTCGAG GACTTGTGAC CCTGGATGGT TCTAAATGGA AAAAGCACCG CCAGATTGTG  420
AAACCTGGCT TCAACATCAG CATTCTGAAA ATATTCATCA CCATGATGTC TGAGAGTGTT  480
CGGATGATGC TGAACAAATG GGAGGAACGC ATTGCCCAAA ACTCACGTCT GGAGCTCTTT  540
CAACATGTCT CCCTGATGAC CCTGGACAGC ATCATGAAGT GTGCCTTCAG CCACCAGGGC  600
AGCATCCAGT TGGACAGTAC CCTGGACTCA TACCTGAAAG CAGTGTTCAA CCTTAGCAAA  660
ATCTCCAACC AGCGCATGAA CAATTTTCTA CATCACAACG ACCTGGTTTT CAAATTCAGC  720
TCTCAAGGCC AAATCTTTTC TAAATTTAAC CAAGAACTTC ATCAGTTCAC AGAGAAAGTA  780
ATCCAGGACC GGAAGGAGTC TCTTAAGGAT AAGCTAAAAC AAGATACTAC TCAGAAAAGG  840
CGCTGGGATT TTCTGGACAT ACTTTTGAGT GCCAAAAGCG AAAACACCAA AGATTTCTCT  900
GAAGCAGATC TCCAGGCTGA AGTGAAAACG TTCATGTTTG CAGGACATGA CACCACATCC  960
AGTGCTATCT CCTGGATCCT TTACTGCTTG GCAAAGTACC CTGAGCATCA GCAGAGATGC 1020
CGAGATGAAA TCAGGGAACT CCTAGGGGAT GGGTCTTCTA TTACCTGGGA ACACCTGAGC 1080
CAGATGCCTT ACACCACGAT GTGCATCAAG GAATGCCTCC GCCTCTACGC ACCGGTAGTA 1140
AACATATCCC GGTTACTCGA CAAACCCATC ACCTTTCCAG ATGGACGCTC CTTACCTGCA 1200
GGAATAACTG TGTTTATCAA TATTTGGGCT CTTCACCACA ACCCCTATTT CTGGGAAGAC 1260
CCTCAGGTCT TTAACCCCTT GAGATTCTCC AGGGAAAATT CTGAAAAAAT ACATCCCTAT 1320
GCCTTCATAC CATTCTCAGC TGGATTAAGG AACTGCATTG GGCAGCATTT TGCCATAATT 1380
GAGTGTAAAG TGGCAGTGGC ATTAACTCTG CTCCGCTTCA AGCTGGCTCC AGACCACTCA 1440
AGGCCTCCCC AGCCTGTTCG TCAAGTTGTC CTCAAGTCCA AGAATGGAAT CCATGTGTTT 1500
GCAAAAAAAG TTTGCTAATT TTAAGTCCTT TCGTATAAGA ATTAATGAGA CAATTTTCCT 1560
ACCAAAGGAA GAACAAAAGG ATAAATATAA TACAAAATAT ATGTATATGG TTGTTTGACA 1620
AATTATATAA CTTAGGATAC TTCTGACTGG TTTTGACATC CATTAACAGT AATTTTAATT 1680
TCTTTGCTGT ATCTGGTGAA ACCCACAAAA ACACCTGAAA AAACTCAAGC TGACTTCCAC 1740
TGCGAAGGGA AATTATTGGT TTGTGTAACT AGTGGTAGAG TGGCTTTCAA GCATAGTTTG 1800
ATCAAAACTC CACTCAGTAT CTGCATTACT TTTATCTCTG CAAATATCTG CATGATAGCT 1860
TTATTCTCAG TTATCTTTCC CCAATAATAA AAAA
```

Seq ID NO: 2 Protein sequence:
Protein Accession #: FGENESH predicted

```
1     11    21    31    41    51
|     |     |     |     |     |
MEPSWLQELM AHPFLLLILL CMSLLLFQVI RLYQRRRWMI RALHLFPAPP AHWFYGHKEF   60
YPVREFEVYH KLMEKYPCAV PLWVGPFTMF FSVHDPDYAK ILLKRQDPKS AVSHKIIESW  120
VGRGLVTLDG SKWKKHRQIV KPGFNISILK IFTMMSESV RMMLNKWEER IAQNSRLELF  180
QHVSLMTLDS IMKCAFSHQG SIQLDSTLDS YLKAVFNLSK ISNQRMNNFL HHNDLVFKFS  240
SQGQIFSKFN QELHQFTEKV IQDRKESLKD KLKQDTTQKR RWDFLDILLS AKSENTKDFS  300
EADLQAEVKT FMFAGHDTTS SAISWILYCL AKYPEHQQRC RDEIRELLGD GSSITWEHLS  360
QMPYTTMCIK ECLRLYAPVV NISRLLDKPI TFPDGRSLPA GITVFINIWA LHHNPYFWED  420
PQVFNPLRFS RENSEKIHPY AFIPFSAGLR NCIGQHFAII ECKVAVALTL LRFKILAPDH S 480
RPPQPVRQVV LKSKNGIHVF AKKVC
```

Seq ID NO: 3 DNA sequence
Nucleic Acid Accession #: NM_052997
Coding sequence: 100-4125 (underlined sequences correspond to start and stop codons)

```
1     11    21    31    41    51
|     |     |     |     |     |
CTAGTCTATA CCAGCAACGA CTCCTACATC GTCCACTCTG GGGATCTTAG AAAGATCCAT   60
AAAGCTGCCT CCCGGGGACA AGTCCGGAAG CTGGAGAAGA TGACAAAGAG GAAGAAGACC  120
ATCAACCTTA ATATACAAGA CGCCCAGAAG AGGACTGCTC TACACTGGGC CTGTGTCAAT  180
GGCCATGAGG AAGTAGTAAC ATTTCTGGTA GACAGAAAGT GCCAGCTTGA CGTCCTTGAT  240
GGCGAACACA GGACACCTCT GATGAAGGCT CTACAATGCC ATCAGGAGGC TTGTGCAAAT  300
ATTCTGATAG ATTCTGGTGC CGATATAAAT CTCGTAGATG TGTATGGCAA CATGGCTCTC  360
CATTATGCTG TTTATAGTGA GATTTTGTCA GTGGTGGCAA AACTGCTGTC CCATGGTGCA  420
GTCATCGAAG TGCACAACAA GGCTAGCCTC ACACCACTTT TACTATCCAT AACGAAAAGA  480
```

AGTGAGCAAA TTGTGGAATT TTTGCTGATA AAAAATGCAA ATGCGAATGC AGTTAATAAG 540
TATAAATGCA CAGCCCTCAT GCTTGCTGTA TGTCATGGAT CATCAGAGAT AGTTGGCATG 600
CTTCTTCAGC AAAATGTTGA CGTCTTTGCT GCAGATATAT GTGGAGTAAC TGCAGAACAT 660
TATGCTGTTA CTTGTGGATT TCATCACATT CATGAACAAA TTATGGAATA TATACGAAAA 720
TTATCTAAAA ATCATCAAAA TACCAATCCA GAAGGAACAT CTGCAGGAAC ACCTGATGAG 780
GCTGCACCCT TGGCGGAAAG AACACCTGAC ACAGCTGAAA GCTTGGTGGA AAAAACACCT 840
GATGAGGCTG CACCCTTGGT GGAAAGAACA CCTGACACGG CTGAAAGCTT GGTGGAAAAA 900
ACACCTGATG AGGCTGCATC CTTGGTGGAG GGAACATCTG ACAAAATTCA ATGTTTGGAG 960
AAAGCGACAT CTGGAAAGTT CGAACAGTCA GCAGAAGAAA CACCTAGGGA AATTACGAGT 1020
CCTGCAAAAG AAACATCTGA GAAATTTACG TGGCCAGCAA AAGGAAGACC TAGGAAGATC 1080
GCATGGGAGA AAAAAGAAGA CACACCTAGG GAAATTATGA GTCCCGCAAA AGAAACATCT 1140
GAGAAATTTA CGTGGGCAGC AAAAGGAAGA CCTAGGAAGA TCGCATGGGA GAAAAAAGAA 1200
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Seq ID NO: 4 Protein sequence:
Protein Accession #: NP_443723.1

1 11 21 31 41 51
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Seq ID NO: 5 DNA sequence
Nucleic Acid Accession #: none found
Coding sequence: 273-1785 (underlined sequences correspond to start and stop codons)

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CTTTCAGGGA GCCACCTGGG CAAAGACAGA GAAGCTCCCA GAAGGAGAGA TTGATCCGTG 1980
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Seq ID NO: 6 Protein sequence:
Protein Accession #: none found

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GPIHHRALLI SVTVCSLLLV LIILFCYFRY KRQETRPRYS IGLEQDETYI PPGESLRDLI 180
EQSQSSGSGS GLPLLVQRTI AKQIQMVKQI GKGRYGEVWM GKWRGEKVAV KVFFTTEEAS 240
WFRETEIYQT VLMRHENILG FIAADIKGTG SWTQLYLITD YHENGSLYDY LKSTTLDAKS 300
MLKLAYSSVS GLCHLHTEIF STQGKPAIAH RDLKSKNILV KKNGTCCIAD LGLAVKFISD 360
TNEVDIPPNT RVGTKRYMPP EVLDESLNRN HFQSYIMADM YSFGLILWEV ARRCVSGGIV 420

EEYQLPYHDL VPSDPSYEDM REIVCIKKLR PSFPNRWSSD ECLRQMGKLM TECWAHNPAS 480
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Seq ID NO: 7 DNA sequence
Nucleic Acid Accession #: none found
Coding sequence: 482-3007(underlined sequences correspond to start and stop codons)

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Seq ID NO: 8 Protein sequence:
Protein Accession #: none found

1 11 21 31 41 51
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RFVPLTHLDL RGNQLQTLPY VGFLEHIGRI LDLQLEDNKW ACNCDLLQLK TWLENMPPQS 240
IIGDVVCNSP PFFKGSILSR LKKESICPTP PVYEEHEDPS GSLHLAATSS INDSRMSTKT 300
TSILKLPTKA PGLPYITKP STQLPGPYCP IPCNCKVLSP SGLLIHCQER NIESLSDLRP 360

PPQNPRKLIL AGNIIHSLMK SDLVEYPTLE MLHLGNNRIE VLEEGSFMNL TRLQKLYLNG 420
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GVPLTKVNLK TNQFTHLPVS NILDDLDLLT QIDLEDNPWD CSCDLVGLQQ WIQKLSKNTV 540
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YGHKTTHHTT ERPSASLYEQ HMVSPMVHVY RSPSPQPKHL EEEEERNEKE GSDAKHLQRS 720
LLEQENHSPL TGSNMKYKTT NQSTEFLSFQ DASSLYRNIL EKERBLQQLG ITEYLRKNIA 780
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Seq ID NO: 9 DNA sequence
Nucleic Acid Accession #: NM_003474
Coding sequence: 307-3036 (underlined sequences correspond to start and stop codons)

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CGTGGCTTCC AACCCTGTCA GGCTCACCTC GGCCACCTTG GAAAAGGCCT GATTAGGAAG 2640
CCGCCAGATT CCTACCCACC GAAGGACAAT CCCAGGAGAT TGCTGCAGTG TCAGAATGTT 2700
GACATCAGCA GACCCCTCAA CGGCCTGAAT GTCCCTCAGC CCCAGTCAAC TCAGCGAGTG 2760
CTTCCTCCCC TCCACCGGGC CCCACGTGCA CCTAGCGTCC CTGCCAGACC CCTGCCAGCC 2820
AAGCCTGCAC TTAGGCAGGC CCAGGGGACC TGTAAGCCAA ACCCCCCTCA GAAGCCTCTG 2880
CCTGCAGATC CTCTGGCCAG AACAACTCGG CTCACTCATG CCTTGGCCAG GACCCCAGGA 2940
CAATGGGAGA CTGGGCTCCG CCTGGCACCC CTCAGACCTG CTCCACAATA TCCACACCAA 3000
GTGCCCAGAT CCACCCACAC CGCCTATATT AAGTGAAAG CCGACACCTT TTTTCAACAG 3060
TGAAGACAGA AGTTTGCACT ATCTTTCAGC TCCAGTTGGA GTTTTTGTA CCAACTTTTA 3120
GGATTTTTTT TAATGTTTAA AACATCATTA CTATAAGAAC TTTGAGCTAC TGCCGTCAGT 3180
GCTGTGCTGT GCTATGGTGC TCTGTCTACT TGCACAGGTA CTTGTAAATT ATTAATTTAT 3240
GCAGAATGTT GATTACAGTG CAGTGCGCTG TAGTAGGCAT TTTTACCATC ACTGAGTTTT 3300
CCATGGCAGG AAGGCTTGTT GTGCTTTTAG TATTTTAGTG AACTTGAAAT ATCCTGCTTG 3360
ATGGGATTCT GGACAGGATG TGTTTGCTTT CTGATCAAGG CCTTATTGGA AAGCAGTCCC 3420
CCAACTACCC CCAGCTGTGC TTATGGTACC AGATGCAGCT CAAGAGATCC CAAGTAGAAT 3480
CTCAGTTGAT TTTCTGGATT CCCCATCTCA GGCCAGAGCC AAGGGGCTTC AGGTCCAGGC 3540
TGTGTTTGGC TTTCAGGGAG GCCCTGTGCC CCTTGACAAC TGGCAGGCAG GCTCCCAGGG 3600

ACACCTGGGA GAAATCTGGC TTCTGGCCAG GAAGCTTTGG TGAGAACCTG GGTTGCAGAC 3660
AGGAATCTTA AGGTGTAGCC ACACCAGGAT AGAGACTGGA ACACTAGACA AGCCAGAACT 3720
TGACCCTGAG CTGACCAGCC GTGAGCATGT TTGGAAGGGG TCTGTAGTGT CACTCAAGGC 3780
GGTGCTTGAT AGAAATGCCA AGCACTTCTT TTTCTCGCTG TCCTTTCTAG AGCACTGCCA 3840
CCAGTAGGTT ATTTAGCTTG GGAAAGGTGG TGTTTCTGTA AGAAACCTAC TGCCCAGGCA 3900
CTGCAAACCG CCACCTCCCT ATACTGCTTG GAGCTGAGCA AATCACCACA AACTGTAATA 3960
CAATGATCCT GTATTCAGAC AGATGAGGAC TTTCCATGGG ACCACAACTA TTTTCAGATG 4020
TGAACCATTA ACCAGATCTA GTCAATCAAG TCTGTTTACT GCAAGGTTCA ACTTATTAAC 4080
AATTAGGCAG ACTCTTTATG CTTGCAAAAA CTACAACCAA TGGAATGTGA TGTTCATGGG 4140
TATAGTTCAT GTCTGCTATC ATTATTCGTA GATATTGGAC AAAGAACCTT CTCTATGGGG 4200
CATCCTCTTT TTCCAACTTG GCTGCAGGAA TCTTTAAAAG ATGCTTTTAA CAGAGTCTGA 4260
ACCTATTTCT TAAACACTTG CAACCTACCT GTTGAGCATC ACAGAATGTG ATAAGGAAAT 4320
CAACTTGCTT ATCAACTTCC TAAATATTAT GAGATGTGGC TTGGGCAGCA TCCCCTTGAA 4380
CTCTTCACTC TTCAAATGCC TGACTAGGGA GCCATGTTTC ACAAGGTCTT TAAAGTGACT 4440
AATGGCATGA GAAATACAAA AATACTCAGA TAAGGTAAAA TGCCATGATG CCTCTGTCTT 4500
CTGGACTGGT TTTCACATTA GAAGACAATT GACAACAGTT ACATAATTCA CTCTGAGTGT 4560
TTTATGAGAA AGCCTTCTTT TGGGGTCAAC AGTTTTCCTA TGCTTTGAAA CAGAAAAATA 4620
TGTACCAAGA ATCTTGGTTT GCCTTCCAGA AAACAAAACT GCATTTCACT TTCCCGGTGT 4680
TCCCCACTGT ATCTAGGCAA CATAGTATTC ATGACTATGG ATAAACTAAA CACGTGACAC 4740
AAACACACAC AAAAGGGAAC CCAGCTCTAA TACATTCCAA CTCGTATAGC ATGCATCTGT 4800
TTATTCTATA GTTATTAAGT TCTTTAAAAT GTAAAGCCAT GCTGGAAAAT AATACTGCTG 4860
AGATACATAC AGAATTACTG TAACTGATTA CACTTGGTAA TTGTACTAAA GCCAAACATA 4920
TATATACTAT TAAAAAGGTT TACAGAATTT TATGGTGCAT TACGTGGGCA TTGTCTTTTT 4980
AGATGCCCAA ATCCTTAGAT CTGGCATGTT AGCCCTTCCT CCAATTATAA GAGGATATGA 5040
ACCAAAAAAA AAAAAAAAAA AA

Seq ID NO: 10 Protein sequence:
Protein Accession #: NP_003465.2

1 11 21 31 41 51
| | | | | |
MAARPLPVSP ARALLLALAG ALLAPCEARG VSLWNEGRAD EVVSASVRSG DLWIPVKSFD 60
SKNHPEVLNI RLQRESKELI INLERNEGLI ASSFTETHYL QDGTDVSLAR NYTVILGHCV 120
YHGHVRGYSD SAVSLSTCSG LRGLIVFENE SYVLEPMKSA TNRYKLFPAK KLKSVRGSCG 180
SHHNTPNLAA KNVFPPPSQT WARRHKRETL KATKYVELVI VADNREFQRQ GKDLEKVKQR 240
LIEIANHVDK FYRPLNIRIV LVGVEVWNDM DKCSVSQDPF TSLHEFLDWR KMKLLPRKSH 300
DNAQLVSGVY FQGTTIGMAP IMSMCTADQS GGIVMDHSDN PLGAAVTLAH ELGHNFGMNH 360
DTLDRGCSCQ MAVEKGGCIM NASTGYPFPM VFSSCSRKDL ETSLEKGMGV CLFNLPEVRE 420
SFGGQKCGNR FVEEGEECDC GEPEECMNRC CNATTCTLKP DAVCAHGLCC EDCQLKPAGT 480
ACRDSSNSCD LPEFCTGASP HCPANVYLHD GHSCQDVDGY CYNGICQTHE QQCVTLWGPG 540
AKPAPGICFE RVNSAGDPVG NCGKVSKSSP AKCEMRDAKC GKIQCQGGAS RFVIGTNAVS 600
IETNIPLQGG GRILCRGTHV YLGDDMPDPG LVLAGTKCAD GKICLNRQCQ NISVPGVHEC 660
AMQCHGRGVC NNRKNCHCEA HWAPPFCDKF GFGGSTDSGP IRQADNQGLT IGILVTILCL 720
LAAGPVVYLK RKTLIRLLFT NKKTTIEKLR CVRPSRPPRG FQPCQAHLGH LGKGLMRKPP 780
DSVPPKDNPR RLLQCQNVDI SRPLNGLNVP QPQSTQRVLP PLIIRAPRAPS VPARPLPAKP 840
ALRQAQGTCK PNPPQKPLPA DPLARTTRLT HALARTPGQW ETGLRLAPLR PAPQYPHQVP 900
RSTHTAYIK

Seq ID NO; 11 DNA sequence
Nucleic Acid Accession #: NM_001394
Coding sequence: 400-1584(underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
| | | | | |
GGCACGAGGG CTGAGCGCCG GAGGAGCGTA GGCAGGGCAG CGCTGGCGCC AGCGGCGACA 60
GGAGCCGCGC GACCGGCAAA AATACACGGG AGGCCGTCGC CGAAAAGAGT CCGCGGTCCT 120
CTCTCGTAAA CACACTCTCC TCCACCGGCG CCTCCCCCTC CGCTCTGCGC GCCGCCCGGC 180
TGGGCGCCCG AGGCCGCTCC GACTGCTATG TGACCGCGAG GCTGCGGGAG GAAGGGGACA 240
GGGAAGAAGA GGCTCTCCCG CGGGAGCCCT TGAGGACCAA GTTTGCGGCC ACTTCTGCAG 300
GCGTCCCTTC TTAGCTCTCG CCTGCCCCTT TCTGCAGCCT AGGCGGCCCA GGTTCTCTTC 360
TCTTCCTCGC GCACCCAGCC GCCTCGGTTC CCGGCGACCA TGTGTACGAT GUAGGAGCTG 420
CGGGAGATGG ACTGCAGTGT GCTCAAAAGG CTGATGAACC GGGACGAGAA TGGCGGCGGC 480
GCGGGCGGCA GCGGCAGCCA CGGCACCCTG GGGCTGCCGA GCGGCGGCAA GTGCCTGCTG 540
CTGGACTGCA GACCGTTCCT GGCGCACAGC GCGGGCTACA TCCTAGGTTC GGTCAACGTG 600
CGCTGTAACA CCATCGTGCG GCGGCGGCCT AAGGGCTCCG TGAGCCTGGA GCAGATCCTG 660
CCCGCCGAGG AGGAGGTACG CGCCCGCTTG CGCTCCGGCC TCTACTCGGC GGTCATCGTC 720
TACGACGAGC GCAGCCCGCG CGCCGAGAGC CTCCGCGAGG ACAGCACCGT GTCGCTGGTG 780
GTGCAGGCGC TGCGCCGCAA CGCCGAGCGC ACCGACATCT GCCTGCTCAA AGGCGGCTAT 840
GAGAGGTTTT CCTCCGAGTA CCCAGAATTC TGTTCTAAAA CCAAGGCCCT GGCAGCCATC 900
CCACCCCCGG TTCCCCCCAG CGCCACAGAG CCCTTGGACC TGGGCTGCAG CTCCTGTGGG 960
ACCCCACTAC ACGACCAGGG GGGTCCTGTG GAGATCCTTC CCTTCCTCTA CCTCGGCAGT 1020
GCCTACCATG CTGCCCGGAG AGACATTCTG GACGCCCTGG GCATCACGGC TCTGTTGAAT 1080
GTCTCCTCGG ACTGCCCAAA CCACTTTGAA GGACACTATC AGTACAAGTG CATCCCAGTG 1140
GAAGATAACC ACAAGGCCGA CATCAGCTCC TGGTTCATGG AAGCCATAGA GTACATCGAT 1200
GCCGTGAAGG ACTGCCGTGG GCGCGTGCTG GTGCACTGCC AGGCGGGCAT CTCGCGGTCG 1260
GCCACCATCT GCCTGGCCTA CCTGATGATG AAGAAACGGG TGAGGCTGGA GGAGGCCTTC 1320

GAGTTCGTTA AGCAGCGCCG CAGCATCATC TCGCCCAACT TCAGCTTCAT GGGGCAGCTG 1380
CTGCAGTTCG AGTCCCAGGT GCTGGCCACG TCCTGTGCTG CGGAGGCTGC TAGCCCCTCG 1440
GGACCCCTGC GGGAGCGGGG CAAGACCCCC GCCACCCCCA CCTCGCAGTT CGTCTTCAGC 1500
TTTCCGGTCT CCGTGGGCGT GCACTCGGCC CCCAGCAGCC TGCCCTACCT GCACAGCCCC 1560
ATCACCACCT CTCCCAGCTG TTAGAGCCGC CCTGGGGGCC CCAGAACCAG AGCTGGCTCC 1620
CAGCAAGGGT AGGACGGGCC GCATGCGGCA GAAAGTTGGG ACTGAGCAGC TGGGAGCAGG 1680
CGACCGAGCT CCTTCCCCAT CATTTCTCCT TGGCCAACGA CGAGGCCAGC CAGAATGGCA 1740
ATAAGGACTC CGAATACATA ATAAAAGCAA ACAGAACACT CCAACTTAGA GCAATAACCG 1800
GTGCCGCAGC AGCCAGGGAA GACCTTGGTT TGGTTTATGT GTCAGTTTCA CTTTTCCGAT 1860
AGAAATTTCT TACCTCATTT TTTTAAGCAG TAAGGCTTGA AGTGATGAAA CCCACAGATC 1920
CTAGCAAATG TGCCCAACCA GCTTTACTAA AGGGGGAGGA AGGGAGGGCA AAGGGATGAG 1980
AAGACAAGTT TCCCAGAAGT GCCTGGTTCT GGGTACTTGT CCCTTTGTTG TCGTTGTTGT 2040
AGTTAAAGGA ATTTCATTTT TAAAAGAAAT CTTCGAAGGT GTGGTTTTCA TTTCTCAGTC 2100
ACCAACAGAT GAATAATTAT GCTTAATAAT AAAGTATTTA TTAAGACTTT CTTCAGAGTA 2160
TGAAAGTACA AAAAGTCTAG TTACAGTGGA TTTAGAATAT ATTTATGTTG ATGTCAAACA 2220
GCTGAGCACC GTAGCATGCA GATGTCAAGG CAGTTAGGAA GTAAATGGTG TCTTGTAGAT 2280
ATGTGCAAGG TAGCATGATG AGCAACTTGA GTTTGTTGCC ACTGAGAAGC AGCCGGGTTG 2340
GGTGGGAGGA GGAAGAAAGG GAAGAATTAG GTTTGAATTG CTTTTTAAAA AAAAAAGAAA 2400
AGAAAAAGAC AGCATCTCAC TATGTTGCCA AGGCTCATCT TGAGAAGCAG GCGGGTTGGG 2460
TGGGAGGAGG AAGAAAGGGA AGAATTAGGT TTGAATTGCT TTTTTAAAAA AAAA

Seq ID NO: 12 Protein sequence:
Protein Accession #: NP_001385

1 11 21 31 41 51
| | | | | |
MVTMEELREM DCSVLKRLMN RDENGGGAGG SGSHGTLGLP SGGKCLLLDC RPFLAHSAGY 60
ILGSVNVRCN TIVRRRAKGS VSLEQILPAE EEVRARLRSG LYSAVIVYDE RSPRAESLRE 120
DSTVSLVVQA LRRNAERTDI CLLKGGYERF SSEYPEFCSK TKALAAIPPP VPPSATEPLD 180
LGCSSCGTPL HDQGGPVEIL PFLYLGSAYH AARRDMLDAL GITALLNVSS DCPNHFEGHY 240
QYKCIPVEDN HKADISSWFM EAIEYIDAVK DCRGRVLVHC QAGISRSATI CLAYLMMKKR 300
VRLEEAFEFV KQRRSIISPN FSFMGQLLQF ESQVLATSCA AEAASPSGPL RERGKTPATP 360
TSQFVFSFPV SVGVHSAPSS LPVLHSPITT SPSC

Seq ID NO: 13 DNA sequence
Nucleic Acid Accession #: none found
Coding sequence: 68-340(underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
| | | | | |
AGCGCCTTGC CTTCTCTTAG GCTTTGAAGC ATTTTTGTCT GTGCTCCCTG ATCTTCAGGT 60
CACCACCATG AAGTTCTTAG CAGTCCTGGT ACTCTTGGGA GTTTCCATCT TTCTGGTCTC 120
TGCCCAGAAT CCGACAACAG CTGCTCCAGC TGACACGTAT CCAGCTACTG GTCCTGCTGA 180
TGATGAAGCC CCTGATGCTG AAACCACTGC TGCTGCAACC ACTGCGACCA CTGCTGCTCC 240
TACCACTGCA ACCACCGCTG CTTCTACCAC TGCTCGTAAA GACATTCCAG TTTTACCCAA 300
ATGGGTTGGG GATCTCCCGA ATGGTAGAGT GTGTCCCTGA GATGGAATCA GCTTGAGTCT 360
TCTGCAATTG GGTCACAACT ATTCATGCTT CCTGTGATTT CATCCAACTA CTTACCTTGC 420
CTACGATATC CCCTTTATCT CTAATCAGTT TATTTTCTTT CAAATAAAAA ATAACTATGA 480
GCGAGCTAAC AT

Seq ID NO: 14 Protein sequence:
Protein Accession #: none found

1 11 21 31 41 51
| | | | | |
MKFLAVLVLL GVSIFLVSAQ NPTTAAPADT YPATGPADDE APDAETTAAA TTATTAAPTT 60
ATTAASTTAR KDIPVLPKWV GDLPNGRVCP

Seq ID NO: 15 DNA sequence
Nucleic Acid Accession #: NM_016640.2
Coding sequence: 39-1358(underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
| | | | | |
GCTTAAGTTG ACCTCTGGGT CCGGAATCGC GGGCAAAGAT GGCGGCGGCC AGGTGTTGGA 60
GGCCTTTGCT ACGCGGTCCG AGGCTTTCAT TGCACACCGC GGCTAATGCC GCCGCCACGG 120
CTACAGAAAC GACCTCCCAA GACGTCGCGG CGACCCCGGT CGCGCGGTAC CCGCCGATTG 180
TGGCCTCCAT GACAGCCGAC AGCAAAGCTG CACGGCTGCG GCGGATCGAG CGCTGGCAGG 240
CGACGGTGCA CGCTGCGGAG TCGGTAGACG AGAAGCTGCG AATCCTCACC AAGATGCAGT 300
TTATGAAGTA CATGGTTTAC CCGCAGACCT TCGCACTGAA TGCCGACCGC TGGTACCAGT 360
ACTTCACCAA GACCGTGTTC CTGTCGGGTC TGCCGCCGCC CCCAGCGGAG CCCGAGCCCG 420
AGCCCGAACC CGAACCTGAA CCTGCGCTGG ACCTCGCGGC GCTGCGTGCG GTCGCCTGCG 480
ACTGCCTGCT GCAGGAGCAC TTCTACCTGC GGCGCAGGCG GCGCGTGCAC CGTTACGAGG 540

AGAGCGAGGT CATATCTTTG CCCTTCCTGG ATCAGCTGGT GTCAACCCTC GTGGGCCTCC 600
TCAGCCCACA CAACCCGGCC CTGGCCGCTG CCGCCCTCGA TTATAGATGC CCAGTTCATT 660
TTTACTGGGT GCGTGGTGAA GAAATTATTC CTCGTGGTCA TCGAAGAGGT CGAATTGATG 720
ACTTGCGATA CCAGATAGAT GATAAACCAA ACAACCAGAT TCGAATATCC AAGCAACTCG 780
CAGAGTTTGT GCCATTGGAT TATTCTGTTC CTATAGAAAT CCCCACTATA AAATGTAAAC 840
CAGACAAACT TCCATTATTC AACGGCAGT ATGAAAACCA CATATTTGTT GGCTCAAAAA 900
CTGCAGATCC TTGCTGTTAC GGTCACACCC AGTTTCATCT GTTACCTGAC AAATTAAGAA 960
GGGAAAGGCT TTTGAGACAA AACTGTGCTG ATCAGATAGA AGTTGTTTTT AGAGCTAATG 1020
CTATTGCAAG CCTTTTTGCT TGGACTGGAG CACAAGCTAT GTATCAAGGA TTCTGGAGTG 1080
AAGCAGATGT TACTCGACCT TTTGTCTCCC AGGCTGTGAT CACAGATGGA AAATACTTTT 1140
CCTTTTTCTG CTACCAGCTA AATACTTTGG CACTGACTAC ACAAGCTGAT CAAAATAACC 1200
CTCGTAAAAA TATATGTTGG GGTACACAAA GTAAGCCTCT TTATGAAACA ATTGAGGATA 1260
ATGATGTGAA AGGTTTTAAT GATGATGTTC TACTTCAGAT AGTTCACTTT CTACTGAATA 1320
GACCAAAAGA AGAAAAATCA CAGCTGTTGG AAAACTGAAA AAGCATATTT GATTGAGAAC 1380
TGTGGGAATA TTTAAATTTT ACTGAAGGAA CAATAATGAT GAGATTTGTA ACTGTCAACT 1440
ATTAAATACA TTGATTTTTG AGACAAATAT TTCTTATGTC AACCTGTTAT TAGATCTCTT 1500
ACTCTGCTCA AATTCATCAC TGAAAGATTT AATTTTAGTT ACCTTTTGTT GATTTAAAAA 1560
TAATTGCATT TGTATATTGC TAACTGATAA GACAAATTGA GTTATTUAGC TATTAAATGC 1620
ACATTTTAAT ATAAATGCAG AAATCCCAAA TAAAATGCTA ACATACTGAA TTCAGTAATT 1680
AAAAGAACCC ACTGC

Seq ID NO: 16 Protein sequence:
Protein Accession #: NP_057724.1

1 11 21 31 41 51
MAAARCWRPL LRQPRLSLHT AANAAATATE TTSQDVAATP VARYPPIVAS MTADSKAARL 60
RRIERWQATV HAAESVDEKL RILTKMQFMK YMVYPQTFAL NADRWYQVPT KTVFLSGLPP 120
PPAEPEPEPE PEPEPALDLA ALRAVACDCL LQEHFYLRRR RRVHRYEESE VISLPFLDQL 180
VSTLVGLLSP HNPALAAAAL DYRCPVHPYW VRGEEIIPRG HRRGRIDDLR YQIDDKPNNQ 240
IRISKQLAEF VFLDYSVPIE IPTIKCKPDK LPLFKRQYEN HIFVGSKTAD PCCYGHTQFH 300
LLPDKLRRER LLRQNCADQI EVVFRANAIA SLFAWTGAQA MYQQFWSEAD VTRPFVSQAV 360
ITDGKYPSFP CYQLNTLALT TQADQNNPRK NICWGTQSKP LYETIEDNDV KGFNDDVLLQ 420
IVHFLLNRPK EEKSQLLEN

Seq ID NO: 17 DNA sequence
Nucleic Acid Accession #: NM_025059.1
Coding sequence: 3-2150 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
GCATGAGCCT GGACTGCACC AGCCATATCG CGCTGGGTGC CGCTTCGCCA GCGCCCGAGG 60
AAACTTACGA TCATCTTTCG GAAGTCCCGG TCACGCGGGA GCAGTTAAAC CACTATCGGA 120
ATGTGGCTCA AAATGCTCGA AGTGAACTTG CAGCAACTTT GGTCAAATTT GAATGTGCTC 180
AGTCTGAGCT TCAAGACCTC CGATCCAAGA TGCTTTCTAA AGAAGTCTCC TGTCAAGAAC 240
TGAAAGCTGA AATGGAGAGC TACAAGGAAA ACAATGCCAG AAAATCATCT CTCCTTACCT 300
CTTTGAGAGA CAGAGTTCAG GAACTAGAAG AAGAATCAGC AGCACTTTCC ACTTCTAAAA 360
TCAGAACAGA AATCACAGCT CACGCTGCAA TCAAGGAGAA CCAGGAATTA AAGAAGAAAG 420
TTGTAGAGTT AAATGAAAAA TTACAAAAGT GTTCAAAAGA AAATGAGGAG AATAAGAAAC 480
AAGTTTCAAA GAATTGCAGG AAACATGAGG AATTTCTGAC TCAACTGCGT GACTGCTTGG 540
ATCCAGATGA GAGGAATGAC AAGGCATCAG ATGAAGATTT AATTTTAAAG CTTAGAGACC 600
TGCGCAAAGA AAATGAATTC GTGAAAGGAC AAATTGTTAT TCTTGAAGAG ACTATAAATG 660
TCCATGAGAT GGAAGCAAAA GCTAGCAGAG AAACGATCAT GAGGCTGGCT TCAGAAGTCA 720
ACAGAGAGCA GAAAAAAGCT GCCTCCTGTA CTGAAGAGAA AGAGAAGCTG AACCAGGACC 780
TGCTCAGTGC TGTAGAAGCA AAAGAAGCTC TTGAAAGGGA AGTTAAGATC TTCCAAGAAA 840
GGCTGCTTGC TGGCCAGCAG GTCTGGGATG CCTCAAAGCA GGAAGTGAGC CTCCTGAAGA 900
AAAGCTCTTC TGAGTTGGAG AAGAGTTTGA AGGCCAGTCA GGATGCAGTC ACAACCTCAC 960
AAAGCCAGTA CTCCTCATTT AGGGAGAAAA TCGCAGCCCT CCTTAGGGGC AGATTGAGCA 1020
TGACTGGGTC CACTGAGGAC ACCATTTTGG AGAAGATTCG AGAAATGGAC AGCCGGGAAG 1080
AAAGCAGGGA CCGGATGGTC TCCCAGCTTG AAGCCCAAAT ATCTGAGCTT GTTGAACAGT 1140
TGGGAAAGGA GTCTGGGTTT CACCAGAAAG CTCTCCAGAG GGCCCAGAAA GCAGAGAATA 1200
TGTTGGAGAC TCTTCAGGGT CAGCTGACAC ACCTGGAGGC AGAGCTGGTT TCTGGAGGTG 1260
TTTTGCAGA CAACTTGAAT TTTGAGAAAC AAAAATATCT TAAATTTCTG GATCAGCTTT 1320
CTCAGAAAAT GAAGTTGGAC CAGATGGCTG CCGAACTTGG CTTTGACACG CGGCTGGACG 1380
TGGTTTTAGC TCGAACAGAG CAGCTGGTTC GTCTTGAGAG CAATGCAGTC ATTGAGAACA 1440
AGACCATTGC CCACAATTTG CAGAGAAAGC TAAAGACACA GAAAGAGAGA CTGGAGAGCA 1500
AAGAATTACA CATGAGCCTC CTCCGCCAGA AAATAGCCCA GCTGGAGGAG GAGAAGCAGG 1560
CACGCACGGC CTTGGTGGTT GAGAGGGACA ACGCGCATCT TACCATCAGG AACTTGCAGA 1620
AGAAGGTGGA GAGGCTGCAG AAAGAGCTGA ACACGTGTCG AGACTTGCAC ACCGAGCTCA 1680
AAGCCAAACT GGCCGACACC AATGAACTGA AGATTAAAAC TTTGGAACAG ACTAAAGCCA 1740
TTGAAGATCT AAACAAATCC AGAGACCAAC TGGAGAAGAT GAAGGAGAAA GCTGAGAAAA 1800
AGCTCATGTC TGTCAAGTCA GAACTGGATA CCACAGAACA TGAGGCTAAG GAGAATAAAG 1860
AAAGGGCCAG AAACATGATA GAAGTGGTAA CCAGTGAAAT GAAGACACTA AAAAAATCTC 1920
TGGAAGAAGC AGAAAAGAGA GAAAAGCAGC TGGCAGACTT CAGGGAGGTG GTGTCGCAGA 1980
TGCTAGGCTT GAACGTGACC AGCCTTGCTC TTCCTGATTA TGAAATCATC AAGTGTCTTG 2040

AAAGATTGGT CCATTCACAT CAGCATCACT TTGTTACCTG TGCCTGCCTC AAAGATGTGA 2100
CTACTGGGCA AGAGAGGCAC CCACAAGGCC ATTTACAGCT TCTTCATTGA ACACTGTATC 2160
TCTTGAGAGA GGTGGCCATA AGACATGGCA CACAATTCCC AATTTCACAA ATTCCTCATG 2220
TCTTTGAGAT TTGATCAGTT TGTGAATATT TTATGCTTTG ATGATATAGT GAGAATGCAT 2280
CACTTGCAAA AACGATCTCA AAAGTGTCAG CCTTAGATAA ACGTCAGCAT TAAAAAACGC 2340
CAAAAAAAAA AAAAAAAAGC ATTTTAGGAT CCAGAAGAAT TCCACCAGAT TGCATGAGTT 2400
AGATTGGGAA ATGGGAGTGG GAGATAATAT TGGGAGGTAT CTATTTTAAG TCAGGGGCTT 2460
TACTAGCCGA TTTAGTTCTC ACAATAACCA TGTGGAGAAG CTGTGACATT TTTAATTTAC 2520
AACCTTTCTG GGGCTCAGAC ATAAAGTTAC CTATCCAAGG TTGCAGTTGG GTAGTGGTGG 2580
GACCAGGATG GACAACTCAT TGGCCCTGCC TCAAAAGCCA TACCTCTTCT CCTGCTATGC 2640
AGAATCTGTT TCTCCTGAAT CTCTGTGATG CTGGTGGGAA TTGTTTGCAT AGAGGAAGGA 2700
CAATAACCCT GCCATCGTGA GTTAATGTCC GGGCTGGTCA CAGTGGTTCA TGCCTGTAAT 2760
CCCAGCACTT TGGGAGTCCA AGGCAGGCAT ATCATTTGAG GTCAGGAGTT TAAGACCAGC 2820
CTGGCTAACA TAGTGAGACC CTGTTTCTAC TAAAAATACA AAAATAAGCC AGGTGTGGTG 2880
GTGCATGACT GTAATCCCAA CTACTCAGCA GGAGAAGCAC TTGAACCCAG GAGACGGAGG 2940
CGGCAGTGAG CCAAGATTGT GCCACTGCAC TCCAGCCTGG GCGACAGAGT GAAACTACAT 3000
CTCAGAAAAA AAAAAAAAAA AAAAAAAAAA AAGTTAATGT CCAAAAATGA CAGATTTACA 3060
AGTGTAAGCT ATATGATTTC TTCAAAAAGC AAAAQCAATA TACCTAATTC ATTTGGATCA 3120
AACTTACATA GGTCTCAGGT CCTGTAAGAA ACTTGCCTGT TCTAACTGTT GCTACCAGAT 3180
TATATCTGGT GGTAATTGTT AATGTTTCAG CAGGGCTGGT CTCAGTCCTT TAAAATGGAA 3240
AGCTTTATTT GGAGCCCAAC CCTATAAGAT GAAGAAATCC TATATAGTCT TATTCACCAA 3300
TATATCCAAT ACACCCACAG CAATGGTACC TTTTTAAGAT CAGGATTTTA TTATGAATTC 3360
CTGTCACTTT CTGTTTTCCA TTTAAATTTC TATTTTACAA ATTTTTCAGG GAATCATATT 3420
CTTAACTTCA CTGAGAAAAA TGTGTTACTC TTTTGGACAA TTTATCTTAT TTCTATCATA 3480
TAAGATGTAT TTTTTTATTG TCCTTAAAAG AAGCTCTAGC ATGAAATTAA AGGAAAGGGA 3540
AAGAAATAGA TCTGGTGCAC CCGAACATTA GGAGAAAATG AAAAATATAC AACCAACCGT 3600
TCGTGAGTCA TCAAAAAGTC AAAGTCAGCC TGGCCAACAT GGCAAAACTC CGTCTCTGCA 3660
AAAAATACAA AAATGAGCCC GGTATGTTGG CATATGCCTG TAATCCCAGC TACTCGAGAG 3720
GCTGAGACAC GAAAATTGCT TGAACCTGGG AGGCGGAGGT TGCAATGAGC CGAGATCGCG 3780
CTACTGCACT CCAGCCTGGG CAACAGAGAG AGACCTTGTC TCAAAAAACA ACAACAACAA 3840
AAAGTCAAAG TCATAATAAG CAAATTATTG GCTTCTTTCT TCTAGACTAA AAGAAATTAA 3900
AGAGATGAAA CAATCAATTG CAAGGGTCAA AACTAGATTG GATCTTGGTT TGAATGAAAA 3960
AAAGCATAAA ATATTCTTGC AATAATTGTA AAAATTTGAA TGTGGACTAA GTCCTAGATT 4020
ATATTAAAAT ATTTTTAATT TTTTAAGCTT GACAAATGCA CTGATTGTTA TACTTTAAAT 4080
AACTAAAAAT CTGAGAATCC ACAGTGCTAC AGACAATAAA TGATAAAATG GGAAAAAAAA 4140
AAAAAAAAAA A

Seq ID NO: 18 Protein sequence:
Protein Accession #: NP_079335.1

1 11 21 31 41 51
MSLDCTSHIA LGAASPAPEE TYDHLSEVPV TREQLNHYRN VAQNARSELA ATLVKFECAQ 60
SELQDLRSKM LSKEVSCQEL KAEMESYKEN NARKSSLLTS LRDRVQELEE ESAALSTSKI 120
RTEITAHAAI KENQELKKKV VELNEKLQKC SKENEENKKQ VSKNCRKHEE FLTQLRDCLD 180
PDERNDKASD EDLILKLRDL RKENEPVKGQ IVILEETINV HEMEAKASRE TIMRLASEVN 240
REQKKAASCT EEKEKLNQDL LSAVEAKEAL EREVKIFQER LLAGQQVWDA SKQEVSLLKK 300
SSSELERKSLK ASQDAVTTSQ SQVSSPREKI AALLRGRLSM TGSTEDTILE KIREMDSREE 360
SRDRMVSQLE AQISELVEQL GKESGFHQKA LQRAQKAENM LSTLQQQLTH LEAELVSQGV 420
LRDNLNFEKQ KYLKFLDQLS QKMKLDQMAA ELGFDTRLDV VLARTEQLVR LESNAVIENK 480
TIAHNLQRKL KTQKERLESK ELHMSLLRQK IAQLEEEKQA RTALVVERDN AHLTIRNLQK 540
KVERLQKBLN TCRDLHTELK AKLADTNELK IKTLEQTKAI BDLNKSRDQL EKMKEKAEKK 600
LMSVKSELDT TEHEAKENKB RARNMIEVVT SEMKTLKKSL BDAEKRIKQL ADTRIVVSQM 660
LGLNVTSLAL PDYEIIKCLE RLVHSHQHHF VTCACLKDVT TGQERHPQGH LQLLH

Seq ID NO: 19 DNA sequence
Nucleic Acid Accession #: AF071552, NM_000662
Coding sequence: 441-1313 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
CTTTGTATAA GGCTCAGCTA AAAGGGAAAT TGAGTGGGTC AGGTACCACG GATACTATAC 60
ACTCTATTGC ATGATTCTCC TGCCTACATC AGAAGACGTT TATAAGCCTA TTTTAAAGGA 120
TACCAGTTGG AATCTCTCTT TTATTAATCA CCAAGAGAAC CATGAACAAG CTGTTTATCA 180
TTTGACTCAT CATTTAATCT TGATTTCCAG CTTCTCACAC TTGAAAGAAG ACATAATACA 240
TTTCTCACAG GATTCTGGGA CTATTAACTG AACTTATGTG TGTAAAAGGA ATTCATACAA 300
TGAAAGCACT AGAAATAATT ATTATACTTA TAACCATTGT ATTTTTACAT GTTTAAAATA 360
TAGCCATAAT TAGCCTACTC AAATCCAAGT GTAAAAGTAA AATGATTTGC TTTCGTTTTG 420
TTTTCCTTGC TTAGGGGATC ATGGACATTG AAGCATATCT TGAAAGAATT GGCTATAAGA 480
AGTCTAGGAA CAAATTGGAC TTGGAAACAT TAACTGACAT TCTTCAACAC CAGATCCGAG 540
CTGTTCCCTT TGAGAACCTT AACATCCATT GTGGGGATGC CATGGACTTA GGCTTAGAGG 600
CCATTTTTGA TCAAGTTGTG AGAAGAAATC GGGGTGGATG GTGTCTCCAG GTCAATCATC 660
TTCTGTACTG GGCTCTGACC ACTATTGGTT TTGAGACCAC GATGTTGGGA GGGTATGTTT 720
ACAGCACTCC AGCCAAAAAA TACAGCACTG GCATGATTCA CCTTCTCCTG CAGGTGACCA 780

TTGATGGCAG GAACTACATT GTCGATGCTG GGTTTGGACG CTCATACCAG ATGTGGCAGC 840
CTCTGGAGTT AATTTCTGGG AAGGATCAGC CTCAGGTGCC TTGTGTCTTC CGTTTGACGG 900
AAGAGAATGG ATTCTGGTAT CTAGACCAAA TCAGAAGGGA ACAGTACATT CCAAATGAAG 960
AATTTCTTCA TTCTGATCTC CTAGAAGACA GCAAATACCG AAAAATCTAC TCCTTTACTC 1020
TTAAGCCTCG AACAATTGAA GATTTTGAGT CTATGAATAC ATACCTGCAG ACATCTCCAT 1080
CATCTGTGTT TACTAGTAAA TCATTTTGTT CCTTGCAGAC CCCAGATGGG GTTCACTGTT 1140
TGGTGGGCTT CACCCTCACC CATAGGAGAT TCAATTATAA GGACAATACA GATCTAATAG 1200
AGTTCAAGAC TCTGAGTGAG GAAGAAATAG AAAAAGTGCT GAAAAATATA TTTAATATTT 1260
CCTTGCAGAG AAAGCTTGTG CCCAAACATG GTGATAGATT TTTTACTATT TAGAATAAGG 1320
AGTAAAACAA TCTTGTCTAT TTGTCATCCA GCTCACCAGT TATCAACTGA CGACCTATCA 1380
TGTATCTTCT GTACCCTTAC CTTATTTTGA AGAAAATCCT AGACATCAAA TCATTTCACC 1440
TATAAAAATG TCATCATATA TAATTAAACA GCTTTTTAAA GAAACATAAC CACAAACCTT 1500
TTCAAATAAT AATAATAATA ATAATAATAA ATGTATTTTA AAGATGGCCT GTGGTTATCT 1560
TGGAAATTGG TGATTTATGC TAGAAAGCTT TTAATGTTGG TTTATTGTTG AATTC

Seq ID NO: 20 Protein sequence:
Protein Accession #: NP_000653.1

1 11 21 31 41 51
MDIEAYLERI GYKKSRNKLD LETLTDILQH QIRAVPFENL NIHCGDAMDL GLEAIPDQVV 60
RRNRGGWCLQ VNHLLVYWALT TIGFETTMLG GYVVYSTPAKK YSTGMIHLLL QVTIDGRNYI 120
VDAGFGRSYQ MWQPLELISG KDQPQVPCVF RLTEENGFWY LDQIRREQYI PNEEFLHSDI. 180
LEDSKYRKIY SFTLKPRTIE DFESMNTYLQ TSPSSVFTSK SFCSLQTPDG VHCLVGFTLT 240
HRRFNYKINT DLIEFKTLSE EEIEKVLKNI FNISLQRKLV PKHGDRFFTI

Seq ID NO: 21 DNA sequence
Nucleic Acid Accession #: NM_003714
Coding sequence: 123-1031(underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
CGGCACGAGC AAAAAGGAAG AGTGGGAGGA GGAGGGGAAG CGGCGAAGGA GGAAGAGGAG 60
GAGGAGGAAG AGGGGAGCAC AAAGGATCCA GGTCTCCCGA CGGGAGGTTA ATACCAAGAA 120
CCATGTGTGC CGAGCGGCTG GGCCAGTTCA TGACCCTGGC TTTGGTGTTG GCCACCTTTG 180
ACCCGGCGCG GGGGACCGAC GCCACCAACC CACCCGAGGG TCCCCAAGAC AGGAGCTCCC 240
AGCAGAAAGG CCGCCTGTCC CTGCAGAATA CAGCGGAGAT CCAGCACTGT TTGGTCAACG 300
CTGGCGATGT GGGGTGTGGC GTGTTTGAAT GTTTCGAGAA CAACTCTTGT GAGATTCGGG 360
GCTTACATGG GATTTGCATG ACTTTTCTGC ACAACGCTGG AAAATTTGAT GCCCAGGGCA 420
AGTCATTCAT CAAAGACGCC TTGAAATGTA AGGCCCACGC TCTGCGGCAC AGGTTCGGCT 480
GCATAAGCCG GAAGTGCCCG GCCATCAGGG AAATGGTGTC CCAGTTGCAG CGGGAATGCT 540
ACCTCAAGCA CGACCTGTGC GCGGCTGCCC AGGAGAACAC CCGGGTGATA GTGGAGATGA 600
TCCATTTCAA GGACTTGCTG CTGCACGAAC CCTACGTGGA CCTCGTGAAC TTGCTGCTGA 660
CCTGTGGGGA GGAGGTGAAG GAGGCCATCA CCCACAGCGT GCAGGTTCAG TGTGAGCAGA 720
ACTGGGGAAG CCTGTGCTCC ATCTTGAGCT TCTGCACCTC GGCCATCCAG AAGCCTCCCA 780
CGGCGCCCCC CGAGCGCCAG CCCCAGGTGG ACAGAACCAA GCTCTCCAGG GCCCACCAGG 840
GGGAAGCAGG ACATCACCTC CCAGAGCCCA GCAGTAGGGA GACTGGCCGA GGTGCCAAGG 900
GTGAGCGAGG TAGCAAGAGC CACCCAAACG CCCATGCCCG AGGCAGAGTC GGGGGCCTTG 960
GGGCTCAGGG ACCTTCCGGA AGCAGCGAGT GGGAAGACGA ACAGTCTGAG TATTCTGATA 1020
TCCGGAGGTG AAATGAAAGG CCTGGCCACG AAATCTTTCC TCCACGCCGT CCATTTTCTT 1080
ATCTATGGAC ATTCCAAAAC ATTTACCATT AGAGAGGGGG GATGTCACAC GCAGGATTCT 1140
GTGGGGACTG TGGACTTCAT CGAGGTGTGT GTTCCGCGAA CGGACAGGTG AGATGGAGAC 1200
CCCTGGGGCC GTGGGGTCTC AGGGGTGCCT GGTGAATTCT GCACTTACAC GTACTCAAGG 1260
GAGCGCGCCC GCGTTATCCT CGTACCTTTG TCTTCTTTCC ATCTGTGGAG TCAGTGGGTG 1320
TCGGCCGCTC TGTTGTGGGG GAGGTGAACC AGGGAGGGGC AGGGCAAGGC AGGGCCCCCA 1380
GAGCTGGGCC ACACAGTGGG TGCTGGGCCT CGCCCCGAAG CTTCTGGTGC AGCAGCCTCT 1440
GGTGCTGTCT CCGCGGAAGT CAGGGCGGCT GGATTCCAGG ACAGGAGTGA ATGTAAAAAT 1500
AAATATCGCT TAGAATGCAG GAGAAGGGTG GAGAGGAGGC AGGGGCCGAG GGGGTGCTTG 1560
GTGCCAAACT GAAATTCAGT TTCTTGTGTG GGGCCTTGCG GTTCAGAGCT CTTGGCGAGG 1620
GTGGAGGGAG GAGTGTCATT TCTATGTGTA ATTTCTGAGC CATTGTACTG TCTGGGCTGG 1680
GGAGGACACT GTCCAAGGGA GTGGCCCCTA TGAGTTTATA TTTTAACCAC TGCTTCAAAT 1740
CTCGATTTCA CTTTTTTTAT TTATCCAGTT ATATCTACAT ATCTGTCATC TAAATAAATG 1800
GCTTTCAAAC AAAAAAAAAA AAAAAAAAAA AAAAAAA

Seq ID NO: 22 Protein sequence:
Protein Accession #: NP_003705

1 11 21 31 41 51
MCAERLGQPM TLALVLATPD PARGTDATNP PEGPQDRSSQ QKGRLSLQNT AEIQHCLVNA 60
GDVGCQVFEC FENNSCEIRG LHGICMTFLH NAGKFDAQGK SFIKDALKCK AHALRHRFGC 120
ISRKCPAIRB MVSQLQRECV LKHDLCAAAQ ENTRVIVEMI HFKDLLLHEP YVDLVNLLLT 180
CGEEVKEAIT HSVQVQCEQN WGSLCSILSF CTSAIQKPPT APPERQPQVD RTKLSRAHHG 240
BAGHHLPEPS SRETGRGARG ERGSKSHPNA HARGRVGGLG AQGPSGSSEW EDEQSEYSDI 300

RR

Seq ID NO: 23 DNA sequence
Nucleic Acid Accession #: NM_005264.1
Coding sequence: 557-1954(underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
GAATTCCGGC CAGAAGAAAT CTGGCCTCGG AACACGCCAT TCTCCGCGCC GCTTCCAATA 60
ACCACTAACA TCCCTAACGA GCATCCGAGC CGAGGGCTCT GCTCGGAAAT CGTCCTGGCC 120
CAACTCGGCC CTTCGAGCTC TCGAAGATTA CCGCATCTAT TTTTTTTTTC TTTTTTTCT 180
TTTCCTAGCG CAGATAAAGT GAGCCCGGAA AGGGAAGGAG GGGGCGGGGA CACCATTGCC 240
CTGAAAGAAT AAATAAGTAA ATAAACAAAC TGGCTCCTCG CCGCAGCTGG ACGCGGTCGG 300
TTGAGTCCAG GTTGGGTCGG ACCTGAACCC CTAAAAGCGG AACCGCCTCC CGCCCTCGCC 360
ATCCCGGAGC TGAGTCGCCG GCGGCGGTGG CTGCTGCCAG ACCCGGAGTT TCCTCTTTCA 420
CTGGATGGAG CTGAACTTTG GGCGGCCAGA GCAGCACAGC TGTCCGGGGA TCGCTGCACG 480
CTGAGCTCCC TCGGCAAGAC CCAGCGGCGG CTCGGGATTT TTTTGGGGGG GCGGGGAACA 540
GCCCCGCGCC GGCACCATGT TCCTGGCGAC CCTGTACTTC GCGCTGCCGC TCTTGGACTT 600
GCTCCTGTCG GCCGAAGTGA GCGGCGGAGA CCGCCTGGAT TGCGTGAAAG CCAGTGATCA 660
GTGCCTGAAG GAGCAGAGCT GCAGCACCAA GTACCGCACG CTAAGGCAGT GCGTGGCGGG 720
CAAGGAGACC AACTTCAGCC TGGCATCCGG CCTGGAGGCC AAGGATGAGT GCCGCAGCGC 780
CATGGAGGCC CTGAAGCAGA AGTCGCTCTA CAACTGCCGC TGCAAGCGGG GTATGAAGAA 840
GGAGAAGAAC TGCCTGCGCA TTTACTGGAG CATGTACCAG AGCCTGCAGG GAAATGATCT 900
GCTGGAGGAT TCCCCATATG AACCAGTTAA CAGCAGATTG TCAGATATAT TCCGGGTGGT 960
CCCATTCATA TCAGATGTTT TTCAGCAAGT GGAGCACATT CCCAAAGGGA ACAACTGCCT 1020
GGATGCAGCG AAGGCCTGCA ACCTCGACGA CATTTGCAAG AAGTACAGGT CGGCGTACAT 1080
CACCCCGTGC ACCACCAGCG TGTCCAACGA TGTCTGCAAC CGCCGCAAGT GCCACAAGGC 1140
CCTCCGGCAG TTCTTTGACA AGGTCCCGGC CAAGCACAGC TACGGAATGC TCTTCTGCTC 1200
CTGCCGGGAC ATCGCCTGCA CAGAGCGGAG GCGACAGACC ATCGTGCCTG TGTGCTCCTA 1260
TGAAGAGAGG GAGAAGCCCA ACTGTTTGAA TTTGCAGGAC TCCTGCAAGA CGAATTACAT 1320
CTGCAGATCT CGCCTTGCGG ATTTTTTTAC CAACTGCCAG CCAGAGTCAA GGTCTGTCAG 1380
CAGCTGTCTA AAGGAAAACT ACGCTGACTG CCTCCTCGCC TACTCGGGGC TTATTGGCAC 1440
AGTCATGACC CCCAACTACA TAGACTCCAG TAGCCTCAGT GTGGCCCCAT GGTGTGACTG 1500
CAGCAACAGT GGGAACGACC TAGAAGAGTG CTTGAAATTT TTGAATTTCT TCAAGGACAA 1560
TACATGTCTT AAAAATGCAA TTCAAGCCTT TGGCAATGGC TCCGATGTGA CCGTGTGGCA 1620
GCCAGCCTTC CCAGTACAGA CCACCACTGC CACTACCACC ACTGCCCTCC GGGTTAAGAA 1680
CAAGCCCCTG GGGCCAGCAG GGTCTGAGAA TGAAATTCCC ACTCATGTTT TGCCACCGTG 1740
TGCAAATTTA CAGGCACAGA AGCTGAAATC CAATGTGTCG GGCAATACAC ACCTCTGTAT 1800
TTCCAATGGT AATTATGAAA AAGAAGGTCT CGGTGCTTCC AGCCACATAA CCACAAAATC 1860
AATGGCTGCT CCTCCAAGCT GTGGTCTGAG CCCACTGCTG GTCCTGGTGG TAACCGCTCT 1920
GTCCACCCTA TTATCTTTAA CAGAAACATC ATAGCTGCAT TAAAAAAATA CAATATGGAC 1980
ATGTAAAAAG ACAAAAACCA AGTTATCTGT TTCCTGTTCT CTTGTATAGC TGAAATTCCA 2040
GTTTAGGAGC TCAGTTGAGA AACAGTTCCA TTCAACTGGA ACATTTTTTT TTTTCCTTTT 2100
AAGAAAGCTT CTTGTGATCC TTCGGGGCTT CTGTGAAAAA CCTGATGCAG TGCTCCATCC 2160
AAACTCAGAA GGCTTTGGGA TATGCTGTAT TTTAAAGGGA CAGTTTGTAA CTTGGGCTGT 2220
AAAGCAAACT GGGGCTGTGT TTTCGATGAT GATGATCATC ATGATCATGA TGATTTTAAC 2280
AGTTTTACTT CTGGCCTTTC CTAGCTAGAG AAGGAGTTAA TATTTCTAAG GTAACTCCCA 2340
TATCTCCTTT AATGACATTG ATTTCTAATG ATATAAATTT CAGCCTACAT TGATGCCAAG 2400
CTTTTTTGCC ACAAAGAAGA TTCTTACCAA GAGTGGGCTT TGTGGAAACA GCTGGTACTG 2460
ATGTTCACCT TTATATATGT ACTAGCATTT TCCACGCTGA TGTTTATGTA CTGTAAACAG 2520
TTCTGCACTC TTGTACAAAA GAAAAAACCA CCCGGAATTC

Seq ID NO: 24 Protein sequence:
Protein Accession #: NP_005255

1 11 21 31 41 51
MFLATLVFAL PLLDLLLSAE VSGGDRLDCV KASDQCLKEQ SCSTKYRTLR QCVAGKETNF 60
SLASGLEAKD ECRSAMEALK QKSLYNCRCK RGMKKEKNCL RIYWSMYQSL QGNDLLEDSP 120
YEPVNSRLSD IFRVVPFISD VFQQVEHIPK GNNCLDAAKA CNLDDICKKY RSAYITPCTT 180
SVSNDVCNRR KCHKALRQFF DKVPAKHSYG MLFCSCRDIA CTERRRQTIV PVCSYEEREK 240
PNCLNLQDSC KTNYICRSRL ADFFTNCQPE SRSVSSCLKE NYADCLLAYS GLIGTVMTPN 300
YIDSSSLSVA PWCDCSNSGN DLEECLKFLN FFKDNTCLKN AIQAFGNGSD VTVWQPAFPV 360
QTTTATTITA LRVKNKPLGP AGSENRIPTH VLPPCANLQA QKLKSNVSGN THLCISNGNY 420
EKEGLGAASH ITTKSMAAPP SCGLSPLLVL VVTALSTLLS LTETS

Seq ID NO: 25 DNA sequence
Nucleic Acid Accession #: FGENESH predicted
Coding sequence: 1576(entire sequence represents open reading frame)

1 11 21 31 41 51
CTTTTGTTTC GCCATGCCTA GTCTAGTGGT ATCTGGAATA ATGGAAAGAA ATGGGGGCTT 60
TGGAGAACTA GGATGTTTCG GGGGAAGCGC TAAGGACCGA GGGCTGCTGG AAGACGAGCG 120
CGCCCTTCAG CTGGCTCTCG ATCAACTCTG CCTCCTGGGT TTGGGGGAGC CCCCCGCCCC 180

CAGGGCGGGC GAGGACGGGG GAGGTGGGGG GGGCGGCGCC CCCGCCGCAGC CGACAGCCCC 240
CCCGCAGCCG GCGCCGCCGC CGCCGCCCGC GGCGCCCCCG GCCGCCCCGA CGACGCCCCC 300
CGCAGCGCAG ACGCCCCAGC CCCCCACCGC CCCCAAAGGG GCGAGCGACG CCAAGCTCTG 360
CGCTCTCTAC AAAGAGGCCG AGCTGCGCCT GAAGGGCAGC AGCAACACCA CGGAGTGTGT 420
TCCCCGTGCC ACCTCCGAGC ACGTGGCCGA GATCGTGGGC AGGCAAGGCT GCAAGATTAA 480
GGCCTTGAGG GCCAAGACCA ACACCTACAT CAAGACACCG GTGAGGGCG AGGAACCAGT 540
GTTCATGGTG ACAGGGCGAC GGGAGGACGT GGCCACAGCC CGGCGGGAAA TCATCTCAGC 600
AGCGGAGCAC TTCTCCATGA TCCGTGCCTC CGGCAACAAG TCAGGCGCCG CCTTTGGTGT 660
GGCTCCTGCT CTGCCCGGCC AGGTGACCAT CCGTGTGCGG GTGCCCTACC GCGTGGTGGG 720
GCTGGTGGTG GGCCCCAAAG GGGCAACCAT CAAGCGCATC CAGCAGCAAA CCAACACATA 780
CATTATCACA CCAAGCCGTG ACCGCGACCC CGTGTTCGAG ATCACGGGTG CCCCAGGCAA 840
CGTGGAGCGT GCGCGCGAGG AGATCGAGAC GCACATCGCG GTGCGCACTG GCAAGATCCT 900
CGAGTACAAC AATGAAAACG ACTTCCTGGC GGGGAGCCCC GACGCAGCAA TCGATAGCCG 960
CTACTCCGAC GCCTGGCGGG TGCACCAGCC CGGCTGCAAG CCCCTCTCCA CCTTCCGGCA 1020
GAACAGCCTG GGCTGCATCG GCGAGTGCGG AGTGGACTCT GGCTTTGAGG CCCCACGCCT 1080
GGGTGAGCAG GGCNGGGACT TTGGCTACGG CGGGTACCTC TTTCCGGGCT ATGGCGTGGG 1140
CAAGCAGGAT GTGTACTACG GCGTGGCCGA GACTACGCCC CCGCTGTGGG CGGGCCAGGA 1200
GAACGCCACG CCCACCTCCG TGCTCTTCTC CTCTGCCTCC TCCTCCTCCT CCTCTTCCGC 1260
CAAGGCCCGC GCTGGGCCCC CGGGCGCACA CCGCTCCCCT GCCACTTCCG CGGGACCCGA 1320
GCTGGCCGGA CTCCCGAGGC GCCCCCCGGG AGAGCCGCTC CAGGGCTTCT CTAAACTTGG 1380
TGGGGGCGGC CTGCGGAGCC CCGCCGGCGG GCGGGATTGC ATGGTCTGCT TTGAGAGCOA 1440
AGTGACTGCC GCCCTTGTGC CCTGCGACA CAACCTGTTC TGCATGGAGT GTGCAGTACG 1500
CATCTGCGAG AGGACGGACC CAGAGTGTCC CGTCTGCCAC ATCACAGCCA CGCAAGCCAT 1560
CCGAATATTC TCCTAA

Seq ID NO: 26 Protein sequence:
Protein Accession #: FGENESH predicted

1 11 21 31 41 51
| | | | | |
FCFAMPSLVV SGIMERNGGF GELGCFGGSA KDRGLLEDER ALQLALDQLC LLGLGEPPAP 60
RAGEDGGGGG GGAPAQPTAP PQPAPPPPPA APPAAPTTAP AAQTPQPPTA PKGASDAKLC 120
ALYKEAELRL KGSSNTTECV PVPTSEHVAE IVGRQGCKIK ALRAKTNTYI KTPVRGEEPV 180
FMVTGRREDV ATARREIISA AEHPSMIRAS RNKSGAAFGV APALPGQVTI RVRVPYRVVG 240
LVVGPKGATI KRIQQQTNTY IITPSRDRDP VFEITGAPGN VERAREEIBT HIAVRTGKIL 300
EYNNENDFLA GSPDAAIDSR YSDAWRVHQP GCKPLSTFRQ NSLGCIGECG VDSGFEAPRL 360
GEQGGDFGYG GYLFPGYGVG KQDVYYGVAE TSPPLWAGQE NATPTSVLFS SASSSSSSSA 420
KARAGPPGAH RSPATSAGPE LAGLPRRPPG EPLQGFSKLG GGGLRSPGGG RDCMVCFESE 480
VTAALVPCGH NLFCMECAVR ICERTDPECP VCHITATQAI RIPS

Seq ID NO: 27 DNA sequence
Nucleic Acid Accession #: FGENESH predicted
Coding sequence: 1-2070 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
| | | | | |
ATGAGCGGTG CGGGGGTGGC GGCTGGGACG CGGCCCCCCA GCTCGCCUAC CCCGGGCTCT 60
CGGCGCCGGC GCCAGCGCCC CTCTGTGGGC GTCCAGTCCT TGAGGCCGCA GAGCCCGCAG 120
CTCAGGCAGA GCGACCCGCA GAAACGGAAC CTGGACCTGG AGAAAAGCCT GCAGTTCCTG 180
CAGCAGCAGC ACTCGGAGAT GCTGGCCAAG CTCCATGAGG AGATCGAGCA TCTGAAGCGG 240
GAAAACAAGG GTGAGCCGGC GCGGGGCCCT AGGCCGGCCC TGCCTCCCCA GGCACACTCA 300
ACACTGCCGC TCCCGCAGCA CAGAAACACA GCCATCAACT CCAGCACACG CCTGGGCTCA 360
GGGGGAACAC AGGACGGGGA GCCCCTCCAG ACTGTCCTTG CCCACCTGGC TGCACTGGCC 420
CCTGTATGCC AACCCAGTGG GTACAGGTTC TGGGGGACCT GGACAGATGC CGCTACCTCT 480
AGCCGTGGCT GGACGATGTT ATGCAGCCAA GCACAGCACG TGCTGCTCTC GGGAAGCCCA 540
GGGCCTGAGG TCATTGCAGG GCGGCAGGTG GCCACAGGGT GCTCCCCAGA CCTCCCTCCT 600
CCAAGTAGAG CTGAAATGGG AAGGAACCCC TGGGACAGCC CCTGCCCTGC TAGATCTTTG 660
CCTCAGATTG CTGCTGTGGC CAGGCCCAGG ATTTCCAGCC CTATGGCTCT GAGTCCTCAC 720
ATGCTGGGGG CCCAGGGGAT ATGGACACAC TCCATCCAGG GATCCCTTCC TGCCATCTGG 780
GCAGCAACCA TGGGGACAAA GGGAGGAAGC AGAGTCCTGT TTCCTTGCCA CTTGTCCAAG 840
GCACTTCCCC ATCCTGACAG CGGCCCCCAC CCAGCCCAGG ATCCTGGGCT GTGGTCTCAA 900
GCTCACTTCC CATTATCTTT GGGGCTGGGG CTGACATCAG GAGGACATCT GACTGGTGGA 960
TGGAGCCAGC CTGGGAACAT CGCAGCTGGG GCAGTGCCTA GGGCTCTCCC TTCCCAGGGA 1020
GACATGGAGA AGGGGGTTGA GGGAGGGCCC TTCCCTAGCC GCTGTGGCAA CTCCAGTGAG 1080
CTGTTCTGGG CAAAGTGTGG CCCAAGTGGG CAGCCCCAGC CCTGCAGTGC TGGGGACGCT 1140
GACAGGACAC GGGAAGAGGC CATGCTTTCC CTCGGGACCT GCTGTTCCAT GTGTCCCAAG 1200
CCCTCCTGCT TTCCAGATGG CCCCTCAGGA AACCACCTTT CCAGGGCCTC TGCTCCCTTG 1260
GGCGCTCGCT GGGTCTGCAT CAACGGAGTG TGGGTAGAGC CGGGAGGACC CAGCCCTGCC 1320
AGGCTGAAGG AGGGCTCCTC ACGGACACAC AGGCCAGGAG GCAAGCGTGG GCGTCTTGCG 1380
GGCGGTAGCG CCGACACTGT GCGCTCTCCT GCAGACAGCC TCTCCATGTC AAGCTTCCAG 1440
TCTGTCAAGT CCATCTCTAA TTCAGCCAAC TCTCAAGGCA AGGCCAGGCC CCAGCCCGGC 1500
TCCTTCAACA AGCAAGATTC AAAAGCTGAC GTCTCCCAGA AGGCGGACCT GGAAGAGGAG 1560
CCCCTACTTC ACAACAGCAA GCTGGACAAA GTTCCTGGGG TACAAGGGCA GGCCAGAAAG 1620
GAGAAAGCAG AGGCCTCTAA TGCAGGAGCT GCCTGTATGG GGAACAGCCA GCACCAGGGC 1680
AGGCAGATGG GGGCGGGGGC ACACCCCCCA ATGATCCTGC CCCTTCCCCT GCGAAAGCCC 1740
ACCACACTTA GGCAGTGCOA AGTGCTCATC CGCGAGCTGT GGAATACCAA CCTCCTGCAG 1800

ACCCAAGAGC TGCGGCACCT CAAGTCCCTC CTGGAAGGGA GCCAGAGGCC CCAGGCAGCC 1860
CCGGAGGAAG CTAGCTTTCC CAGGGACCAA GAAGCCACGC ATTTCCCCAA GGTCTCCACC 1920
AAGAGCCTCT CCAAGAAATG CCTGAGCCCA CCTGTGGCGG AGCGTGCCAT CCTGCCCGCA 1980
CTGAAGCAGA CCCCGAAGAA CAACTTTGCC GAGAGGCAGA AGAGGCTGCA GGCAATGCAG 2040
AAACGGCGCC TGCATCGCTC AGTGCTTTGA

Seq ID NO: 28 Protein sequence:
Protein Accession #: FGENESH predicted

1 11 21 31 41 51
| | | | | |
MSQAGVAAGT RPPSSPTPQS RRRRQRPSVG VQSLRPQSPQ LRQSDPQKRN LDLEKSLQFL 60
QQQHSEMLAK LHEEIEHLKR ENKGEPARGP RPALPPQAHS TLPLPQHRNT AINSSTRLGS 120
GGTQDGEPLQ TVLAHLAALA PVCQPSGYRF WGTWTDAATS SRGWTMLCSQ AQIVLLSGSP 180
GPEVIAGRQV ATGCSPDLPP PSRAEMGRNP WDSPCPARSL PQIAAVARPR ISSPMALSPH 240
MLGAQGIWTH SIQGSLPAIW AATMGTKGGS RVLFPCHLSK ALPHPDSGPH PAQDPGLWSQ 300
AIFPLSLGLG LTSGGHLTGG WSQPQNIAAG AVPRALPSQG DMEKGVEGGP FPSRCGNSSB 360
LFWAKCGPSR QPQPCSAGDA DRTREAAMLS LGTCCSMCPK PSCPPDGPSG NHLSRASAPL 420
GARWVCINGV WVEPGGPSPA RLKEGSSRTH RPGGKRGRLA GGSADTVRSP ADSLSMSSFQ 480
SVKSISNSAN SQGKARPQPG SFNKQDSKAD VSQKADLEEE PLLHNSKLDK VPQVQGQARK 540
EKAEASNAGA ACMGNSQHQG RQMGAGAHPP MILPLPLRKP TTLRQCEVLI RELWNTNLLQ 600
TQELRHLKSL LEGSQRPQAA PEEASFPRDQ EATHFPKV8T K8LSKKCLSP PVAERAILPA 660
LKQTPKNNFA ERQKRLQAMQ KRRLHRSVL

Seq ID NO: 29 DNA sequence
Nucleic Acid Accession #: NM_012319.2
Coding sequence: 138-2405 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
| | | | | |
CTCGTGCCGA ATTCGGCACG AGACCGCGTG TTCGCGCCTG GTAGAGATTT CTCGAAGACA 60
CCAGTGGGGC CGTGTGGAAC CAAACCTGCG CGCGTGGCCG GGCCGTGGGA CAACGAGGCC 120
GCGGAGACGA AGGCGCAATG GCGAGGAAGT TATCTGTAAT CTTGATCCTG ACCTTTGCCC 180
TCTCTGTCAC AAATCCCCTT CATGAACTAA AAGCAGCTGC TTTCCCCCAG ACCACTGAGA 240
AAATTAGTCC GAATTGGGAA TCTGGCATTA ATGTTGACTT GGCAATTTCC ACACGGCAAT 300
ATCATCTACA ACAGCTTTTC TACCGCTATG GAGAAAATAA TTCTTTGTCA GTTGAAGGGT 360
TCAGAAAATT ACTTCAAAAT ATAGGCATAG ATAAGATTAA AAGAATCCAT ATACACCATG 420
ACCACGACCA TCACTCAGAC CACGAGCATC ACTCAGACCA TGAGCGTCAC TCAGACCATG 480
AGCATCACTC AGACCACGAG CATCACTCTG ACCATGATCA TCACTCTCAC CATAATCATG 540
CTGCTTCTGG TAAAAATAAG CGAAAAGCTC TTTGCCCAGA CCATGACTCA GATAGTTCAG 600
GTAAAGATCC TAGAAACAGC CAGGGGAAAG GAGCTCACCG ACCAGAACAT GCCAGTGGTA 660
GAAGGAATGT CAAGGACAGT GTTAGTGCTA GTGAAGTGAC CTCAACTGTG TACAACACTG 720
TCTCTGAAGG AACTCACTTT CTAGAGACAA TAGAGACTCC AAGACCTGGA AAACTCTTCC 780
CCAAAGATGT AAGCAGCTCC ACTCCACCCA GTGTCACATC AAAGAGCCGG GTGAGCCGGC 840
TGGCTGGTAG GAAAACAAAT GAATCTGTGA GTGAGCCCCG AAAAGGCTTT ATGTATTCCA 900
GAAACACAAA TGAAAATCCT CAGGAGTGTT TCAATGCATC AAAGCTACTG ACATCTCATG 960
GCATGGGCAT CCAGGTTCCG CTGAATGCAA CAGAGTTCAA CTATCTCTGT CCAGCCATCA 1020
TCAACCAAAT TGATGCTAGA TCTTGTCTGA TTCATACAAG TGAAAAGAAG GCTGAAATCC 1080
CTCCAAAGAC CTATTCATTA CAAATAGCCT GGGTTGGTGG TTTTATAGCC ATTTCCATCA 1140
TCAGTTTCCT GTCTCTGCTG GGGGTTATCT TAGTGCCTCT CATGAATCGG GTGTTTTTCA 1200
AATTTCTCCT GAGTTTCCTT GTGGCACTGG CCGTTGGGAC TTTGAGTGGT GATGCTTTTT 1260
TACACCTTCT TCCACATTCT CATGCAAGTC ACCACCATAG TCATAGCCAT GAAGAACCAG 1320
CAATGGAAAT GAAAAGAGGA CCACTTTTCA GTCATCTGTC TTCTCAAAAC ATAGAAGAAA 1380
GTGCCTATTT TGATTCCACG TGGAAGGGTC TAACAGCTCT AGGAGGCCTG TATTTCATGT 1440
TTCTTGTTGA ACATGTCCTC ACATTGATCA AACAATTTAA AGATAAGAAG AAAAAGAATC 1500
AGAAGAAACC TGAAAATGAT GATGATGTGG AGATTAAGAA GCAGTTGTCC AAGTATGAAT 1560
CTCAACTTTC AACAAATGAG GAGAAAGTAG ATACAGATGA TCGAACTGAA GGCTATTTAC 1620
GAGCAGACTC ACAAGAGCCC TCCCACTTTG ATTCTCAGCA GCCTGCAGTC TTGGAAGAAG 1680
AAGAGGTCAT GATAGCTCAT GCTCATCCAC AGGAAGTCTA CAATGAATAT GTACCCAGAG 1740
GGTGCAAGAA TAAATGCCAT TCACATTTCC ACGATACACT CGGCCAGTCA GACGATCTCA 1800
TTCACCACCA TCATGACTAC CATCATATTC TCCATCATCA CCACCACCAA AACCACCATC 1860
CTCACAGTCA CAGCCAGCGC TACTCTCGGG AGGAGCTGAA AGATCCCGGC GTCGCCACTT 1920
TGGCCTGGAT GGTGATAATG GGTGATGGCC TGCACAATTT CAGCGATGGC CTAGCAATTG 1980
GTGCTGCTTT TACTGAAGGC TTATCAAGTG GTTTAAGTAC TTCTGTTGCT GTGTTCTGTC 2040
ATGAGTTGCC TCATGAATTA GGTGACTTTG CTGTTCTACT AAAGGCTGGC ATGACCGTTA 2100
AGCAGGCTGT CCTTTATAAT GCATTGTCAG CCATGCTGGC GTATCTTGGA ATGGCAACAG 2160
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GCTTATTCAT GTATGTTGCT CTGGTTGATA TGGTACCTGA AATGCTGCAC AATGATGCTA 2280
GTGACCATGG ATGTAGCCGC TGGGGGTATT TCTTTTTACA GAATGCTGGG ATGCTTTTGG 2340
GTTTTGGAAT TATGTTACTT ATTTCCATAT TTGAACATAA AATCGTGTTT CGTATAAATT 2400
TCTAGTTTAG GTTTAAATGC TAGAGTAGCT TAAAAAGTTG TCATAGTTTC AGTAGGTCAT 2460
AGGGAGATGA GTTTGTATGC TGTACTATGC AGCGTTTAAA GTTAGTGGGT TTTGTGATTT 2520
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TATTCTATCT TGGAGATAAA ATCTGTATGT GCAATTCACC GGTATTACCA GTTTATTATG 2640
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TTTTCAAGAA CTAACACAGT TATTCCTATA CTGGATTTTA GGTCTCTGAA GAACTGCTGG 2760
TGTTTAGGAA TAAGAATGTG CATGAAGCCT AAAATACCAA GAAAGCTTAT ACTGAATTTA 2820
AGCAAAGAAA TAAAGGAGAA AAGAGAAGAA TCTGAGAATT GGGGAGGCAT AGATTCTTAT 2880
AAAAATCACA AAATTTGTTG TAAATTAGAG GGGAGAAATT TAGAATTAAG TATAAAAAGG 2940
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GTAGTTGAGCA CTCTCATATA CTAATTAGTG TACATTTAAC TTTGTATAAT ACAGAAATCT 3060
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TTCGTGCGGG TTATATACCA GATGAGTACA GTGAGTAGTT TATGTATCAC CAGACTGGGT 3180
TATTGCCAAG TTATATATCA CCAAAAGCTG TATGACTGGA TGTTCTGGTT ACCTGGTTTA 3240
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Seq ID NO: 30 Protein sequence:
Protein Accession #: NP_036451.2

1 11 21 31 41 51
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FYRYGENNSL SVSGFRKLLQ NIGIDKIKRI HHHDHDHHS DHEHHSDHER HSDHEHHSDH 120
EHHSDHDHHS HHNHAASGKN KRKALCPDHD SDSSGKDPRN SQQKGAHRPE HASGRRNVKD 180
SVSASEVTST VYNTVSEGTH FLETIETPRP GKLFPKDVSS STPPSVTSKS RVSRLAGRKT 240
NESVSEPRKG FMYSRNTNEN PQECFNASKL LTSHGMGIQV PLNATEPNYL CPAIINQIDA 300
RSCLIHTSEK KAEIPPKTYS LQIAWVGGFI AISIISFLSL LGVILVPLMN RVFFKFLLSF 360
LVALAVGTLS GDAFLHLLPH SHASHHHSHS HEEPAMEMKR GPLFSHLSSQ NIEESAYFDS 420
TWKGLTALGG LYFMFLVEHV LTLIKQFKDK KKKNQKKPEN DDDVEIKKQL SKYESQLSTN 480
EEKVDTDDRT EGYLRADSQE PSHFDSQQPA VLEEEEVMIA HAHPQEVYNE YVPRGCKNKC 540
IISHFHDTLGQ SDDLIHHHHD YHHILHHHHH QNIHPHSHSQ RYSREELKDA GVATLAWMVI 600
MGDGLHNFSD GLAIGAAFTE GLSSGLSTSV AVFCHELPHE LGDFAVLLKA GMTVKQALLY 660
NALSAMLAYL GMATGIFIGH YAENVSMWIF ALTAGLFMYV ALVDMVPEML HNDASDHGCS 720
RWGYFFLQNA GMLLGFGIML LISIFEHKIV FRINF

Seq ID NO: 31 DNA sequence
Nucleic Acid Accession #: NM_002184.1
Coding sequence: 256-3012(underlined sequences correspond to start and stop codons)

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AGACGCGGAG GGTCGAGGCG GCGCTGCCTG AGTGAAACGC AATGGAAAAA GCATGACATT 180
TAGAAGTAGA AGACTTAGCT TCAAATCCCT ACTCCTTCAC TTACTAATTT TGTGATTTGG 240
AAATATCCGC GCAAGATGTT GACGTTGCAG ACTTGGGTAG TGCAAGCCTT GTTTATTTTC 300
CTCACCACTG AATCTACAGG TGAACTTCTA GATCCATGTG GTTATATCAG TCCTGAATCT 360
CCAGTTGTAC AACTTCATTC TAATTTCACT GCAGTTTGTG TGCTAAAGGA AAAATGTATG 420
GATTATTTTC ATGTAAATGC TAATTACATT GTCTGGAAAA CAAACCATTT TACTATTCCT 480
AAGGAGCAAT ATACTATCAT AAACAGAACA GCATCCAGTG TCACCTTTAC AGATATAGCT 540
TCATTAAATA TTCAGCTCAC TTGCAACATT CTTACATTCG GACAGCTTGA ACAGAATGTT 600
TATGGAATCA CAATAATTTC AGGCTTGCCT CCAGAAAAAC CTAAAAATTT GAGTTGCATT 660
GTGAACGAGG GGAAGAAAAT GAGGTGTGAG TGGGATGGTG GAAGGGAAAC ACACTTGGAG 720
ACAAACTTCA CTTTAAAATC TGAATGGGCA ACACACAAGT TTGCTGATTG CAAAGCAAAA 780
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GTCTGGGTAG AAGCAGAGAA TGCCCTTGGG AAGGTTACAT CAGATCATAT CAATTTTGAT 900
CCTGTATATA AAGTGAAGCC CAATCCGCCA CATAATTTAT CAGTGATCAA CTCAGAGGAA 960
CTGTCTAGTA TCTTAAAATT GACATGGACC AACCCAAGTA TTAAGAGTGT TATAATACTA 1020
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GACACAGCAT CCACCCGATC TTCATTCACT GTCCAAGACC TTAAACCTTT TACAGAATAT 1140
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GAAGCAAGTG GGATCACCTA TGAAGATAGA CCATCTAAAG CACCAAGTTT CTGGTATAAA 1260
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TATCTAGCAA CCCTAACAGT AAGAAATCTT GTTGGCAAAT CAGATGCAGC TGTTTTAACT 1500
ATCCCTGCCT GTGACTTTCA AGCTACTCAC CCTGTAATGG ATCTTAAAGC ATTCCCCAAA 1560
GATAACATGC TTTGGGTGGA ATGGACTACT CCAAGGGAAT CTGTAAAGAA ATATATACTT 1620
GAGTGGTGTG TGTTATCAGA TAAAGCACCC TGTATCACAG ACTGGCAACA AGAAGATGGT 1680
ACCGTGCATC GCACCTATTT AAGAGGGAAC TTAGCAGAGA GCAAATGCTA TTGATAACA 1740
GTTACTCCAG TATATGCTGA TGGACCAGGA AGCCCTGAAT CCATAAAGGC ATACCTTAAA 1800
CAAGCTCCAC CTTCCAAAGG ACCTACTGTT CGGACAAAAA AAGTAGGGAA AAACGAAGCT 1860
GTCTTAGAGT GGGACCAACT TCCTGTTGAT GTTCAGAATG GATTTATCAG AAATTATACT 1920
ATATTTTATA GAACCATCAT TGGAAATGAA ACTGCTGTGA ATGTGGATTC TTCCCACACA 1980
GAATATACAT TGTCCTCTTT GACTAGTGAC ACATTGTACA TGGTACGAAT GGCAGCATAC 2040
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GGAGTGCTGT TCTGCTTTAA TAAGCGAGAC CTAATTAAAA AACACATCTG GCCTAATGTT 2220
CCAGATCCTT CAAAGAGTCA TATTCCCCAG TGGTCACCTC ACACTCCTCC AAGGCACAAT 2280

TTTAATTCAA AAGATCAAAT GTATTCAGAT GGCAATTTCA CTGATGTAAG TGTTGTGGAA 2340
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AAGGAAAAAA TTAATACTGA AGGACACAGC AGTGGTATTG GGGGTCTTC ATGCATGTCA 2460
TCTTCTAGGC CAAGCATTTC TAGCAGTGAT GAAAATGAAT CTTCACAAAA CACTTCGAGC 2520
ACTGTCCAGT ATTCTACCGT GGTACACAGT GGCTACAGAC ACCAAGTTCC GTCAGTCCAA 2580
GTCTTCTCAA GATCCGAGTC TACCCAGCCC TTGTTAGATT CAGAGGAGCG GCCAGAAGAT 2640
CTACAATTAG TAGATCATGT AGATGGCGGT GATGGTATTT TGCCCAGGCA ACAGTACTTC 2700
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CAAGTTTCAT CAGTCAATGA GGAAGATTTT GTTAGACTTA AACAGCAGAT TTCAGATCAT 2820
ATTTCACAAT CCTGTGGATC TGGGCAAATG AAAATGTTTC AGGAAGTTTC TGCAGCAGAT 2880
GCTTTTGGTC CAGGTACTGA GGGACAAGTA GAAAGATTTG AAACAGTTGG CATGGAGGCT 2940
GCGACTGATG AAGGCATGCC TAAAAGTTAC TTACCACAGA CTGTACGGCA AGGCGGCTAC 3000
ATGCCTCAGT GAAGGACTAG TAGTTCCTGC TACAACTTCA GCAGTACCTA TAAAGTAAAG 3060
CTAAAATGAT TTTATCTGTG AATTC

Seq ID NO: 32 Protein sequence:
Protein Accession #: NP_002175.1

1 11 21 31 41 51
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MLTLQTWVVQ ALFIFLTTES TGELLDPCGY ISPESPVVQL HSNFTAVCVL KEKCMDYFHV 60
NANYIVWKTN HFTIPKEQYT IINRTASSVT PTDIASLNIQ LTCNILTPGQ LEQNVYGITI 120
ISGLPPEKPK NLSCIVNEGK KMRCEWDGGR ETHLETNFTL KSEWATHKFA DCKAKRDTPT 180
SCTVDYSTVY FVNIEVWVEA ENALGKVTSD HINFDPVYKV KPNPPHNLSV INSEELSSIL 240
KLTWTNPSIK SVIILKYMIQ YRTKDASTWS QIPPEDTAST RSSFTVQDLK PFTEYVFRIR 300
CMKEDGKGYW SDWSEEASGI TYEDRPSKAP SFWYKIDPSH TQGYRTVQLV WKTLPPFRAN 360
GKILDYEVTL TRWKSHLQNY TVNATKLTVN LTNDRYLATL TVRNLVGKSD AAVLTIPACD 420
FQATHPVMDL KAPPKDNMLW VEWTTPRESV KKYILEWCVL SDKAPCITDW QQEDGTVHRT 480
YLRGNLAESK CYLITVTPVY ADGPGSPESI KAYLKQAPPS KGPTVRTKKV GKNEAVLEWD 540
QLPVDVQNGF IRNYTIFYRT IIGNETAVNV DSSHTEYTLS SLTSDTLYMV RMAAYTDEGG 600
KDGPEPTFTT PKFAQGEIEA IVVPVCLAFL LTTLLGVLFC FNKRDLIKKH IWPNVPDPSK 660
SHIAQWSPHT PPRHNFNSKD QMYSDGNFTD VSVVEIEAND KKPFPEDLKS LDLFKKEKIN 720
TEGHSSGIGG SSCMSSSRPS ISSSDENESS QNTSSTVQYS TVVHSGYRHQ VPSVQVFSRS 780
ESTQPLLDSE ERPEDLQLVD HVDGGDGILP RQQYFKQNCS QHESSPDISH FERSKQVSSV 840
NEEDFVRLKQ QISDHISQSC GSGQMKMFQE VSAADAFGPG TEGQVERFET VGMEAATDEG 900
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Seq ID NO: 33 DNA sequence
Nucleic Acid Accession #: NM_018255.1
Coding sequence: 11-2491 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
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CTGCTCCGTG GTGCTCTATG ACCCCCTGAA AAGGGTTGTT GTTACCAACT TGAATGGTCA 180
CACCGCCCGA GTCAATTGCA TACAGTGGAT TTGTAAACAG GATGGCTCCC CTTCTACTGA 240
ATTAGTTTCT GGAGGATCTG ATAATCAAGT GATTCACTGG GAAATAGAGG ATAATCAGCT 300
TTTAAAAGCA GTGCATCTTC AAGGCCATGA AGGACCTGTT TATGCGGTGC ATGCTGTTTA 360
CCAGAGGAGG ACATCAGATC CTGCATTATG TACACTGATC GTTTCTGCAG CTGCAGATTC 420
TGCTGTTCGA CTCTGGTCTA AAAAGGGTCC AGAAGTAATG TGCCTTCAGA CTTTAAACTT 480
TGGAAATGGA TTTGCTTTGG CTCTCTGCTT ATCTTTTTTG CCAAATACTG ATGTACCAAT 540
ATTAGCATGT GGCAATGATG ATTGCAGAAT TCACATATTT GCTCAACAAA ATGATCAGTT 600
TCAGAAAGTG CTTTCTCTCT GTGGACATGA GGATTGGATT AGAGGAGTGG AATGGGCAGC 660
CTTTGGTAGA GATCTTTTCC TAGCAAGCTG TTCACAAGAT TGCCTGATAA GAATATGGAA 720
GCTGTATATA AAGTCAACAT CTTTAGAAAC TCAGGATGAC GATAACATAA GACTGAAAGA 780
AAATACTTTT ACCATAGAAA ATGAAAGTGT TAAAATAGCA TTTGCTGTTA CTCTGGAGAC 840
AGTGCTAGCC GGTCATGAAA ACTGGGTAAA TGCAGTTCAC TGGCAACCTG TGTTTTACAA 900
AGATGGTGTC CTACAGCAGC CAGTGAGATT ATTATCTGCT TCCATGGATA AAACCATGAT 960
TCTCTGGGCT CCAGATGAAG AGTCAGGAGT TTGGCTAGAA CAGGTTCGAG TAGGTGAAGT 1020
AGGTGGGAAT ACTTTGGGAT TTTATGATTG CCAGTTCAAT GAAGATGGCT CCATGATCAT 1080
TGCTCATGCT TTCCACGGAG CGTTGCACCT TTGGAAACAG AATACAGTTA ACCCAAGAGA 1140
GTGGACTCCA GAGATTGTCA TTTCAGGACA CTTTGATGGT GTCCAAGACC TAGTCTGGGA 1200
TCCAGAAGGA GAATTTATTA TCACTGTTGG TACTGATCAG ACAACTAGAC TTTTTGCTCC 1260
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TGAAAAAGTT CTTCGGGTTT TTTCTGCACC TCGGAATTTT GTGGAAAATT TTTGTGCCAT 1440
TACAGGACAA TCACTGAATC ATGTGCTCTG TAATCAAGAT AGTGATCTTC CAGAAGGAGC 1500
CACTGTCCCT GCATTGGGAT TATCAAATAA AGCTGTCTTT CAGGGAGATA TAGCTTCTCA 1560
GCCTTCTGAT GAAGAGGAGC TGTTAACTAG TACTGGTTTT GAGTATCAGC AGGTGGCCTT 1620
TCAGCCCTCC ATACTTACTG AGCCTCCCAC TGAGGATCAT CTTCTGCAGA ATACTTTGTG 1680
GCCTGAAGTT CAAAAACTAT ATGGGCACGG TTATGAAATA TTTTGTGTTA CTTGTAACAG 1740
TTCAAAGACT CTGCTTGCCT CAGCTTGTAA GGCAGCTAAG AAAGAGCATG CAGCTATCAT 1800
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CACGCAGATG GCCTTCTCAC CTAATGAGAA GTTCTTACTA GCTGTTTCCA GAGATCGAAC 1920
CTGGTCATTG TGGAAAAAGC AGGATACAAT CTCACCTGAG TTCGAGCCAG TTTTTAGTCT 1980
TTTTGCCTTC ACCAACAAAA TTACTTCTGT GCACAGTAGA ATTATTTGGT CTTGTGATTG 2040

GAGTCCTGAC AGCAAGTATT TCTTCACTGG GAGTCGAGAC AAAAAGGTGG TTGTCTGGGG 2100
TGAGTGCGAC TCCACTGATG ACTGTATTGA GCACAACATT GGCCCCTGCT CCTCAGTCCT 2160
GGACGTGGGT GGGGCTGTGA CAGCTGTCAG CGTCTGCCCA GTGCTCCACC CTTCTCAACG 2220
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GATACACAGA GTCAATAAAT GTGCACTGTA AATGG

Seq ID NO: 34 Protein sequence:
Protein Accession #: NP_060725.1

1 11 21 31 41 51

MVAPVLETSH VFCCPNRVRG VLNWSSGPRG LLAFGTSCSV VLYDPLKRVV VTNLNGHTAR 60
VNCIQWICKQ DGSPSTELVS GGSDNQVIHW EIEDNQLLKA VHLQGHEGPV YAVHAVYQRR 120
TSDPALCTLI VSAAADSAVR LWSKKQPEVM CLQTLNFGNG FALALCLSFL PNTDVPILAC 180
GNDDCRIHIF AQQNDQFQKV LSLCGHEDWI RGVEWAAFGR DLPLASCSQD CLIRIWKLYI 240
KSTSLETQDD DNIRLKENTF TIENESVKIA PAVTLETVLA GHENWVNAVH WQPVFVKDQV 300
LQQPVRILSA SMDKTMILWA PDEESGVWLE QVRVGEVGGN TLGFYDCQFN EDGSMIIAHA 360
FHGALHLWKQ NTVNPREWTP EIVISGHFDG VQDLVWDPEG EFIITVGTDQ TTRLFAPWKR 420
KDQSQVTWHE IARPQIIIGYD LKCLAMINRP QFVSGADEKV LRVFSAPRNF VENFCAITGQ 480
SLNHVLCNQD SDLPEGATVP ALGLSNKAVF QGDIASQPSD EEELLTSTGF BYQQVAFQPS 540
ILTEPPTEDH LLQNTLWPBV QKLYGHGYEI FCVTCNSSKT LLASACKAAK KEHAAIILWN 600
TTSWKQVQNL VFHSLTVTQM APSPNEKFLL AVSRDRTWSL WKKQDTISPE FEPVFSLFAF 660
TNKITSVHSR IIWSCDWSPD SKYFFTGSRD KKVVVWGECD STDDCIEHNI GPCSSVLDVG 720
GAVTAVSVCP VLHPSQRYVV AVGLECGKIC LYTWKKTDQV PEINDWTHCV BTSQSQSHTL 780
AIRKLCWKNC SOKTEQKBAB GAEWLHPASC GEDHTVKIIR VNKCAL

Seq ID NO: 35 DNA sequence
Nucleic Acid Accession #: NM_022131
Coding sequence: 11-2878 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51

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AGGGGAAATC TGTGCGTTCA AGATCCATGG CCAGGAGCTG CCCTTTGAGG CTGTGGTGCT 300
CAACAAGACA TCAGGAGAGG GCCGGCTCCG TGCCAAGAGC CCCATTGACT GTGAGTTGCA 360
GAAGGAGTAC ACATTCATCA TCCAGGCCTA TGACTGTGGT GCTGGGCCCC ACGAGACAGC 420
CTGGAAAAAG TCACACAAGG CCGTGGTCCA TATACAGGTG AAGGATGTCA ACGAGTTTGC 480
TCCCACCTTC AAAGAGCCAG CCTACAAGGC TGTTGTGACG GAGGGCAAGA TCTATGACAG 540
CATTCTGCAG GTGGAGGCCA TTGACGAGGA GTGCTCCCCA CAGTACAGCC AGATCTGCAA 600
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GGAAGATGAG ACTGAGGGAG AAGAGGAGGA AGAAGCCGAG GAAGAAATGA GCTCCAGCAG 2760
TGGCTCTGAC GACAGCGAAG AGGAGGAGGA GGAGGAAGGG ATGGGCAGAG GCAGACATGG 2820
GCAGAATGGA GCCAGGCAAG CCCAGCTGGA GTGGGATGAC TCCACCCTCC CCTACTAGTG 2880
CCCAGGGGTC TGCTGCCTGG CCCACATGTC CCTTTTGTAA ACCCTGACCC AGTGTATGCC 2940
CATGTCTATC ATACCTCACC TCTGATGTCT GTGACATGTC TGGGAAGGCC TTCTCCAGCT 3000
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GGACAACAAG GACACAACAC AACACACAAC AAGGACAGTC ACAACAAGCC TAGAGCCAGA 3780
AAGCAGATGG AAATGCTAAT GAGGTCAAAC GTAGGCTTCA TGGTGGGTGG AGTGGGGGTG 3840
GCTGGGCTCC CCCAGGACAG AGGGGACCCT GAGGTTGGCA AGGCTCTCAC CACTCAGCCT 3900
TATGGTCCCT TATCTCCTAT CTTCCCTCTT GAGAAAATAC ACGCTTTCTG CATGTATTAG 3960
AAACGCACGA GCTCCACCAA GTCTACAATG AAAGTTTGAA ATTTAACTGC AAGGAATTAG 4020
AAGCATATTT GCAATCATTG CAGCTTCTTC TTTCTTCTGC TCATAAAAGG AGGAACACTT 4080
TAGATAGAGG GCAAATATAT CTGAAAACCT AATTTCTTTC TTTTTTTGAT AAGGAAATCT 4140
TTTCCATCTC CATCCTAACA TGCACAACCT GTGAAGAGAA TTGTTTCTAT AGTAACTGGT 4200
CTGTGATCTT TTGTGGCCAA GAGAATAGCA GGCAAGAATT AGGGCCTTGA CAGAATTTCC 4260
ACGAAGCTCT GAGAACATGT TTGTTTCGAA TGTCTGATTC CTCTTTGTCA TCAATGTGTA 4320
TGCTCTGTCC CCATCCTTCA CTCCTCCTCA AGCTCACACC AATTGGTTTG GCACAGGCAC 4380
AGAGCTGGTC CCTAGTTAAG TGGCATTTAT GTTAAAAAAA AATAGTTCAG AATCTCAGCC 4440
TTTTCTTTGT GTCATCAAAA CAGCTTAAGA AGGGGACTAC TGCCAATGTC CTCTAGTCTG 4500
ACCTCCACCC AGGGAGGACC CATGGCAGGT CTTTTCAACT TTCTGATTCA TGAGAACAAC 4560
CTTGTGAAGC TTTTCCCACC TCCTAAAGTG TTTTCTGCAT CTGTTCCTTC CTTTGGACCT 4620
CACAACAAAT CCTGTGAAGT AACTGAGACA TCTGTTGTTA GATACATTTT TGTGATGAGT 4680
AAACTGAGGC TTCG

Seq ID NO: 36 Protein sequence:
Protein Accession #: NP_071414.1

1 11 21 31 41 51

MLPGRLCWVP LLLALGVGSG SGGGGDSRQR RLLAAKVNKH KPWIETSYHG VITENNDTVI 60
LDPPLVALDK DAPVPFAGEI CAFKIHGQEL PFEAVVLNKT SQEGRLRAKS PIDCELQKEV 120
TFIIQAYDCG AGPHETAWKK SHKAVVNIQV KDVNEFAPTF KEPAYKAVVT EQKIYDSILQ 180
VEAIDEDCSP QYSQICNYEI VTTDVPFAID RNGNIRNTEK LSYDKQHQYS ILVTAYDCGQ 240
KPAAQDTLVQ VDVKPVCKPQ WQDWTKRIEV QPQSDSMPLP PSIHLETCDQ AVSSLQIVTE 300
LQTNYIGKGC DRETYSEKSL QKLCQASSGI IDLLPSPSAA TNWTAGLLVD SSEMIFKFDQ 360
RQQAKIPDGI VPKNLTDQFT ITMWMKHGPS FQVRAEKETI LCNSDKTEMN RHGHYALYVHN 420
CRLVFLLRKD FDQADTFRPA EPHWKLDQIC DKEWHYYVIN VBFPVVTLYM DGATYEPYLV 480
TNDWPIHPSH IAMQLTVGAC WQGGEVTKPQ FAQFFHGSLA SLTIRPGKME SQKVISCLQA 540
CKEGLDINSL ESLQQDIKYH FNPSQSILVM EGDDIGNNNR ALQKVSYINS RQFPTAGVRR 600
LKVSSKVQCF GEDVCISIPE VDAYVMVLQA IEPRITLRGT DHPWRPAAQF BSAROVTLPP 660
DIKIVSTFAK TBAPGDVKTT DPKSEVLEEM LHNLDFCDIL VIGGDLDPRQ ECLELNHSEL 720
HQRHLDATNS TAGYSIYGVG SMSRYEQVLH HIRYRNWRPA SLBARRFRIK CSELNGRYTS 780
NEFNLEVSIL HEDQVSDKEH VNHLIVQPFP LQSVHHPESR SSIQHSSVVP SIATVVIIIS 840
VCMLVFVVAM GVYRVRIAHQ HFIQSTEAAK BSEMDWDDSA LTITVNPMEK HEGPGHGEDE 900
TEGEEEEEAE EEMSSSSGSD DSBEEEEEGG MGRGRHGQNG ARQAQLEWDD STLPY

Seq ID NO: 37 DNA sequence
Nucleic Acid Accession #: none found
Coding sequence: 143-874 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51

GGGAGGGAGA GAGGCGCGCG GGTGAAAGGC GCATTGATGC AGCCTGCGGC GGCCTCGGAG 60
CGCGGCGGAG CCAGACGCTG ACCACGTTCC TCTCCTCGGT CTCCTCCGCC TCCAGCTCCG 120
CGCTGCCCGG CAGCCGGGAG CCATGCGACC CCAGGGCCCC GCCGCCTCCC CGCAGCGGCT 180
CCGCGGCCTC CTGCTGCTCC TGCTGCTGCA GCTGCCCGCG CCGTCGAGCG CCTCTGAGAT 240
CCCCAAGGGG AAGCAAAAAG CGCAGCTCCG GCAGAGGGAG GTGGTGCACC TGTATAATGG 300
AATGTGCTTA CAAGGGCCAG CAGGAGTGCC TGGTCGAGAC GGGAGCCCTG GGGCCAATGG 360
CATTCCGGGT ACACCTGGGA TCCCAGGTCG GGATGGATTC AAAGGAGAAA AGGGGAATG 420
TCTGAGGGAA AGCTTTGAGG AGTCCTGGAC ACCCAACTAC AAGCAGTGTT CATGGAGTTC 480
ATTGAATTAT GGCATAGATC TTGGGAAAAT TGCGGAGTGT ACATTTACAA AGATGCGTTC 540
AAATAGTGCT CTAAGAGTTT TGTTCAGTGG CTCACTTCGG CTAAAATGCA GAAATGCATG 600
CTGTCAGCGT TGGTATTTCA CATTCAATGG AGCTGAATGT TCAGGACCTC TTCCCATTGA 660

AGCTATAATT TATTTGGACC AAGGAAGCCC TGAAATGAAT TCAACAATTA ATATTCATCG 720
CACTTCTTCT GTGGAAGGAC TTTGTGAAGG AATTGGTGCT GGATTAGTGG ATGTTGCTAT 780
CTGGGTTGGC ACTTGTTCAG ATTACCCAAA AGGAGATGCT TCTACTGGAT GGAATTCAGT 840
TTCTCGCATC ATTATTGAAG AACTACCAAA ATAAATGCTT TAATTTTCAT TTGCTACCTC 900
TTTTTTTATT ATGCCTTGGA ATGGTTCACT TAAATGACAT TTTAAATAAG TTTATGTATA 960
CATCTGAATG AAAAGCAAAG CTAAATATGT TTACAGACCA AAGTGTGATT TCACACTGTT 1020
TTTAAATCTA GCATTATTCA TTTTGCTTCA ATCAAAAGTG GTTTCAATAT TTTTTTTAGT 1080
TGGTTAGAAT ACTTTCTTCA TAGTCACATT CTCTCAACCT ATAATTTGGA ATATTGTTGT 1140
GGTCTTTTGT TTTTTCTCTT AGTATAGCAT TTTTAAAAAA ATATAAAAGC TACCAATCTT 1200
TGTACAATTT GTAAATGTTA AGAATTTTTT TTATATCTGT TAAATAAAAA TTATTTCCAA 1260
CAACCTTAAA AAAAAAAAAA AAAA

Seq ID NO: 38 Protein sequence:
Protein Accession #: none found

1 11 21 31 41 51
MRPQQPAASP QRLRQLLLLL LLQLPAPSSA SEIPKQKQKA QLRQREVVDL YNGMCLQQPA 60
GVPGRDGSPG ANGIPGTPGI PGRDGFKGEK GECLRESFEE SWTPNYKQCS WSSLNYGIDL 120
GKIAECTPTK MRSNSALRVL FSGSLRLKCR NACCQRWYFT FNGAECSGPI. PIBAIIYLDQ 180
GSPEMNSTIN IHRTSSVEGL CEGIGAGLVD VAIWVGTCSD YPKGDASTGW NSVSRIIEEB 240
LPK

Seq ID NO: 39 DNA sequence
Nucleic Acid Accession #: NM_000949
Coding sequence: 285-2153(underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
GGAGGCTGAA ATCCCCAGAC GCCGGTTTTC TGGGCTGGGC TTTCTGCTTA CTCACTCCTT 60
CTCCCTCTTT CTGGATTTTA CCGACCGTTC GCGAAACAGC TTTCCACACA ATGGAGCTTC 120
ATGTCCTCGT GCAGGAAGTA CTCATCGACT GATGTGGCAG ACTTTGCTCC CTGACAAAAC 180
TAAAGAACTC TCCTATTCAT GGAGGCGAAC ACTGAGGATG CTTTCCACAT GAACCCTGAA 240
GTGAACTTCT GATACATTTC CTGCAGCAAG AGAAGGCAGC CAACATGAAG GAAAATGTGG 300
CATCTGCAAC CGTTTTCACT CTGCTACTTT TTCTCAACAC CTGCCTTCTG AATGGACAGT 360
TACCTCCTGG AAAACCTGAG ATCTTTAAAT GTCGTTCTCC CAATAAGGAA ACATTCACCT 420
GCTGGTGGAG GCCTGGGACA GATGGAGGAC TTCCTACCAA TTATTCACTG ACTTACCACA 480
GGGAAGGAGA GACACTCATG CATGAATGTC CAGACTACAT AACCGGTGGC CCCAACTCCT 540
GCCACTTTGG CAAGCAGTAC ACCTCCATGT GGAGGACATA CATCATGATG GTCAATGCCA 600
CTAACCAGAT GGGAAGCAGT TTCTCGGATG AACTTTATGT GGACGTGACT TACATAGTTC 660
AGCCAGACCC TCCTTTGGAG CTGGCTGTGG AAGTAAAACA GCCAGAAGAC AGAAAACCCT 720
ACCTGTGGAT TAAATGGTCT CCACCTACCC TGATTGACTT AAAAACTGAT TGGTTCACGC 780
TCCTGTATGA AATTCGATTA AAACCCGAGA AAGCAGCTGA GTGGGAGATC CATTTTGCTG 840
GGCAGCAAAC AGAGTTTAAG ATTCTCAGCC TACATCCAGG ACAGAAATAC CTTGTCCAGG 900
TTCGCTGCAA ACCAGACCAT GGATACTGGA GTGCATGGAG TCCAGCCACC TTCATTCAGA 960
TACCTAGTGA CTTCACCATG AATGATACAA CCGTGTGGAT CTCTGTGGCT GTCCTTTCTG 1020
CTGTCATCTG TTTGATTATT GTCTGGGCAG TGGCTTTGAA GGGCTATAGC ATGGTGACCT 1080
GCATCTTTCC GCCAGTTCCT GGGCCAAAAA TAAAAGGATT TGATGCTCAT CTGTTGGAGA 1140
AGGGCAAGTC TGAAGAACTA CTGAGTGCCT TGGGATGCCA AGACTTTCCT CCCACTTCTG 1200
ACTATGAGGA CTTGCTGGTG GAGTATTTAG AAGTAGATGA TAGTGAGGAC CAGCATCTAA 1260
TGTCAGTCCA TTCAAAAGAA CACCCAAGTC AAGGTATGAA ACCCACATAC CTGGATCCTG 1320
ACACTGACTC AGGCCGGGGG AGCTGTGACA GCCCTTCCCT TTTGTCTGAA AAGTGTGAGG 1380
AACCCCAGGC CAATCCCTCC ACATTCTATG ATCCTGAGGT CATTGAGAAG CCAGAGAATC 1440
CTGAAACAAC CCACACCTGG GACCCCCAGT GCATAAGCAT GGAAGGCAAA ATCCCCTATT 1500
TTCATGCTGG TGGATCCAAA TGTTCAACAT GGCCCTACC ACAGCCCAGC CAGCACAACC 1560
CCAGATCCTC TTACCACAAT ATTACTGATG TGTGTGAGCT GGCTGTGGGC CCTGCAGGTG 1620
CACCGGCCAC TCTGTTGAAT GAAGCAGGTA AAGATGCTTT AAAATCCTCT CAAACCATTA 1680
AGTCTAGAGA AGAGGGAAAG GCAACCCAGC AGAGGGAGGT AGAAAGCTTC CATTCTGAGA 1740
CTGACCAGGA TACGCCCCTGG CTGCTGCCCC AGGAGAAAAC CCCCTTTGGC TCCGCTAAAC 1800
CCTTGGATTA TGTGGAGATT CACAAGGTCA ACAAAGATGG TGCATTATCA TTGCTACCAA 1860
AACAGAGAGA GAACAGCGGC AAGCCCAAGA AGCCCGGGAC TCCTGAGAAC AATAAGGAGT 1920
ATGCCAAGGT GTCCGGGGTC ATGGATAACA ACATCCTGGT GTTGGTGCCA GATCCACATG 1980
CTAAAAACGT GGCTTGCTTT GAAGAATCAG CCAAAGAGGC CCCACCATCA CTTGAACAGA 2040
ATCAAGCTGA GAAAGCCCTG GCCAACTTCA CTGCAACATC AAGCAAGTGC AGGCTCCAGC 2100
TGGGTGGTTT GGATTACCTG GATCCCGCAT GTTTTACACA CTCGTTTCAC TGATAGCTTG 2160
ACTAATGGAA TGATTGGTTA AAATGTGATT TTTCTTCAGG TAACACTACA GAGTACGTGA 2220
AATGCTCAAG AATGTAGTCA GACTGACACT ACTAAAGCTC CCAGCTCCTT TCATGCTCCA 2280
TTTTTAACCA CTTGCCTCTT TCTCCAGCAG CTGATTCCAG AACAAATCAT TATGTTTCCT 2340
AACTGTGATT TGTAGATTTA CTTTTTTCTG TTAGTTATAA AACTATGTGT TCAATGAAAT 2400
AAAAGCACAC TGCTTAGTAT TCTTGAGGGA CAATGCCAAT AGGTATATCC TCTGGAAAAG 2460
GCTTTCATGA TTTGGCATGG GACAGACGGA AATGAAATTG TCAAAATTGT TTACCATAGA 2520
AAGATGACAA AAGAAAATTT TCCACATAGG AAAATGCCAT GAAAATTGCT TTTGAAAAAC 2580
AACTGCATAA GCTTTACACT CCTCGTCCAT TTTATTAGGA TTACCCAAAT ATAACCATTT 2640
AAAGAAAGAA TGCATTCCAG AACAAATTGT TTACATAAGT TCCTATACCT TACTGACACA 2700
TTGCTGATAT GCAAGTAAGA AAT

Seq ID NO: 40 Protein sequence:

Protein Accession #: NP_000940.1

1 11 21 31 41 51
MKENVASATV FTLLLPLNTC LLNGQLPPGK PEIFKCRSPN KETFTCWWRP GTDGGLPTNY 60
SLTYHREGET LMHECPDYIT GGPNSCHFGK QYTSMWRTYI MMVNATNQMG SSPSDELYVD 120
VTYIVQPDPP LELAVEVKQP EDRKPYLWIK WSPPTLIDLK TGWFTLLYEI RLKPEKAARW 180
EIHFAGQQTE FKILSLHPGQ KYLVQVRCKP DHGYWSAWSP ATFIQIPSDF TMNDTTVWIS 240
VAVLSAVICL IIVWAVALKQ YSMVTCIFPP VPGPKIKGFD AHLLEKGKSE ELLSALGCQD 300
FPPTSDYEDL LVEYLEVDDS EDQHLMSVHS KEHPSQGMKP TYLDPDTDSQ RGSCDSPSLL 360
SEKCEEPQAN PSTFYDPEVI EKPENPETTH TWDPQCISME GKIPYFHAGG SKCSTWPLPQ 420
PSQHNPRSSY HNITDVCELA VGPAGAPATL LNEAGKDALK SSQTIKSREE GKATQQREVB 480
SPHSETDQDT PWLLPQEKTP FOSAKPLDYV EIHKVNKDGA LSLLPKQREN SGKPKKPGTP 540
ENNKEYAKVS GVMDNNILVL VPDPHAKNVA CPEESAKEAP PSLEQNQAEK ALANFTATSS 600
KCRLQLGGLD YLDPACPTHS FH

Seq ID NO: 41 DNA sequence
Nucleic Acid Accession #: none found, Eos cloned sequence
Coding sequence: 1-1572 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
ATGACCCAAA ATAAATTAAA GCTTTGTTCC AAAGCCAATG TGTATACTGA AGTGCCTGAT 60
GGACGATGGG GCTGGGCGGT AGCTGTTTCA TTTTTCTTCG TTGAAGTCTT CACCTACGGC 120
ATCATCAAGA CATTTGGTGT CTTCTTTAAT GACTTAATGG ACAGTTTTAA TGAATCCAAT 180
AGCAGGATCT CATGGATAAT CTCAATCTGT GTGTTTGTCT TAACATTTTC AGCTCCCCTC 240
GCCACAGTCC TGAGCAATCG TTTCGGACAC CGTCTGGTAG TGATGTTGGG GGGGCTACTT 300
GTCAGCACCG GGATGGTGGC CGCCTCCTTC TCACAAGAGG TTTCTCATAT GTACGTCGCC 360
ATCGGCATCA TCTCTGGTCT GGGATACTGC TTTAGTTTTC TCCCAACTGT AACCATCCTA 420
TCACAATATT TTGGCAAAAG ACGTTCCATA GTCACTGCAG TTGCTTCCAC AGGAGAATGT 480
TTCGCTGTGT TTGCTTTCGC ACCAGCAATC ATGGCTCTGA AGGAGCGCAT TGGCTGGAGA 540
TACAGCCTCC TCTTCGTGGG CCTACTACAG TTAAACATTG TCATCTTCGG AGCACTGCTC 600
AGACCCATCT TTATCAGAGG ACCAGCGTCA CCGAAAATAG TCATCCAGGA AAATCGGAAA 660
GAAGCGCAGT ATATGCTTGA AAATGAGAAA ACACGAACCT CAATAGACTC CATTGACTCA 720
GGAGTAGAAC TAACTACCTC ACCTAAAAAT GTGCCTACTC ACACTAACCT GGAACTGGAG 780
CCGAAGGCCG ACATGCAGCA GGTCCTGGTG AAGACCAGCC CCAGGCCAAG CGAAAAGAAA 840
GCCCCGCTAT TAGACTTCTC CATTTTGAAA GAGAAAAGTT TTATTTGTTA TGCATTATTT 900
GGTCTCTTTG CAACACTGGG ATTCTTTGCA CCTTCCTTGT ACATCATTCC TCTGGGCATT 960
AGTCTGGGCA TTGACCAGGA CCGCGCTGCT TTTTTATTAT CTACGATGGC CATTGCAGAA 1020
GTTTTCGGAA GGATCGGAGC TGGTTTTGTC CTCAACAGGG AGCCCATTCG TAAGATTTAC 1080
ATTGAGCTCA TCTGCGTCAT CTTATTGACT GTGTCTCTGT TTGCCTTTAC TTTTGCTACT 1140
GAATTCTGGG GTCTAATGTC ATGCAGCATA TTTTTTGGGT TTATGGTTGG AACAATAGGA 1200
GGGACTCACA TTCCACTGCT TGCTGAGGAT GATGTCGTGG GCATTGAGAA GATGTCTTCT 1260
GCAGCTGGGG TCTACATCTT CATTCAGAGC ATAGCAGGAC TGGCTGGACC GCCCCTTGCA 1320
GGTTTGTTGG TGGACCAAAG TAAGATCTAC AGCAGGGCCT TCTACTCCTG CGCAGCTGGC 1380
ATGGCCCTGG CTGCTGTGTG CCTCGCCCTG GTGAGACCGT GTAAGATGGG ACTGTGCCAG 1440
CATCATCACT CAGGTGAAAC AAAGGTAGTG AGCCATCGTG GGAAGACTTT ACAGGACATA 1500
CCTGAAGACT TTCTGGAAAT GGATCTTGCA AAAAATGAGC ACAGAGTTCA CGTGCAAATG 1560
GAGCCGGTAT GA

Seq ID NO: 42 Protein sequence:
Protein Accession #: none found, Eos cloned sequence

1 11 21 31 41 51
MTQNKLKLCS KANVYTEVPD GGWGWAVAVS FFFVEVFTYG IIKTPGVFFN DLMDSFNESN 60
SRISWIISIC VFVLTFSAPL ATVLSNRFGH RLVVMLGGLL VSTGMVAASF SQEVSHMYVA 120
IGIISGLGYC PSFLPTVTIL SQYFGKRRSI VTAVASTGEC FAVFAPAPAI MALKERIGWR 180
YSLLFVGLLQ LNIVIFGALL RPIFIRGPAS PKIVIQENRK EAQYMLENEK TRTSIDSIDS 240
GVELTTSPKN VPTHTNLELS PKADMQQVLV KTSPRPSEKK APLLDFSILK EKSPICYALP 300
GLFATLGFFA PSLYIIPLGI SLGIDQDRAA FLLSTMAIAB VFGRIGAGFV LNREPIRKIY 360
IELICVILLT VSLFAPTFAT EFWGLMSCSI PFGFMVGTIG GTHIPLLAED DVVGIEKMSS 420
AAGVYIFIQS IAGLAGPPLA GLLVDQSKIY SRAPVSCAAG MALAAVCLAL VRPCKMGLCQ 480
HHHSGETKVV SHRGKTLQDI PEDFLEMDLA KNEHRVHVQM EPV

Seq ID NO: 43 DNA sequence
Nucleic Acid Accession #: FGENESH predicted ORF
Coding sequence: 1-1749 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
ATGCTGTCTG GCTTCTTGAT GAGTCCCAGT ACCCAGCACA GAGCACAGTA CACTCCCGGA 60
GGAAAGAAAC TTCCGTGGGA GGCTTCCATC GGTGCGCACA CCTCCCGAGG GCGAGGCAGC 120
GACCGGGAGA GGGAGAGCCG GCCGGAGGCT GCCGGGCTCC TGTGGGACCG CGCTGCAGCC 180
GGGGAGGCGG AGAAGGGGAA CCGGGGCGAG CCGCCCCGCT GGATCCCCGC CCAGCAGCAG 240
CCGCCGCCGC CGCCAGCTGG GCAGGCTCCC GGGACTGCGG CTGGGGGCGC GCAGGACCCT 300
CGCCTGCGTC CTGGACGTTC CCGGGGGAGG GTCCCGTTGC CAGTGAAACC TCCAGAGGCT 360

TCCGGACGAC AGCCCCGGGG GCCTTCTGAC TGCATCCCGA GATTTCCATC AGCGAGTGCA 420
ACTCATAAGG CAGTCCCTAA GGGGACCGGG CCACCGGCTG AGGACGGGGA TGGCTTAGGA 480
GCTCCTGGAC CTAGGGCCCG GCGTCGTCGC CTCCTGGGCG TCGCGGCAGA GGGGAGTGGC 540
CCGCGCGGAA AGCGCCGCGG GACAGTCAGT GACGAGGCCC GGGGGTCGCC GGGGCCACGA 600
CTTCTCGGAG ACCGTCCTGC GCTCTCTGGA GACGCGCTGT CCGCGCCCAG GGTGGTGCCA 660
TGTGGGGCGC TCGCCGCTCG TCCGTCTCCT CATCCTGGAA CGCCGCTTCG CTCCTGCAGC 720
TGCTGCTGGC TGCTGCTGCG GCGGCGGGGG CGAGGGCCCA GCGGCGAGTA CTGCCACGGC 780
TGGCTGGACG CGCAGGGCGT CTGGCGCATC GGCTTCCAGT GTCCCGAGCG CTTCGACGGC 840
GGCGACGCCA CCATCTGCTG CGGCAGCTGC GCGTTGCGCT ACTGCTGCTC CAGCGCCGAG 900
GCGCGCCTGG ACCAGGGCGG CTGCGACAAT GACCGCCAGC AGGGCGCTGG CGAGCCTGGC 960
CGGGCGGACA AAGACGGGCC CCGACGGCTC GGCAGGGCTT CATGTCTTAG GGGTACCCAA 1020
GGAGACGGCG AGGGTGCGCC CCCACCCGTG AGGGCCTGGC AGCGGTGCTC CCCTGAAGGC 1080
TCCCCGAAAG GAAGGCAGCT CCTCAGGGCT TTCCCGGGGC TGCTGCCCCG TGCCAGACGC 1140
CGCGGATTCC CATCTTCTCC ACGCGGCGGC CCCTCTCCCC TGCAGCGGCC CGCCTTGCCC 1200
ATCTACGTGC GTTTCCTCAT TGTTGGCTCC GTGTTTGTCG CCTTTACTAT CTTGGGGTCC 1260
CTGGTGGCAG GCTGTTGCTG CAGATGTCTC CGGCCTAAGC AGGATCCCCA GCAGAGCCGA 1320
GCCCCAGGGG GTAACCGCTT GATGGAGACC ATCCCCATGA TCCCCAGTGC CAGCACCTCC 1380
CGGGGGTCGT CCTCACGCCA GTCCAGCACA GCTGCCAGTT CCAGCTCCAG CGCCAACTCC 1440
GGGGCCCGGG CUCCCCCAAC AAGGTCACAG ACCAACTGTT GCTTGCCGGA AGGAACCATG 1500
AACAACGTGT ATGTCAACAT GCCCACGAAT TTCTCTGTGC TGAACTGTCA GCAGGCCACC 1560
CAGATTGTGC CACATCAAGG GCAGTATCTG CATCCCCCAT ACGTGGGGTA CACGGTGCAG 1620
CACGACTCTG TGCCCATGAC AGCTGTGCCA CCTTTCATGG ACGGCCTGCA GCCTGGCTAC 1680
AGGCAGATTC AGTCCCCCTT CCCTCACACC AACAGTGAAC AGAAGATGTA CCCAGCGGTG 1740
ACTGTATAAC CGAGAGTCAC TGGTGGGTTC CTTTACTGAA GGGAGACGAA GGCAGGGGTG 1800
GATTCTCGAG GTGGAAGTCC GCACATGTCA GTGGTATTTA TGGCACGATT CCTTTGGATG 1860
GCTTCATTTG CCCCCAGACT GTATGAAAAC ATCTCCGAAT TAGCATTTCT GGATATGTTT 1920
CATCCAGGGT ATCATTGATT TATGATGGAA AACCGGCCTC AGCTGGAGAT GACTGTGATG 1980
TTGCTGATGG GTGTATAACA AATGCTTGAG TCCGAAGTGC CCTTGAGATA TGGTTGACGA 2040
AAGAATTTTA TAAACTGATA AATTAAGGAT TTTTATTATG TTGTTATTAT TATTTCTTTT 2100
TTGTTGTTGA CTGCACAGGA TCAAAATGCC TGTTATCTCC CTTTTACTGG GACTTTTTTT 2160
TTTTTTTTTT TTTTTTTTAA TCAGACAGGG TCTTGCTCTG TTGCCCAGGC TGGAGTGCAG 2220
TGGTGCGATC TCGGCTCACT GCAACTTCAG CCTCCTGGAT TCAGGCAACA CTCCTGCCTC 2280
AGCCTCCCAC GTGGCTGGGA TTACAGGTGC CTGCCCCCAT GGCTAATTTT TTGTATTTTT 2340
TGTAGAGATG GGGTTTCACC ATGTTGGCTG GGCTGGTCTC ACTCTCCTGA CCTCAAGCAA 2400
TCTGCCTGTC TCAGCCTCCC AAAGTGCTGG GATTACAGGC GTGAGCCACC GCCCCCAGCC 2460
TGAGCCTTTT TTTTTTTCTA ATGCATCCAA GGTTAAGGGG AAGACGCAAA TAACAGGACT 2520
ATTCTAAAAG GAAACCTGTT TGAACTCTGT GAGATCAGTC ATCAGTCTCA GTATTCCACA 2580
GGCACACCTT AATTTCATTG TAAAAAGATA TATATATTTT GTCTATTTTT GTGCTTTTGG 2640
GGGCCTATTT TGTGCTTTTT TACCTTATGT AGAGATCTTA TTACAAAGTG ATTTTCTACA 2700
TTAAAAAGAG ACTGAAATAA ATTGTATAGT TACTTAACTA ATGAAGACAT TTCAGAACTC 2760
TGGGATGATT TTAATCTTGA AGTAGTAGGT GGTATAGTCA TAAAACCATT CATCCCCTTC 2820
TTGATTGTAT CTTAATTTTC TGGCTTTAAG GTGACATCTG AGAGGTAATG CATTCTTTTT 2880
TATATTGAAA TCATAAACTA TCACCCGCTG CTTCTCTGAG TTACTTTTAA TTTTGCCTTG 2940
TGGTTATGGT TTGGCGTTTC CTTCTGTTTG GTTTTCAGAG CCCCATGTCT ATATAGTGCT 3000
GAGTGCAAGT AATTACTATA CTTGTAAATG AAGATCAGTA TTTCTGCCTA GATCTGATAA 3060
AAAAATTTTC TTGTCTTAGT TATAAAAATT CAAAGAAATG TGTTACAAAG ATACTTAGTA 3120
TAGCTCCTCA GCCATAACCT GAGACTTGGG ATGAAATTTA AACCAGATAC GATTTACTTT 3180
GCAGATCATA AGGCTTTTTA TACTCTTGTT ATCAAAATGG CTTATTTTTC AGGCACTAAG 3240
GATTGTTAAG AGAAAAGCTT TTCAACGAAG GATTGCCTTT CTTCTCCCAC ACTGTTCTTG 3300
ATTTCCTCTC TCTTTCAGGC CTCAACAGGC ACTGTATTCA TTGCCAATGT TCCAAATTAT 3360
CAAATTCAAG TGAATTTATT TGTGTGTTCT TTACTTATAT AAAAAAAGAT AACTTTAAGG 3420
ATGTGCAAGT ACATTTCCAA CTGCTAGCAC AACCAGTATT TTGTAATTAA ACAAATCGCT 3480
GTATGGTATG GTCTTCTACA CATTTATGTC TATAGATATC TATCGATCAT CTTTCTATTC 3540
TGTTTCATGA CTGAATAATG TAAAACCAGT GTTGGCAATT GGTATCATCA ATGATACTCA 3600
TTTTTTAATA ACCAAAGGCA GGGGAAAATC ATTTTACTTA TTAATAAATA TTTTATGATG 3660
TGAAAAAAAA AAAAAAAAAA AAAAAAAAAA

Seq ID NO: 44 Protein sequence:
Protein Accession #: FGENESH predicted

1 11 21 31 41 51

MLSGFLMSPS TQHRAQYTPG GKKLPWEASI GAHTSRGRGS DRERESRPEA AGLLWDRAAA 60
GEAEKGNRGE PPAWIRAQQQ PRPPPAGQAP GTAAGGAQDP RLRPGRSRGR VRLPVKPPEA 120
SGRQPRGPSD CIPRFPSASA THKAVPKGTG PPAEDGDGLG APGPRARRRR LLQVAAEGSG 180
PRGKRRGTVS DEARGSPGPR LLGDRPALSG DALSAPRVVP CGALAARPSP HPGTPLRSCS 240
CCWLRCWRRG RGPSGEYCHG WLDAQGVWRI GFQCPERFDG GDATICCGSC ALRYCCSSAE 300
ARLDQGGCDN DRQQQAGEPG RADKDGPRRI GRASCLRGTQ GDGEGAPPPV RAWQRCSPEG 360
SPKGRQLLRA FPGLLPRARR RGFPSSPRGG PSPLQRPALP IYVPFLIVGS VPVAFIILGS 420
LVAACCRCL RPKQDPQQSR APGGNRLMET IPMIPSASTS RGSSSRQSST AASSSSANS 480
GARAPPTRSQ TNCCLPEGTM NNVYVNMPTN FSVLNCQQAT QIVPHQGQYL HPPYVGYTVQ 540
HDSVPMTAVP PFMDGLQPGY RQIQSPFPHT NSEQKMYPAV TV

Seq ID NO: 45 DNA sequence
Nucleic Acid Accession #: NM_002285
Coding sequence: 55-3738 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51

GGCCGAGCCT CGGCGGCGGC GGTAGCGGCG GCGGCGACGC TGACACCTCC CACCATGGAC 60
AGCTTCGACT TAGCCCTGCT CCAGGAATGG GACCTCGAGT CACTGTGTGT CTATGAACCA 120
GATAGAAATG CATTACGGAG GAAAGAACGA GAAAGAAGAA ATCAAGAAAC TCAACAGGAT 180
GATGGCACGT TTAATTCTAG TTACTCTCTC TTCAGTGAGC CCTACAAGAC TAACAAGGGG 240
GATGAACTCT CCAACCGGAT CCAGAAACACT TTAGGCAATT ATGATGAAAT GAAAGACTTT 300
TTAACTGATA GAACCAATCA GAGTCATCTC GTTGGAGTTC CCAAACCTGG GGTTCCTCAG 360
ACTCCTGTGA ACAAGATCGA TGAACATTTT GTTGCAGATT CAAGAGCCCA GAACCAGCCC 420
TCGTCTATCT GTAGCACTAC AACTTCCACA CCAGCAGCTG TCCCCGTGCA GCAGAGTAAA 480
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ACACAACAGG GCTCTCTCAG GACCTTGCTT GGAGATGGTG TTGGCAGACA GCAGCCTCGG 600
GCCAAACAAG TGTGCAATGT GGAGGTGGGC CTTCAGACCC AGGAGAGGCC ACCTGCCATG 660
GCGGCCAAGC ACAGCAGCAG CGGACACTGT GTTCAGAACT TTCCTCCATC CCTAGCTTCA 720
AAACCCAGCC TGGTCCAGCA GAAACCGACC GCGTATGTGA GGCCAATGGA CGGCCAAGAT 780
CAGGCCCCTG ATGAGTCTCC TAAGCTGAAG TCGTCTTCGG AAACCAGCGT GCACTGCACA 840
TCATACAGGG GAGTCCCTGC CAGCAAGCCG GAGCCTGCCA GAGCCAAGGC CAAGCTCTCC 900
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GAAGAAATAA TCCGGGAGAT GACCTGGCTT CCACCACTTT CTGCTATTCA AGCACCTGGC 1020
AAAGTGGAAC CAACCAAATT TCCATTTCCA AATAAGGACT CTCAGCTTGT ATCCTCTGGA 1080
CACAATAATC CAAAGAAAGG TGATGCAGAG CCAGAGAGTC CAGACAATGG CACATCGAAT 1140
ACATCAATGC TGGAAGATGA CCTTAAGCTA AGCAGTGATG AAGAGGAGAA TGAACAGCAG 1200
GCAGCTCAGA GAACGGCTCT CCGCGCTCTC TCTGACAGCG CCGTGGTCCA GCAGCCCAAC 1260
TGCAGAACCT CGGTGCCTTC CAGCAAGGGC AGCAGCAGCA GCAGCAGCAG CGGCACGAGC 1320
AGCTCCTCCA GCGACTCAGA GAGCAGCTCC GGATCTGACT CGGAGACCGA GAGCAGCTCC 1380
AGCGAGAGTG AGGGCAGCAA GCCCCCCCAC TTCTCCAGCC CCGAGGTGAA ACCGGCATCC 1440
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CGGTGAACAT TTCCTCA

Seq ID NO: 46 Protein sequence:
Protein Accession #: NP_002276

1 11 21 31 41 51

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PRAKQVGNVE VGLQTQERPP AMAAKHSSSG HCVQNFPPSL ASKPSLVQQK PTAYVRPMDG 240

QDQAPDESPK LKSSSBTSVH CTSYRGVPAS KPEPARAKAK LSKPSIPKQQ EESRSGBTNS 300
CVEEIIREMT WLPPLSAIQA PGKVEPTKFP FPNKDSQLVS SOHNNPKKQD AEPESPDNGT 360
SNTSMLEDDL KLSSDEEENE QQAAQRTALR ALSDSAVVQQ PNCRTSVPSS KGSSSSSSSG 420
TSSSSSDSES SSGSDSETES SSSESEGSKP PHFSSPEAEP ABSNKWQLDK WLNKVNPHKP 480
PILIQNESHG SESNQYYNPV KEDVQDCGKV PDVCQPSLRE KEIKSTCKEB QRPRTANKAP 540
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NCHRPEEPAA ADALGTSVVV PPEPTKTRPC GNNRASHRKE LRSSVTCEKR RTRGLSRIVP 660
KSKEPIETES SSSSSSSDSD LESEQEEYPL SKAQTVAASA SSGNDQRLKE AAANGGSGPR 720
APVGSINART TSDIAKELEE QFYTLVPFGR NELLSPLKDS DEIRSLWVKI DLTLLSRIPE 780
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RPNGNSLFTS ASSSKKPKAD SQLQPHGGDL TKAAHNNSEN IPLHKSRPQT KPWSPGSNGH 960
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GPMESKSPYY LMYSETVELI RYAMRLKTHS GPNATPEDKQ LAALCYRCLA LLYWRMFRLK 1080
RDHAVKYSKA LIDYFKNSSK AAQAPSPWGA SGKSTGTPSP ISPNPFPGSS VGSQGSLSNA 1140
SALSPSTIVS IPQRIHQMAA NHVSITNSIL HSYDYWEMAD NLAKFNREPF NDLDLLMGPV 1200
TLHSSMEHLV QYSQQQLHWL RNSAHLS

Seq ID NO: 47 DNA sequence
Nucleic Acid Accession #: NM_033151
Coding sequence: 351-4499(underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
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ACTAAGTGAT TTGGGCCTGA GGCCTGAGAA GATGTTTAAA AAGAGGGATC AAGCACAGGC 180
TAAGGAGAGG AAAGAGCAGG CACCCAAACC TCTGCATGGC CCCAATATGC TCCCTGCAGG 240
GTAGTGCCCC CTCTTCTGGC TGCTCAAGGC GAGATCTAAG CTTCTTCTAA CTCCTGCTGT 300
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Seq ID NO: 48 Protein sequence:
Protein Accession #: NP_149163.2

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EAPLHMEGTSCPQGWPQHGEIIPQDYHMKYRDNTPTVLHGINLTIRGHEVVGIVGRTGSGKSSLGMALFR
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Seq ID NO: 49 DNA sequence
Nucleic Acid Accession #: NM_033419
Coding sequence: 18-980 (underlined sequences correspond to start and stop codons)

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TCTACATGAG TCTAGCAGGC TGGACCTGTC GGGACGACTG TAAGTATGAG TGTATGTGGG 240
TCACCGTTGG GCTCTACCTC CAGGAAGGTC ACAAAGTGCC TCAGTTCCAT GGCAAGTGGC 300
CCTTCTCCCG GTTCCTGTTC TTTCAAGAGC CGGCATCGGC CGTGGCCTCG TTTCTCAATG 360
GCCTGGCCAG CCTGGTGATG CTCTGCCGCT ACCGCACCTT CGTGCCAGCC TCCTCCCCCA 420
TGTACCACAC CTGTGTGGCC TTCGCCTGGG TGTCCCTCAA TGCATGGTTC TGGTCCACAG 480
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Seq ID NO: 50 Protein sequence:
Protein Accession #: NP_219487.1

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Seq ID NO: 51 DNA sequence
Nucleic Acid Accession #: XM_059098.1
Coding sequence: 178-618(underlined sequences correspond to start and stop codons)

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ATCTCCTGGA TCCTTTACTG CCTGGCTCTG AACCCTGAGC ATCAAGAGAG ATGCCGGGAG 120
GAGGTCAGGG GCATCCTGGG GGATGGGTCT TCTATCACTT GGGACCAGCT GGGTGAGATG 180
TCGTACACCA CAATGTGCAT CAAGGAGACG TGCCGATTGA TTCCTGCAGT CCCGTCCATT 240
TCCAGAGATC TCAGCAAGCC ACTTACCTTC CCAGATGGAT GCACATTGCC TGCAGGGATC 300
ACCGTGGTTC TTAGTATTTG GGGTCTTCAC CACAACCCTG CTGTCTGGAA AAACCCAAAG 360
GTCTTTGACC CCTTGAGGTT CTCTCAGGAG AATTCTGATC AGAGACACCC CTATGCCTAC 420
TTACCATTCT CAGCTGGATC AAGGAACTGC ATTGGGCAGG AGTTTGCCAT GATTGAGTTA 480
AAGGTAACCA TTGCCTTGAT TCTGCTCCAC TTCAGAGTGA CTCCAGACCC CACCAGGCCT 540
CTTACTTTCC CCAACCATTT TATCCTCAAG CCCAAGAATG GGATGTATTT GCACCTGAAG 600
AAACTCTCTG AATGTTAGAT CTCAGGGTAC AATGATTAAA CGTACTTTGT TTTTCGAAGT 660
TAAATTTACA GCTAATGATC CAAGCAGATA GAAAGGGATC AATGTATGGT GGGAGGATTG 720
GAGGTTGGTG GGATAGGGGT CTCTGTGAAG AGATCCAAAA TCATTTCTAG GTACACAGTG 780
TGTCAGCTAG ATCTGTTTCT ATATAACTTT GGGAGATTTT CAGATCTTTT CTGTTAAACT 840
TTCACTACTA TTAATGCTGT ATACACCAAT AGACTTTCAT ATATTTTCTG TTGTTTTTAA 900
AATAGTTTTC AGAATTATGC AAGTAATAAG TGCATGTATG CTCACTGTCA AAAATTCCCA 960
ACACTAGAAA ATCATGTAGA ATAAAAATTT TAAATCTCAC TTCACTTAGC CGACATTCCA 1020
TGCCCTGACC AATCCTACTG CTTTTCCTAA AAACAGAATA ATTTGGTGTG CATTCTTTCA 1080
GACTTTTTCC TATACATTTT ATATGTAGAA ATGTAGCAAT GTATTTGTAT AGATGTGATC 1140
ATTCCTATAT TGTTATTGAT TTTTTTCACT TAATAAAAAT TCACCTTATT CCTT

Seq ID NO: 52 Protein sequence:
Protein Accession #: XP_059098.1

1 11 21 31 41 51
MSYTTMCIKE TCRLIPAVPS ISRDLSKPLT FPDGCTLPAG ITVVLSIWGL HHNPAVWKNP 60
KVFDPLRFSQ ENSDQRHPYA YLPFSAGSRN CIGQEFAMIE LKVTIALILL HFRVTPDFTR 120
PLTPPNHFIL KPKNGMYLHL KKLSEC

Seq ID NO: 53 DNA sequence
Nucleic Acid Accession #: NM_030916
Coding sequence: 1-1533 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
ATGCCCCTGT CCCTGGGAGC CGAGATGTGG GGGCCTGAGG CCTGGCTGCT GCTGCTGCTA 60
CTGCTGGCAT CATTTACAGG CCGGTGCCCC GCGGGTGAGC TGGAGACCTC AGACGTGGTA 120
ACTGTGGTGC TGGGCCAGGA CGCAAAACTG CCCTGCTTCT ACCGAGGGGA CTCCGGCGAG 180
CAAGTGGGGC AAGTGGCATG GGCTCGGGTG GACGCGGGCG AAGGCGCCCA GGAACTAGCG 240
CTACTGCACT CCAAATACGG GCTTCATGTG AGCCCGGCTT ACGAGGGCCG CGTGGAGCAG 300
CCGCCGCCCC CACGCAACCC CCTGGACGGC TCAGTGCTCC TGCGCAACGC AGTGCAGGCG 360
GATGAGGGCG AGTACGAGTG CCGGGTCAGC ACCTTCCCCG CCGGCAGCTT CCAGGCGCGG 420
CTGCGGCTCC GAGTGCTGGT GCCTCCCCTG CCCTCACTGA ATCCTGGTCC AGCACTAAGA 480
GAGGGCCAGG GCCTGACCCT GGCAGCCTCC TGCACAGCTG AGGGCAGCCC AGCCCCCAGC 540
GTGACCTGGG ACACGGAGGT CAAAGGCACA ACGTCCAGCC GTTCCTTCAA GCACTCCCGC 600
TCTGCTGCCG TCACCTCAGA GTTCCACTTG GTGCCTAGCC GCAGCATGAA TGGGCAGCCA 660
CTGACTTGTG TGGTGTCCCA TCCTGGCCTG CTCCAGGACC AAAGGATCAC CCACATCCTC 720
CACGTGTCCT TCCTTGCTGA GGCCTCTGTG AGGGGCCTTG AAGACCAAAA TCTGTGGCAC 780
ATTGGCAGAG AAGGAGCTAT GCTCAAGTGC CTGAGTGAAG GGCAGCCCCC TCCCTCATAC 840
AACTGGACAC GGCTGGATGG GCCTCTGCCC AGTGGGGTAC GAGTGGATGG GGACACTTTG 900
GGCTTTCCCC CACTGACCAC TGAGCACAGC GGCATCTACG TCTGCCATGT CAGCAATGAG 960
TTCTCCTCAA GGGATTCTCA GGTCACTGTG GATGTTCTTG ACCCCCAGGA AGACTCTGGG 1020
AAGCAGGTGG ACCTAGTGTC AGCCTCGGTG GTGGTGGTGG GTGTGATCGC CGCACTCTTG 1080
TTCTGCCTTC TGGTGGTGGT GGTGGTGCTC ATGTCCCGAT ACCATCGGCG CAAGGCCCAG 1140
CAGATGACCC AGAAATATGA GGAGGAGCTG ACCCTGACCA GGGAGAACTC CATCCGGAGG 1200
CTGCATTCCC ATCACACGGA CCCCAGGAGC CAGCCGGAGG AGAGTGTAGG GCTGAGAGCC 1260
GAGGGCCACC CTGATAGTCT CAAGGACAAC AGTAGCTGCT CTGTGATGAG TGAAGAGCCC 1320
GAGGGCCACA GTTACTCCAC GCTGACCACG GTGAGGGAGA TAGAAACACA GACTGAACTG 1380
CTGTCTCCAG GCTCTGGGCG GGCGAGGAG GAGGAAGATC AGGATGAAGG CATCAAACAG 1440
GCCATGAACC ATTTTGTTCA GGAGAATGGG ACCCTACGGG CCAAGCCCAC GGGCAATGGC 1500
ATCTACATCA ATGGGCGGGG ACACCTGGTC TGA

Seq ID NO: 54 Protein sequence:
Protein Accession #: NP_112178.1

1 11 21 31 41 51
MPLSLGAEMW GPSAWLLLLL LLASPTGRCP AGELSTSDVV TVVLGQDAKL PCFYRGDSGE 60
QVGQVAWARV DAGEGAQELA LLHSKYGLHV SPAYEGRVEQ PPPPRNPLDG SVLLRNAVQA 120
DEGEYECRVS TFPAGSPQAR LRLRVLVPPL PSLNPGPALE EGQGLTLAAS CTAEGSPAPS 180
VTWDTEVKGT TSSRSFKHSR SAAVTSEFHL VPSRSMNGQP LTCVVSHPGL LQDQRITHIL 240
HVSPLABASV RGLEDQNLWH IGREGAMLKC LSEGQPPPSY NWTRLDGPLP SGVRVDGDTL 300
GFPPI.TTEHS GIYVCHVSNE PSSRDSQVTV DVLDPQEDSG KQVDLVSASV VVVGVIAALL 360
FCLLVVVVVL MSRYHRRKAQ QMTQKYEEEL TLTRENSIRR LHSHGNTDPRS QPEESVGLRA 420
EGIPDSLKDN SSCSVMSEEP EGRSYSTLTT VREIETQTEL LSPGSGRAEB EEDQDEGIKQ 480
AMNHFVQENG TLRAKPTGNG IYINGRGHLV

Seq ID NO: 55 DNA sequence
Nucleic Acid Accession #: AF007170.1
Coding sequence: 73-1725 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
AAGGAGGCGG CCTCCGGGAA AAGCGACCGC AGGACTCCTG AGAGCAGCCT CCATGAGGCC 60
CTGGACCAGT GCATGACCGC CCTGGACCTC TTCCTCACCA ACCAGTTCTC AGAAGCACTC 120
AGCTACCTCA AGCCCAGAAC CAAGGAAAGC ATGTACCACT CACTGACATA TGCCACCATC 180
CTGGAGATGC AGGCCATGAT GACCTTTGAC CCTCAGGACA TCCTGCTTGC CGGCAACATG 240
ATGAAGGAGG CACAGATGCT GTGTCAGAGG CACCGGAGGA AGTCTTCTGT AACAGATTCC 300
TTCAGCAGCC TGGTGAACCG CCCCACGCTG GGCCAATTCA CTGAAGAAGA AATCCAGCGT 360
GAGGTCTGCT ATGCAGAGTG CCTGCTGCAG CGAGCAGCCC TGACCTTCCT GCAGGACGAG 420
AACATGGTGA GCTTCATCAA AGGCGGCATC AAAGTTCGAA ACAGCTACCA GACCTACAAG 480
GAGCTGGACA GCCTTGTTCA GTCCTCACAA TACTGCAAGG GTGAGAACCA CCCGCACTTT 540
GAAGGAGGAG TGAAGCTTGG TGTAGGGGCC TTCAACCTGA CACTGTCCAT GCTTCCTACT 600
AGGATCCTGA GGCTGTTGGA GTTTGTGGGG TTTTCAGGAA ACAAGGACTA TGGGCTGCTG 660
CAGCTGGAGG AGGGAGCGTC AGGGCACAGC TTCCGCTCTG TGCTCTGTGT CATGCTCCTG 720
CTGTGCTACC ACACCTTCCT CACCTTCGTG CTCGGTACTG GGAACGTCAA CATCGAGGAG 780
GCCGAGAAGC TCTTGAAGCC CTACCTGAAC CGGTACCCTA AGGGTGCCAT CTTCCTGTTC 840
TTTGCAGGGA GGATTGAAGT CATTAAAGGC AACATTGATG CAGCCATCCG GCGTTTCGAG 900
GAGTGCTGTG AGGCCCAGCA GCACTGGAAG CAGTTTCACC ACATGTGCTA CTGGGAGCTG 960
ATGTGGTGCT TCACCTACAA GGGCCAGTGG AAGATGTCCT ACTTCTACGC CGACCTGCTC 1020
AGCAAGGAGA ACTGCTGGTC CAAGGCCACC TACATTTACA TGAAGGCCGC CTACCTCAGC 1080
ATGTTTGGGA AGGAGGACCA CAAGCCGTTC GGGGACGACG AAGTGGAATT ATTTCGAGCT 1140
GTGCCAGCCC TGAAGCTCAA GATTGCTGGG AAATCTCTAC CCACAGAGAA GTTTGCCATC 1200
CGGAAGTCCC GGCGCTACTT CTCCTCCAAC CCTATCTCGC TGCCAGTGCC TGCTCTGGAA 1260
ATGATGTACA TCTGGAACGG CTACGCCGTG ATTGGGAAGC AGCCGAAACT CACGGATGGG 1320
ATACTTGAGA TTATCACTAA GGCTGAAGAG ATGCTGGAGA AAGGCCCAGA GAACGAGTAC 1380

TCAGTGGATG ACGAGTGCTT GGTGAAATTG TTGAAAGGCC TGTGTCTGAA ATACCTGGGC 1440
CGTGTCCAGG AGGCCGAGGA GAATTTTAGG AGCATCTCTG CCAATGAAAA GAAGATTAAA 1500
TATGACCACT ACTTGATCCC AAACGCCCTG CTGGAGCTGG CCCTGCTGCT TATGGAGCAA 1560
GACAGAAACG AAGAGGCCAT CAAACTTTTG GAATCTGCCA AGCAAAACTA CAAGAATTAC 1620
TCCATGGAGT CAAGGACACA CTTTCGAATC CAGGCAGCCA CACTCCAAGC CAAGTCTTCC 1680
CTAGAGAACA GCAGCAGATC CATGGTCTCA TCAGTGTCCT TGTAGCTTTG TGCAGCAGTT 1740
CCGGGCTGGA AGACAGAGAC AGCTGGACAG AGCTCCTGAA AACATTTCAA AATACCCCCT 1800
CCCCCTGCCC TGCCCTGCCT TTGGGGTCCA CCGGCACTCC AGTTGGATGG CACAACATAG 1860
TGTATCCGTG CAGAAGCCGA GCTGGCATTT TCACCAGTGT AGCCAAGGGC CTTTGCCAAG 1920
GGCAGAGCAG GTGGAGCCCT CTGCCTGCCC TATCACACAT ACGGGTACTT GCTTTTCACT 1980
GTGATGTTTA AGAGAATGTA TGAACAGTTT ACATTTTCCT TAGAAATACA TTGATGGGAT 2040
CACAGTTGGC TTTAAAAACC AACAACAATC AACCACCTGT AAGTCTTTGT CTTCACCTAT 2100
TATCATCTGG AGGTAAATCT CTTTATATGA TGATGCCAAA GGGCAAATTG CTTTTCAAAT 2160
TCAGCAAGTT CTCAGCTTGT GTGACGGAAG GTCCTTCAGA GGACCTGAGG AATGCCTGGG 2220
AGAGGCTAAG CCTCAGGCTT CAATGCTTCT GGGGTTGGGC ATGAGGATGT ACACAGACAC 2280
CCACTACCTT ACTACTCACA CTTCATTTCA CTCCTTTTGT AAATTTCCAA TTTAAAAATC 2340
AAGCACGTCT TTTTAGTGAG ATAAAATCTG AGCTCTTCTG TAGAAAAATC AATCTCTACC 2400
AGTAGAAAAT GCCAGGGCTT GATGGAAGAG CTGTGTAGCC CTTTCTATGC CAAAGCCAGG 2460
AAATTTGGGG GGCAGGAGGA GGTTCTCAGA ATCCAGTCTG TATCTTTGCT GTATGCCAAA 2520
CTGAAACCAC TGGGAATAAT TTATGAAACA TAAAAATCTT CTGTACTTCA CTCCAAGGTA 2580
CATTTGCTTA CTGACAGCAT TTTTGTTAAA ACTGTTATTC TTGAAAAAAA AAAAAAAAAA 2640
AA

Seq ID NO: 56 Protein sequence:
Protein Accession #: AAC39582.1

1 11 21 31 41 51
| | | | | |
MTALDLFLTN QFSEALSYLK PRTKESMVHS LTVATILEMQ AMMTFDPQDI LLAGNMMKEA 60
QMLCQRHRRK SSVTDSFSSL VNRPTLGQFT EEEIHAEVCY AECLLQRAAL TFLQDENMVS 120
FIKGGIKVRN SYQTYKELDS LVQSSQYCKG ENHPHFEGGV KLGVGAFNLT LSMLPTRLLR 180
LLEFVGFSQN KDYGLLQLEE GASGHSFRSV LCVMLLLCYH TFLTFVLGTG NVNIEEAEKL 240
LKPYLNRYPK GAIFLFPAGR IEVIKGNIDA AIRRFEECCE AQQHWKQFHH MCYWELMWCF 300
TYKGQWKMSY FYADLLSKEN CWSKATYIYM KAAYLSMFGK EDHKPPGDDE VELPRAVPGL 360
KLKIAGKSLP TEKFAIRKSR RYFSSNPISL PVPALEMMYI WNGYAVIGKQ PKLTDGILEI 420
ITKAEEMLEK GPENGYSVDD ECLVKLLKGL CLKYLGRVQE AEENFRSISA NEKKIKYDIY 480
LPNALLELA LLLMEQDRNE EAIKLLESAK QNYKNYSMES RTHFRIQAAT LQAKSSLENS 540
SRSMVSSVSL

Seq ID NO: 57 DNA sequence
Nucleic Acid Accession #: NM_006670.1
Coding sequence: 1-927 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
| | | | | |
ATGCCTGGGG GGTGCTCCCG GGGCCCCGCC GCCGGGGACG GGCGTCTGCG GCTGGCGCGA 60
CTAGCGCTGG TACTCCTGGG CTGGGTCTCC TCGTCTTCTC CCACCTCCTC GGCATCCTCC 120
TTCTCCTCCT CGGCGCCGTT CCTGGCTTCC GCCGTGTCCG CCCAGCCCCC GCTGCCGGAC 180
CAGTGCCCCG CGCTGTGCGA GTGCTCCGAG GCAGCGCGCA CAGTCAAGTG CGTTAACCGC 240
AATCTGACCG AGGTGCCCAC GGACCTGCCC GCCTACGTGC GCAACCTCTT CCTTACCGGC 300
AACCAGCTGG CCAGCAACCA CTTCCTTTAC CTGCCGCGGG ATGTGCTGGC CCAACTGCCC 360
AGCCTCAGGC ACCTGGACTT AAGTAATAAT TCGCTGGTGA GCCTGACCTA CGTGTCCTTC 420
CGCAACCTGA CACATCTAGA AAGCCTCCAC CTGGAGGACA ATGCCCTCAA GGTCCTTCAC 480
AATGGCACCC TGGCTGAGTT GCAAGGTCTA CCCCACATTA GGGTTTTCCT GGACAACAAT 540
CCCTGGGTCT GCGACTGCCA CATGGCAGAC ATGGTGACCT GGCTCAAGGA AACAGAGGTA 600
GTGCAGGGCA AAGACCGGCT CACCTGTGCA TATCCGGAAA AAATGAGGAA TCGGGTCCTC 660
TTGGAACTCA ACAGTGCTGA CCTGGACTGT GACCCGATTC TTCCCCCATC CCTGCAAACC 720
TCTTATGTCT TCCTGGGTAT TGTTTTAGCC CTGATAGGCG CTATTTTCCT CCTGGTTTTG 780
TATTTGAACC GCAAGGGGAT AAAAAAGTGG ATGCATAACA TCAGAGATGC CTGCAGGGAT 840
CACATGGAAG GGTATCATTA CAGATATGAA ATCAATGCGG ACCCCAGATT AACAAACCTC 900
AGTTCTAACT CGGATGTCCT CGAGTGA

Seq ID NO: 58 Protein sequence
Protein Accession #: NP_006661.1

1 11 21 31 41 51
| | | | | |
MPGGCSRGPA AGDGRLRLAR LALVLLGWVS SSSPTSSASS FSSSAPFLAS AVSAQPPLPD 60
QCPALCECSE AARTVKCVNR NLTEVPTDLP AYVRNLFLTG NQLASNHFLY LPRDVLAQLP 120
SLRHLDLSNN SLVSLTYVSF RNLTHLESLH LEDNALKVLH NGTLAELQGL PHIRVFLDNN 180
PWVCDCHMAD MVTWLKETEV VQGKDRLTCA YPEKMRNRVL LELNSADLDC DPILPPSLQT 240
SYVFLGIVLA LIGAIFLLVL YLNRKGIKKW MHNIRDACRD HMEGYHYRYE INADPRLTNL 300
SSNSDVLS

Seq ID NO: 59 DNA sequence
Nucleic Acid Accession #: NM_024022

Coding sequence: 1-1362(underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
| | | | | |
ATGGGGGAAA ATGATCCGCC TGCTGTTGAA GCCCCCTTCT CATTCCGATC GCTTTTTGGC 60
CTTGATGATT TGAAAATAAG TCCTGTTGCA CCAGATGCAG ATGCTGTTGC TGCACAGATC 120
CTGTCACTGC TGCCATTGAA GTTTTTTCCA ATCATCGTCA TTGGGATCAT TGCATTGATA 180
TTAGCACTGG CCATTGGTCT GGGCATCCAC TTCGACTGCT CAGGGAAGTA CAGATGTCGC 240
TCATCCTTTA AGTGTATCGA GCTGATAGCT CGATGTGACG GAGTCTCGGA TTGCAAAGAC 300
GGGGAGGACG AGTACCGCTG TGTCCGGGTG GGTGGTCAGA ATGCCGTGCT CCAGGTGTTC 360
ACAGCTGCTT CGTGGAAGAC CATGTGCTCC GATGACTGGA AGGGTCACTA CGCAAATGTT 420
GCCTGTGCCC AACTGGGTTT CCCAAGCTAT GTGAGTTCAG ATAACCTCAG AGTGAGCTCG 480
CTGGAGGGGC AGTTCCGGGA GGAGTTTGTG TCCATCGATC ACCTCTTGCC AGATGACAAG 540
GTGACTGCAT TACACCACTC AGTATATGTG AGGGAGGGAT GTGCCTCTGC CCACGTGGTT 600
ACCTTGCAGT GCACAGCCTG TGGTCATAGA AGGGGCTACA GCTCACGCAT CGTGGGTGGA 660
AACATGTCCT TGCTCTCGCA GTGCCCCTGG CAGGCCAGCC TTCAGTTCCA GGGCTACCAC 720
CTGTGCGGGG GCTCTGTCAT CACGCCCCTG TGGATCATCA CTGCTGCACA CTGTGTTTAT 780
GACTTGTACC TCCCCAAGTC ATGGACCATC CAGGTGGGTC TAGTTTCCCT GTTGGACAAT 840
CCAGCCCCAT CCCACTTGGT GGAGAAGATT GTCTACCACA GCAAGTACAA GCCAAAGAGG 900
CTGGGCAATG ACATCGCCCT TATGAAGCTG GCCGGGCCAC TCACGTTCAA TGAAATGATC 960
CAGCCTGTGT GCCTGCCCAA CTCTGAAGAG AACTTCCCCG ATGGAAAAGT GTGCTGGACG 1020
TCAGGATGGG GGGCCACAGA GGATGGAGGT GACGCCTCCC CTGTCCTGAA CCACGCGGCC 1080
GTCCCTTTGA TTTCCAACAA GATCTGCAAC CACAGGGACG TGTACGGTGG CATCATCTCC 1140
CCCTCCATGC TCTGCGCCGG CTACCTGACG GGTGGCGTGG ACAGCTGCCA GGGGGACAGC 1200
GGGGGGCCCC TGGTGTGTCA AGAGAGGAGG CTGTGGAAGT TAGTGGGAGC GACCAGCTTT 1260
GGCATCGGCT GCGCAGAGGT GAACAAGCCT GGGGTGTACA CCCGTGTCAC CTCCTTCCTG 1320
GACTGGATCC ACGAGCAGAT GGAGAGAGAC CTAAAAACCT GA

Seq ID NO: 60 Protein sequence
Protein Accession #: NP_076927

1 11 21 31 41 51
| | | | | |
MGENDPPAVB APPSPRSLFQ LDDLKISPVA PDADAVAAQI LSLLPLKPFP IIVIGIIALI 60
LALAIGLGIH FDCSGKYRCR SSFKCIELIA RCDGVSDCKD GEDEYRCVRV GGQNAVLQVF 120
TAASWKTMCS DDWKGHYANV ACAQLGFPSY VSSDNLRVSS LEGQFREEFV SIDHLLPDDK 180
VTALHHSVYV REGCASGHVV TLQCTACGHR RGYSSRIVGG NMSLLSQWPW QASLQFQGYH 240
LCGGSVITPL WIITAAHCVY DLYLPKSWTI QVGLVSLLDN PAPSHLVEKI VYHSKYKPKR 300
LGNDIALMKL AGPLTFNEMI QPVCLPNSEB NFPDGKVCWT SGWGATEDGG DASPVLNHAA 360
VPLISNKICN HRDVYGGIIS PSMLCAGYLT GGVDSCQGDS GGPLVCQERR LWKLVGATSF 420
GIGCAEVNKP GVYTRVTSFL DWIHEQMERD LKT

Seq ID NO: 61 DNA sequence
Nucleic Acid Accession #: NM_006475
Coding sequence: 28-2538 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
| | | | | |
AACAGAACTG CAACGGAGAG ACTCAAGATG ATTCCCTTTT TACCCATGTT TTCTCTACTA 60
TTGCTGCTTA TTGTTAACCC TATAAACGCC AACAATCATT ATGACAAGAT CTTGGCTCAT 120
AGTCGTATCA GGGGTCGGGA CCAAGGCCCA AATGTCTGTG CCCTTCAACA GATTTTGGGC 180
ACCAAAAAGA AATACTTCAG CACTTGTAAG AACTGGTATA AAAAGTCCAT CTGTGGACAG 240
AAAACGACTG TTTTATATGA ATGTTGCCCT GGTTATATGA GAATGGAAGG AATGAAAGGC 300
TGCCCAGCAG TTTTGCCCAT TGACCATGTT TATGGCACTC TGGGCATCGT GGGAGCCACC 360
ACAACGCAGC GCTATTCTGA CGCCTCAAAA CTGAGGGAGG AGATCGAGGG AAAGGGATCC 420
TTCACTTACT TTGCACCGAG TAATGAGGCT TGGGACAACT TGGATTCTGA TATCGGTAGA 480
GGTTTGGAGA GCAACGTGAA TGTTGAATTA CTGAATGCTT TACATAGTCA CATGATTAAT 540
AAGAGAATGT TGACCAAGGA CTTAAAAAAT GGCATGATTA TTCCTTCAAT GTATAACAAT 600
TTGGGGCTTT TCATTAACCA TTATCCTAAT GGGGTTGTCA CTGTTAATTG TGCTCCAATC 660
ATCCATGTGA ACCAGATTTC AACAAATGGT GTTGTCCATG TCATTGACCG TGTGCTTACA 720
CAAATTGGTA CCTCAATTCA AGACTTCATT GAAGCAGAAG ATGACCTTTC ATCTTTTAGA 780
GCAGCTGCCA TCACATCGGA CATATTGGAG GCCCTTGGAA GAGACGGTCA CTTCACACTC 840
TTTGCTCCCA CCAATGAGGC TTTTGAGAAA CTTCCACGAG GTGTCCTAGA AAGGTTCATG 900
GGAGACAAAG TGGCTTCCGA AGCTCTTATG AAGTACCACA TCTTAAATAC TCTCCAGTGT 960
TCTGAGTCTA TTATGGGAGG AGCAGTCTTT GAGACGCTGG AAGGAAATAC AATTGAGATA 1020
GGATGTGACG GTGACAGTAT AACAGTAAAT GGAATCAAAA TGGTGAACAA AAAGGATATT 1080
GTGACAAATA ATGGTGTGAT CCATTTTATT GATCAGGTCC TAATTCCTGA TTCTGCCAAA 1140
CAAGTTATTG AGCTGGCTGG AAAACAGCAA ACCACCTTCA CGGATCTTGT GGCCCAATTA 1200
GGCTTGGCAT CTGCTCTGAG GCCAGATGGA GAATACACTT TGCTGGCACC TGTGAATAAT 1260
GCATTTTCTG ATGATACTCT CAGCATGGTT CAGCGCCTCC TTAAATTAAT TCTGCAGAAT 1320
CACATATTGA AAGTAAAAGT TGGCCTTAAT GAGCTTTACA ACGGGCAAAT ACTGGAAACC 1380
ATCGGAGGCA AACAGCTCAG AGTCTTCGTA TATCGTACAG CTGTCTGCAT TGAAAATTCA 1440
TGCATGGAGA AAGGGAGTAA GCAAGGGAGA AACGGTGCGA TTCACATATT CCGCGAGATC 1500
ATCAAGCCAG CAGAGAAATC CCTCCATGAA AAGTTAAAAC AAGATAAGCG CTTTAGCACC 1560
TTCCTCAGCC TACTTGAAGC TGCAGACTTG AAAGAGCTCC TGACACAACC TGGAGACTGG 1620
ACATTATTTG TGCCAACCAA TGATGCTTTT AAGGGAATGA CTAGTGAAGA AAAAGAAATT 1680
CTGATACGGG ACAAAAATGC TCTTCAAAAC ATCATTCTTT ATCACCTGAC ACCAGGAGTT 1740

TTCATTGGAA AAGGATTTGA ACCTGGTGTT ACTAACATTT TAAAGACCAC ACAAGGAAGC 1800
AAAATCTTTC TGAAAGAAGT AAATGATACA CTTCTGGTGA ATGAATTGAA ATCAAAAGAA 1860
TCTGACATCA TGACAACAAA TGGTGTAATT CATGTTGTAG ATAAACTCCT CTATCCAGCA 1920
GACACACCTG TTGGAAATGA TCAACTGCTG GAAATACTTA ATAAATTAAT CAAATACATC 1980
CAAATTAAGT TTGTTCGTGG TAGCACCTTC AAAGAAATCC CCGTGACTGT CTATACAACT 2040
AAAATTATAA CCAAAGTTGT GGAACCAAAA ATTAAAGTGA TTGAAGGCAG TCTTCAGCCT 2100
ATTATCAAAA CTGAAGGACC CACACTAACA AAAGTCAAAA TTGAAGGTGA ACCTGAATTC 2160
AGACTGATTA AAGAAGGTGA AACAATAACT GAAGTGATCC ATGGAGAGCC AATTATTAAA 2220
AAATACACCA AAATCATTGA TGGAGTGCCT GTGGAAATAA CTGAAAAAGA GACACGAGAA 2280
GAACGAATCA TTACAGGTCC TGAAATAAAA TACACTAGGA TTTCTACTGG AGGTGGAGAA 2340
ACAGAAGAAA CTCTGAAGAA ATTGTTACAA GAAGAGGTCA CCAAGGTCAC CAAATTCATT 2400
GAAGGTGGTG ATGGTCATTT ATTTGAAGAT GAAGAAATTA AAAGACTGCT TCAGGGAGAC 2460
ACACCCGTGA GGAAGTTGCA AGCCAACAAA AAAGTTCAAG GTTCTAGAAG ACGATTAAGG 2520
GAAGGTCGTT CTCAGTGAAA ATCCAAAAAC CAGAAAAAAA TGTTTATACA ACCCTAAGTC 2580
AATAACCTGA CCTTAGAAAA TTGTGAGAGC CAAGTTGACT TCAGGAACTG AAACATCAGC 2640
ACAAAGAAGC AATCATCAAA TAATTCTGAA CACAAATTTA ATATTTTTTT TTCTGAATGA 2700
GAAACATGAG GGAAATTGTG GAGTTAGCCT CCTGTGGTAA AGGAATTGAA GAAAATATAA 2760
CACCTTACAC CCTTTTTCAT CTTGACATTA AAAGTTCTGG CTAACTTTGG AATCCATTAG 2820
AGAAAAATCC TTGTCACCAG ATTCATTACA ATTCAAATCG AAGAGTTGTG AACTGTTATC 2880
CCATTGAAAA GACCGAGCCT TGTATGTATG TTATGGATAC ATAAAATGCA CGCAAGCCAT 2940
TATCTCTCCA TGGGAAGCTA AGTTATAAAA ATAGGTGCTT GGTGTACAAA ACTTTTTATA 3000
TCAAAAGGCT TTGCACATTT CTATATGAGT GGGTTTACTG GTAAATTATG TTATTTTTTA 3060
CAACTAATTT TGTACTCTCA GAATGTTTGT CATATGCTTC TTGCAATGCA TATTTTTTAA 3120
TCTCAAACGT TTCAATAAAA CCATTTTTCA GATATAAAGA GAATTACTTC AAATTGAGTA 3180
ATTCAGAAAA ACTCAAGATT TAAGTTAAAA AGTGGTTTGG ACTTGGGAA

Seq ID NO: 62 Protein sequence:
Protein Accession #: NP_006466

1 11 21 31 41 51
MIPFLPMFSL LLLLIVNPIN ANNHYDKILA HSRIRGRDQG PNVCALQQIL GTKKKYPSTC 60
KNWVKKSICG QKTTVLYECC PGYMRMEGMK GCPAVLPIDH VYGTLGIVGA TTTQRYSDAS 120
KLREEIEGKG SFTYFAPSNE AWDNLDSDIR RGLESNVNVE LLNALHSHMI NKRMLTKDLK 180
NGMIIPSMYN NLGLFINHYP NGVVTVNCAR IIHGNQIATN GVVHVIDRVL TQIGTSIQDF 240
IEAEDDLSSF RAAAITSDIL EALGRDGHFT LFAPTNEAFE KLPRGVLERP MGDKVASEAL 300
MKYHILNTLQ CSESIMGGAV FETLEGNTIE IGCDGDSITV NGIKMVNKKD IVTNNGVIHL 360
IDQVLIPDSA KQVIELAGKQ QTTFTDLVAQ LGLASALRPD GEYTLLAPVN NAFSDDTLSM 420
VQRLLKLILQ NHILKVKVGL NELYNGQILE TIGGKQLRVF VYRTAVCIEN SCMEKGSKQG 480
RNGAIHIFRE IIKPAEKSLH EKLKQDKRFS TFLSLLEAAD LKELLTQPGD WTLFVPTNDA 540
FKGMTSEEKE ILIRDKNALQ NIILYHLTPG VFIGKGFEPG VTNILKTTQG SKIFLKEVND 600
TLLVNELKSK ESDIMTTNGV IHVVDKLLVP ADTPVGNDQL LEILNKLIKY IQIKFVRGST 660
FKEIPVTVYT TKITTKVVEP KIKVIEGSLQ PIIKTEGPTL TKVKIEGEPE FRLIKEGETI 720
TEVIIGEPII KKYTKIIDGV PVEITEKETR EERITTGPEI KYTRISTGGG ETEETLKKLL 780
QEEVTKVTKF IEGGDGHLFE DEEIKRLLQG DTPVRKLQAN KKVQGSRRRL REGRSQ

Seq ID NO: 63 DNA sequence
Nucleic Acid Accession #: NM_020974
Coding sequence: 81-3080 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
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CGGGTCGGGG CCGTGCCGCG GGGCCGCAGG AGGATGTAGA TGAGTGTGCC CAAGGGCTAG 240
ATGACTGCCA TGCCGACGCC CTGTGTCAGA ACACACCCAC CTCCTACAAG TGTCCTGCA 300
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TTGATGGCTT CATGTTGGCT CATGACGGTC ATAATTGTCT TGATGTGGAC GAGTGCCTGG 480
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GCAAGGAGGG GTTTTTCCTG AGTGACAATC AGCACACCTG CATTCACGGC TCGGAAGAGG 600
GCCTGAGCTG CATGAATAAG GATCACGGCT GTAGTCACAT CTGCAAGGAG GCCCCAAGGG 660
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GCCCAGAGTG CAGCTGCCAT CCACAGTACA AGATGCACAC AGATGGGAGG AGCTGCCTTG 840
AGCGAGAGGA CACTGTCCTG GAGGTGACAG AGAGCAACAC CACATCAGTG GTGGATGGGG 900
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Seq ID NO: 64 Protein sequence:
Protein Accession #: NP_066025.1

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DHGCSHICKE APRGSVACEC RPGFELAKNQ RDCILTCNHG NGGCQHSCDD TADGPECSCH 240
PQYKMHTDGR SCLEREDTVL BVTESNTTSV VDGDKRVKRR LLMETCAVNN GGCDRTCKDT 300
STGVHCSCPV GFTLQLDGKT CKDIDECQTR NGGCDHPCKN IVGSFDCGCK KGFKLLTDEK 360
SCQDVDECSL DRTCDHSCIN HPGTFACACN RGYTLVGFTH CGDTNECSIN NGGCQQVCVN 420
TVGSYECQCH PGYKLHWNKK DCVEVKGLLP TSVSPRVSLH CGKSGGGDGC FLRCHSGIHL 480
SSDVTTIRTS VTFKLNEGKC SLKNAELFPE GLRPALPEKH SSVKESFRYV NLTCSSCIKQV 540
PQAPGHPSTP KEMPITVVEFB LETNQKEVTA SCDLSCIVKR TEKRLRKAIR TLRKAVHREQ 600
FHLQLSGMNL DVAKKPPRTS ERQAESCQVQ QGHAENQCVS CRAGTYYDGA RERCILCPNG 660
TFQNEEQQMT CEPCPRPGNS GALKTPEAWN MSECGGLCQP GEYSADGFAP CQLCALGTFQ 720
PEAGRTSCFP CGGGLATKHQ GATSFQDCET RVQCSPQHPY NTTTHRCIRC PVGTYQPEFG 780
KNNCVSCPGN TTTDFDGSTN ITQCKNRRCG GELGDFTGYI ESPNYPQNYP ANTECTWTIN 840
PPPKRRILIV VPEIFLPIED DCGDYLVMRK TSSSNSVTTY BTCQTVERPI APTSRSKKLW 900
IQFKSNEGNS ARGFQVPYVT YDEDYQELIE DIVRDGRLYA SENHQEILKD KKLIKALPDV 960
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Seq ID NO: 65 DNA sequence
Nucleic Acid Accession #: NM_007210
Coding sequence: 1-1869 (underlined sequences correspond to start and stop codons)

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ATGAACAACC TTAGAGATTC AATGCCCAAG CTCCAAATCA GGGCTCCAGA AGCCCAGCAG 240
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CCCTTCTGGG AACGGCCACC ACAGGACCCC AATGCCCCTG GGGCAGATGG AAAAGCATTT 360
CAGAAGAGCA AGTGGACCCC CCTGGAGACC CAGGAAAAGG AAGAAGGCTA TAAGAAGCAC 420
TGTTTCAATG CCTTTGCCAG CGACCGGATC TCCCTGCAGA GGTCCCTGGG GCCAGACACC 480
CGACCACCTG AGTGTGTGGA CCAGAAGTTC CGGCGCTGCC CCCCACTGGC CACCACCAGC 540

GTGATCATTG TGTTCCACAA CGAAGCCTGG TCCACACTGC TGCGAACAGT GTACAGCGTC 600
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GAGGAGCACC TAAAGGAGAA GCTGGAGCAG TACGTGAAGC AGCTGCAGGT GGTGAGGGTG 720
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TTTGTCTAGG ACCCAGATCA TCCCCAGAGA GAGCCCCCAC AAGCTCCTCA GGAAACAGGA 1920
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Seq ID NO: 66 Protein sequence:
Protein Accession #: NP_009141

1 11 21 31 41 51

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QKSKWTPLET QEKEEQVKKH CPNAPASDRI SLQRSLGPDT RPPECVDQKP RRCPPLATTS 180
VITVFIINEAW STLLRTVVSV LHTTPAILLK EIILVDDAST EEHLKEKLEQ YVKQLQVVRV 240
VRQEERKGLI TARLLQASVA QAEVLTFLDA HCECFHGWLE PLLARIAEDK TVVVSPDIVT 300
IDLNTFEFAK PVQRGRVHSR GNFDWSLTFG WETLPPHEKQ RRKDETYPIK SPTFAGGLFS 360
IPKSYFEHIG TYDNQMEIWG GENVEMSFRV WQCGGQLEII PCSVVGHVFR TKSPHTFPKG 420
TSVIARNQVR LAEVWMDSYK KIFYRRNLQA AKMAQEKSPQ DISERLQLRE QLHCHNFSWY 480
LHNVYPEMFV PDLTPTFYQA IKNLOTNQCL DVGENNRGGK PLIMYSCHGL GGNQYPEYTT 540
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Seq ID NO: 67 DNA sequence
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Coding sequence: 600-4484 (underlined sequences correspond to start and stop codons)

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TTTAATAATT TGCATTATAT TGTCCCAACC AGTAGTTTAT TTTTTGCCAC GGAGATGTAG 5880
AAGATATTAC AAGCTACTGG ATGCACTGTC AGATTAACTT ATTTCATTAA AGAAGTTGGG 5940
AGAACAAATA GGAAAAAAAA AACTTATTTT TCTAGTAAAT ATTAATGTAT TACATTTCAA 6000
ATAATGGTGC CTGACATATT GAATAATTAT TTTCTACAGT GTACGTATGC AACAAAGATA 6060
TTCCATCATG CATTAGAGTC AGTTCTGGCT CTGCCTAGCT GTTTACATTT GCAAATGTAG 6120
CAAACAAGGT AATGAAGCAA CTATTTCTAT TGCAGTAGAT ATCCTTTTGT GTGTGTGTGT 6180
GTGCATTAAA GTTGTAAACG GTAACATGAA ACAAATGAAA GTTCTTGCTA TAATGGTATG 6240
GAAAACAAGA AGGAAATGAA AATATTTTTA TGCCTACTTA GGAAAAAAAG GGTAGCACTT 6300
ATTCATTCCA AGTACTTTTT TTTTTTTAAT TTTTAAGCTC TTAACTCACA TTGTTATGCT 6360
TAAGATGATA AACATATATC CTCTTTTTAT TGCTTTGTCT ATGTTTCATA TGAAACATTT 6420
CAGAAATTAT TTTGATAAGT GTTGCTGGAA TCTGCAACGC TGATTTTTTT TTGCATTCTG 6480
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TTGTGTTGTC ATTTTCATTT TTGCATTTTT TTGTTTGCAT ATTAAAAAAA GAGAAAAGAG 6720
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TATTCTGATC TCACCTGTCG CGTAGCTCTA ATATTCACAT AAACTGAAAT AAAGAAGTGG 6840
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AATACATATC ACTATTCTTG GAATATTTAT GGTCAGTCTA CTTTTTAGTA AAATATTTTT 7320
GGATAGCGTT GACACGATAG ATCTTATTCC ATACTTCTTT ATTATTGATA ATTTTATTTT 7380
CATTTTTTGC TTTCATTATT ATACATATTT TGGTGGAGAA GAGGTTGGGC TTTTTTGAAA 7440
GAGACAAAAA TTTATTATAA CACTAAACAC TCCTTTTTTG ACATATTAAA GCCTTTATTC 7500
CATCTCTCAA GATATATTAT AAAATTTATT TTTTTAATTT AAGATTTCTG AATTATTTTA 7560
TCTTAAATTG TGATTTTAAA CGAGCTATTA TGGTACGGAA CTTTTTTTAA TGAGGAATTT 7620
CATGATGATT TAGGAATTTT CTCTCTTGGA AAAGGCTTCC CCTGTGATGA AAATGATGTG 7680
CCAGCTAAAA TTGTGTGCCA TTTAAAAACT GAAAATATTT TAAAATTATT TGTCTATATT 7740
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AGTTAATTGC AGTAATTAGA ACTTCTGGAA TATGCTAGGG CAGAAGTATG TCAAGTATGT 9000
CACATGAAGA AAATGTGAAA TTCAAGAGTA ATCCACACGT GAGAAACTAG ACAATGTACA 9060
TTCATGTGTT CTCTTGAAAG GAAAGGGAGA GCTGTAAGCT TCACTCTGTC CTACACCGGA 9120
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CTTCTAGAGC ATAGAGTCCC AAAACTCAAT TCTGGTTTTC CCCTGTTTTT TTTTTTTTTT 9240
TTTTTCCCAA CATATGAACT GCAGCATATC ACTTTTTCTT TTTGTGCCTC AGGTTCCTCA 9300
CCTGTAAAAT TGAAAAATAT ATGTATTAAT AATATTATTA ATAATAATAA TGGTAATGTA 9360
GTACTTGTTT GTAAAGCACT TTGAGATCCT TGGTTGAAAG GCACCATAGG AGTGCCAAGT 9420
ATTATTATGT GGCCAAGGGG GTTATTTAAA CTGTCAGTTC CCAAAGGCCA GGAAAGGTTG 9480
GGGTCATTTT TCTTAAAGAC GAGCTGTAAA TATCAACTAG GCAGCCAATA GTGTTGACTA 9540
TGAAGATGCA AAACTATTAC TAGGCTGATA AAATCATAGT TTCTTAATGG CTACCAATAA 9600
GGCAAATATC ACAATAATAA ACGCCAAATT CCTTAGGGCG GACTATTTGA CAACCACATG 9660
GAAAACTTTG GGGGAGGCAT GAGGGGGGAA CATCTCAAAA TGCCAATGTA AAATTTAACT 9720
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AAAAGAATTC AATTTGTAGT CCTGATTTGA ATACTAGAAT GTTGGCTATA ATAGTTCTGT 9840
TCTTACAACA CATGAAAATT TTTCGTTTTA TTTTATTTTG TTTTCATAGT GCATGTTCAT 9900
TTCTACTCAC AAACATGTTC TTGGTGTATT TCTTATGCAA ACAATCTTCA GGCAGCAAAG 9960
ATGTCTGTTA CATCTAAACT TGAATAATAA AGTTTTACCA CCAGTTTACAC A

Seq ID NO: 68 Protein sequence:
Protein Accession #: NP_054831

1 11 21 31 41 51

MPYEVNAGYD FTNMVRKKNP PLRNVASEGB GQILEPIGTE SKVSGKNKEF SADQMSFNTD 60
QSDAAELNHK EEHSLHVQDP SSSSKKDLKS AVLSEKAGFN YESPSKGGNF PSFPHDEVTD 120
RNMLAFSFPA AGGVCEPLKS PQRAEADDPQ DMACTPSGDS LETKEDQKMS PKATEETGQA 180
QSGQANCQGI. SPVSVASKNP QVPSDGGVRL NKSKTDLLVN DNPDPAPLSP ELQDFKCNIC 240
GYGYYGNDPT DLIKHFRKYII LGLHNRTRQD AELDSKILAL HNMVQFSHSK DFQKVNRSVF 300
SQVLQDNSS RPVLLNGTYD VQVTSGGTPI GIGRKTPDCQ GNTKYFRCKP CNFTYMGNSS 360
TELEQHFLQT HPNKJKASLP SSEVAKPSEK NSNKSIPALQ SSDSGDLQKW QDKITVKAGD 420
DTPVGVSVPI KPLDSSRQNG TEATSYYWCK PCSFSCESSS SLKLLEHYGK QHGAVQSGGL 480
NPELNDKLSR QSVNQNDLA KSSEGETMTK TDKSSSQAKK KDFESKQAED NMVTSYNCQF 540
CDFRYSKSHQ PDVIVVCPLI. RHVQQLHNIH KCTIKHCPPC PRGLCSPEKH LGETYPPAC 600
RKSNCSHCAL LLLHLSPOAA GSSRVKHQCH QCSFTTPDVD VLLPHYESVH ESQASDVKQE 660
ANHLQQSDGQ QSVKESKEHS CTKCDFITQV EEEISRHYRR AHSCYKCRQC SFTAADTQSL 720
LEHFNTVHCQ EQDITTANGE EDGHAISTIK EEPKIDFRVY NLLTPDSKMQ EFVSESVVKR 780
EKLEEKDGLK EKVWTESSSD DLRNVTWRGA DILRGSPSYT QASLGLLTPV SGTQEQTKTL 840
RDSPNVEAAH LARPIYGLAV ETKGFLQGAP AGGEKSQALP QQYPASGENK SKDESQSLLR 900
RRRGSGVFCA NCLTTKTSLW RKNANGGYVC NACGLYQKLH STPRPLNIJK QNNQEQIRRR 960
RTRKRLNPEA LQAEQLNKQQ RGSNEEQVNG SPLERRSEDH LTESHQREIP LPSLSKYEAQ 1020
GSLTKSHSAQ QPVLVSQTLD IHKRMQPLHI QIKSPQESTG DPGNSSSVSE GKGSSERGSP 1080
IEKYMRPAKH PNYSPPQSPI EKYQYPLPGL PFVHNDFQSE ADWLRPWSKY KLSVPGNPHY 1140
LSHVPGLPNP CQNYVPYPTP NLPPHFSAVG SDNDIPLDLA IKHSRPGPTA NGASKEKTKA 1200
PPNVKNEGPL NVVKTEKVDR STQDELSTKC VHCGIVFLDE VMYALHMSCH GDSQPFQCSI 1260
CQHLCTDKYD PTTHIQRGLH RNNAQVEKNG KPKE

Seq ID NO: 69 DNA sequence
Nucleic Acid Accession #: XM_073879
Coding sequence: 1-387(underlined sequences correspond to start and stop codons)

1 11 21 31 41 51

ATGGGGTTTG GAGACCAGGG AACGGTGGAA GGGAGCCTAG GAACGTCGAA AAAACCACCT 60
GAAGTGAAAA TGTTTGGAGC CAGTCAAGGT TTGCTGACAA TGGAAACAAA CCAGTCCCTG 120
GCACAAGGCA CAGGCTGCTC AGTAGTAAAG GTAGACACTG TTCTCTTCGA GAGTTTATAC 180
CACTGCGGCT TTGAACACGG GAGCGTGATG CACTGCCTTG GGGATGATCA CCCCCAGGAA 240
GACAGGAAGG CTCACTTCTC TGCCCCAGTT GCAGCCATCG CCTCTCCAGC ACCGACTCCT 300
GTCTGTCCTG CACACCACTC AACACAGAGC ATCTGCCAGT TTCTACAGCA CTGCAGGCAG 360
AACACTCACT TGCAGGCTGC TAACTAA

Seq ID NO: 70 Protein sequence:
Protein Accession #: XP_073879

1 11 21 31 41 51

MGFGDQGTVE GSLGTSKKPP EVKMPGASQG LLTMETNQSL AQGTGCSVVK VDTVLPESLV 60
HCGFEHGSVM HCLGDDHPQE DRKAHPSAPV AAIASPAPTP VCPAMHSTQS ICQFLQHCRQ 120
NTHLQAAN

Seq ID NO: 71 DNA sequence
Nucleic Acid Accession #: AB033064
Coding sequence: 826-1986 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51

GGGGAACAGC AAATTCAGTC ACAGACAATC CTCCACTCGG TCAAGAGCCA CTTTTCTCTT 60
CCTGCCTTGC CCCCCCGCAG GGGGTAAGGA ACTGAGCGTT TAATCTTTAG CCGGTTGGCT 120
ACCAGCTAAA ATTCTACTTA TCTTAGTTTC TAGTGGATAG CTTTCTTATT TTGCCCATGT 180
TTTCTTAGAA TCCCTGTTTA ATATACTTTT GTCAGTAGTA GTATCTAGGA GTAGCAGGGA 240
GAGTGACAAT AAATTAGCCC CTTCTTTTTT CCCTTGTCAT TCAGGCCCCT TTTCCTCTCC 300
AGAGGGAAAT TACCAGTAAA CTCTTCTAAA TCTTCCACCC CTTCTCAGTC ATACTGTGAA 360
GAAACACACT AAAGTGGACA TTATTTGACC AGTGAACACG AACCCAGCTT CAGGCATTGG 420
TTTGTTGTGG CACATGGAGA AACATCTCTT TTAAAATATC TCCCAATTAC CCTTTTCACA 480
ATTTGTATCC ACCTAGGATT TGCTGCTGGG GTAAGTCACT AGATTTATTT CTCAAAGCTC 540
CCCTCTCTAT GAGCTGAAAG ACTGACCAAC CATGAACACT AGTAGGGGAT GGGGAAAGGG 600
GACAGAGCAG AGCCAGTTGT TCCACACTTT GGGAAGCAGG AGTAGCTTTT ATCATCTTCC 660
TCTGGGGAGC AGGCATAGAG ACATAAACTG AGTGAAAATG GGTGGAGGAA GAACTTCTAT 720
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ATTTTACGAG CATTGAAGGC CAAATGTTGT GAGGAGGAAC TGGACTTTAG GGCTGTGGTG 960
ATGGATGAGG TGGTGCTGAC AATCGAGCAA GGAAACCTGG GTCTGCGGAT CAATGGAGAG 1020
CTAATCACTG CCTACCCACA AGTGGTGGTA GTCAGAGTAC CAACCCCTTG GGTGCAAAGT 1080
GATAGTGACA TCACTGTTTT GCGCCATCTA GAGAAGATGG GATGTCGGTT AATGAACCGA 1140

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ATGCAAAGCA ACTGCTCATT AGGTGGTGTG GGGATGATGT GCTCATTGAG TGAACAAGGG 1560
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GCAAGTTCCA GCTCTGTTGA CAGCGACCCT GAAAGCACGG AGCGAGAGCT GCTCACCAAG 1920
CTCCCAGGGG GCCTGTTCAA CATGAACCAG CTGCTAGCCA ATGAAATCAA ACTACTGGTG 1980
GACTGACTCC ACTGGTAATT AACCAACAAA ACCCTTGTAA AACTTTCTTT CTTCTTTTCT 2040
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TAGTAGGATT AGTTGGAGAG AGTGGGAGAT AGATGAGACC TCTGCTAGTA AGATGTTACT 2160
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TTCTAAGTAT AAAGCTGAAG TGATTTCGAA TGCCAGCGTT ATATATTTGC ATTTTTCACA 3060
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CATAGAATTA AATAATATTA AAATTGAGTG AAAGGTTGAT TGTTGATGAA TAGAATAGTA 3960
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ATGGGCTATT TGGCTGGTGA GACACGATCC CCTCCTAAGA AAATGTAGGT GCTCAGACAG 5280
GTAACCACTG CTGCTACTGT TTTTATTTGT TTGTTTGTTC AATTTTATTT AAGATTTGTT 5340
TTTGTTGTAC TAGGATTTTA AAAAATGTAA TATATTGCAG GATTTATAAC CAG

Seq ID NO: 72 Protein sequence:
Protein Accession #: BAA86552

1 11 21 31 41 51

MCSSVAAKLW FLTDRRIRED VPQKEILRAL KAKCCEEELD FRAVVMDEVV LTIEQGNLGL 60
RINGELITAY PQVVVVRVPT PWVQSDSDIT VLRHLEKMGC RLMNRPQAIL NCVNKFWTFQ 120
ELAGHGVPLP DTFSYGGHEN FAKMIDEAEV LEFPMVVKNT RGHRGKAVFL ARDKHHLADL 180
SHLIRHEAPY LFQKYVKESH GRDVRVIVVG GRVVGTMLRC STDGRMQSNC SLGGVGMMCS 240
LSEQGKQLAI QVSNILGMDV CGIDLLMKDD GSFCVCEANA NVGFIAFDKA CNLDVAGHIA 300
DYAASLLPSG RLTRRMSLLS VVSTASETSE PELQPPASTA VDNMSASSSS VDSDPESTER 360
ELLTKLPGQL FNMNQLLANE IKLLVD

Seq ID NO: 73 DNA sequence
Nucleic Acid Accession #: XM_040080.2
Coding sequence: 159-1104 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51

CTGAGTGGGG GCGGGGACTG CTGGAGTTGC GGGGCCTGCC TGGGGTAGGG CGGGGCAGGA 60
CAGCTTGGAG ATAGGGCCCG GAATTGCGGG CGTCACTCTG CTCCTGCGAC CTAGCCAGGC 120
GTGAGGGAGT GACAGCAGCG CATTCGCGGG ACGAGAGCGA TGAGTGAGAA CGCCGCACCA 180
GGTCTGATCT CAGAGCTGAA GCTGGCTGTG CCCTGGGGCC ACATCGCAGC CAAAGCCTGG 240
GGCTCCCTGC AGGGCCCTCC AGTTCTCTGC CTGCACGGCT GGCTGGACAA TGCCAGCTCC 300
TTCGACAGAC TCATCCCTCT TCTCCCGCAA GACTTTTATT ACGTTGCCAT GGATTTCGGA 360
GGTCATGGGC TCTCGTCCCA TTACAGCCCA GGTGTCCCAT ATTACCTCCA GACTTTTGTG 420
AGTGAGATCC GAAGAGTTGT GGCAGCCTTG AAATGGAATC GATTCTCCAT TCTGGGCCAC 480
AGCTTCGGTG GCGTCGTGGG CGGAATGTTT TTCTGTACCT TCCCCGAGAT GGTGGATAAA 540
CTTATCTTGC TGGACACGCC GCTCTTTCTC CTGGAATCAG ATGAAATGGA GAACTTGCTG 600
ACCTACAAGC GGAGAGCCAT AGAGCACGTG CTGCAGGTAG AGGCCTCCCA GGAGCCCTCG 660
CACGTGTTCA GCCTGAAGCA GCTGCTGCAG AGGTTACTGA AGAGCAATAG CCACTTGAGT 720
GAGGAGTCCG GGGAGCTTCT CCTGCAAAGA GGAACCACGA AGGTGGCCAC AGGTCTGGTT 780
CTGAACAGAG ACCAGAGGCT CGCCTGGGCA GAGAACAGCA TTGACTTCAT CAGCAGGGAG 840
CTGTGTGCGC ATTCCATCAG GAAGCTGCAG GCCCATGTCC TGTTGATCAA AGCAGTCCAC 900
GGATATTTTG ATTCAAGACA GAATTACTCT GAGAAGGAGT CCCTGTCGTT CATGATAGAC 960
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GTCCACATGA GCGAACCCCA GCACGTGGCC AGTATCATCA GCTCCTTCTT ACAGTGCACA 1080
CACATGCTCC CAGCCCAGCT GTAGCTCTGG GCCTGGAACT ATGAAGACCT AGTGCTCCCA 1140
GACTCAACAC TGGGACTCTG AGTTCCTGAG CCCCACAACA AGGCCAGGGA TGGTGGGGAC 1200
AGGCCTCACT AGTCTTGAGG CCCAGCCTAG GATGGTAGTC AGGGGAAGGA GCGAGATTCC 1260
AACTTCAACA TCTGTGACCT CAAGGGGGAG ACAGAGTCTG GGTTCCAGGG CTGCTTTCTC 1320
CTGGCTAATA ATAAATATCC AGCCAGCTGG AGGAAGGAAG GGCAGGCTGG GCCCACCTAG 1380
CCTTTCCCTG CTGCCCAACT GGATGGAAAA TAAAAGGTTC TTGTATTCTC A

Seq ID NO: 74 Protein sequence:
Protein Accession #: XP_040080.1

1 11 21 31 41 51

MSENAAPGLI SELKLAVPWG HIAAKAWGSL QGPPVLCLHG WLDNASSFDR LPLLPQDFY 60
YVAMDFGGHG LSSHYSPGVP YYLQTFVSEI RRVVAALKWN RFSILGHSFG GVVGGMFFCT 120
FPEMVDKLIL LDTPLFLLES DEMENLLTYK RRAIEHVLQV BASQEPSHVF SLKQLLQRLL 180
KSNSHLSEEC GELLLQRQTT KVATGLVLNR DQRLAWAENS IDFISRELCA HSIRKLQAHV 240
LLIKAVHGYF DSRQNYSEKB SLSFMIDTMK STLKEQFQFV EVPGNHCVHM SEPQHVASII 300
SSFLQCTHML PAQL

Seq ID NO: 75 DNA sequence
Nucleic Acid Accession #: NM_005794
Coding sequence: 434-1276 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51

GGTTCCCTTC CACGCTGTGA AGCTTTGTTC TTTTGGTCTT CATGATAAAT CTTGCTGCTG 60
CTCACTCGTT GGGTCCGTGC CACCTTTAAG AGCTGTAACA CTCACCGCGA AGGTCTGCAA 120
CTTCACTCCT GGGGCCAGCA AGACCACGAA TGCACCGAGA GGAATGAACA ACTCTGGACA 180
CACCATCTTT AAGAACCGTA ATACTCACCG CAAGGGTCTG CAACTTCATT CTTGAAGTCA 240
GTGAGGCCAA GAACCCATCA ATTCCGTACA CATTTTGGTG ACTTTGAAGA GACTGTCACC 300
TATCACCAAG TGGTGAGACT ATTGCCAAGC AGTGAGACTA TTGCCAAGTG GTGAGACCAT 360
CACCAAGCGG TGAGACTATC ACCTATCGCC AAGTGGCCTG ATTCAGCAGG AAGCATCTCA 420
GACACCAACC ACTATGCTGT CAGCAGTTGC CCGGGCTACA CAGGGCTGGT TTCATCCCTG 480
TGCTAGGCTT TCTGTGAGGA TGAGCAGCAC CGGGATAGAC AGGAAGGGCG TCCTGGCTAA 540
CCGGGTAGCC GTGGTCACGG GGTCCACCAG TGGGATCGGC TTTGCCATCG CCCGACGTCT 600
GGCCCGGGAC GGGGCCCACG TGGTCATCAG CAGCCGGAAG CAGCAGAACG TGGACCGGGC 660
CATGGCCAAG CTGCAGGGGG AGGGGCTGAG TGTGGCGGGC ATTGTGTGCC ACGTGGGGAA 720
GGCTGAGGAC CGGGAGCAGC TGGTGGCCAA GGCCCTGGAG CACTGTGGGG GCGTCGACTT 780
CCTGGTGTGC AGCGCAGGGG TCAACCCTCT GGTAGGGAGC ACTCTGGGGA CCAGTGAGCA 840
GATCTGGGAC AAGATCCTAA GTGTGAACGT GAAGTCCCCA GCCCTGCTGC TGAGCCAGTT 900
GCTGCCCTAC ATGGAGAACA GGAGGGGTGC TGTCATCCTG GTCTCTTCCA TTGCAGCTTA 960
TAATCCAGTA GTGGCGCTGG GTGTCTACAA TGTCAGCAAG ACAGCGCTGC TGGGTCTCAC 1020
TAGAACACTG GCATTGGAGC TGGCCCCCAA GGACATCCGG GTAAACTGCG TGGTTCCAGG 1080
AATTATAAAA ACTGACTTCA GCAAAGTGTT TCATGGGAAT GAGTCTCTCT GGAAGAACTT 1140
CAAGGAACAT CATCAGCTGC AGAGGATTGG GGAGTCAGAG GACTGTGCAG GAATCGTGTC 1200

CTTCCTGTGC TCTCCAGATG CCAGCTACGT CAACGGGGAG AACATTGCGG TGGCAGGCTA 1260
CTCCACTCGG CTCTGAGAGG AGTGGGGGCG GCTGCGTAGC TGTGGTCCCA GCCCAGGAGC 1320
CTGAGGGGGT GTCTAGGTGA TCATTTGGAT CTGGAGCAGA GTCTGCCATT CTGCCAGACT 1380
AGCAATTTGG GGGCTTACTC ATGCTAGGCT TGAGGAAGAA GAAAAACGCT TCGGCATTCT 1440
CC

Seq ID NO: 76 Protein sequence;
Protein Accession #: NP_005785

1 11 21 31 41 51
MLSAVARGYQ GWFHPCARLS VRMSSTGIDR KGVLANRVAV VTGSTSGIGF AIARRLARDG 60
AHVVISSRKQ QNVDRAMAKL QGEGLSVAGI VCHVGKAEDR EQLVAKALEH CGGVDFLVCS 120
AGVNPLVGST LGTSEQIWDK ILSVNVKSPA LLLSQLLPYM ENRRGAVILV SSIAAYNPVV 180
ALGVYNVSKT ALLGLTRTLA LELAPKDIRV NCVVPGIIKT DFSKVFHGNE SLWKNFKEHH 240
QLQRIGESED CAGIVSFLCS PDASYVNGEN IAVAGYSTRL

Seq ID NO: 77 DNA sequence
Nucleic Acid Accession #: NM_002425
Coding sequence: 26-1453 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
AAAGAAGGTA AGGGCAGTGA GAATGATGCA TCTTGCATTC CTTGTGCTGT TGTGTCTGCC 60
AGTCTGCTCT GCCTATCCTC TGAGTGGGGC AGCAAAAGAG GAGGACTCCA ACAAGGATCT 120
TGCCCAGCAA TACCTAGAAA AGTACTACAA CCTCGAAAAG GATGTGAAAC AGTTTAGAAG 180
AAAGGACAGT AATCTCATTG TTAAAAAAAT CCAAGGAATG CAGAAGTTCC TTGGGTTGGA 240
GGTGACAGGG AAGCTAGACA CTGACACTCT GGAGGTGATG CGCAAGCCCA GGTGTGGAGT 300
TCCTGACGTT GGTCACTTCA GCTCCTTTCC TGGCATGCCG AAGTGGAGGA AAACCCACCT 360
TACATACAGG ATTGTGAATT ATACACCAGA TTTGCCAAGA GATGCTGTTG ATTCTGCCAT 420
TGAGAAAGCT CTGAAAGTCT GGGAAGAGGT GACTCCACTC ACATTCTCCA GGCTGTATGA 480
AGGAGAGGCT GATATAATGA TCTCTTTCGC AGTTAAAGAA CATGGAGACT TTTACTCTTT 540
TGATGGCCCA GGACACAGTT TGGCTCATGC CTACCCACCT GGACCTGGGC TTTATGGAGA 600
TATTCACTTT GATGATGATG AAAAATGGAC AGAAGATGCA TCAGGCACCA ATTTATTCCT 660
CGTTGCTGCT CATGAACTTG GCCACTCCCT GGGGCTCTTT CACTCAGCCA ACACTGAAGC 720
TTTGATGTAC CCACTCTACA ACTCATTCAC AGAGCTCGCC CAGTTCCGCC TTTCGCAAGA 780
TGATGTGAAT GGCATTCAGT CTCTCTACGG ACCTCCCCCT GCCTCTACTG AGGAACCCCT 840
GGTGCCCACA AAATCTGTTC CTTCGGGATC TGAGATGCCA GCCAAGTGTG ATCCTGCTTT 900
GTCCTTCGAT GCCATCAGCA CTCTGAGGGG AGAATATCTG TTCTTTAAAG ACAGATATTT 960
TTGGCGAAGA TCCCACTGGA ACCCTGAACC TGAATTTCAT TTGATTTCTG CATTTTGGCC 1020
CTCTCTTCCA TCATATTTGG ATGCTGCATA TGAAGTTAAC AGCAGGGACA CCGTTTTTAT 1080
TTTTAAAGGA AATGAGTTCT GGGCCATCAG AGGAAATGAG GTACAAGCAG GTTATCCAAG 1140
AGGCATCCAT ACCCTGGGTT TTCCTCCAAC CATAAGGAAA ATTGATGCAG CTGTTTCTGA 1200
CAAGGAAAAG AAGAAAACAT ACTTCTTTGC AGCGGACAAA TACTGGAGAT TTGATGAAAA 1260
TAGCCAGTCC ATGGAGCAAG GCTTCCCTAG ACTAATAGCT GATGACTTTC CAGGAGTTGA 1320
GCCTAAGGTT GATGCTGTAT TACAGGCATT TGGATTTTTC TACTTCTTCA GTGGATCATC 1380
ACAGTTTGAG TTTGACCCCA ATGCCAGGAT GGTGACACAC ATATTAAAGA GTAACAGCTG 1440
GTTACATTGC TAGGCGAGAT AGGGGGAAGA CAGATATGGG TGTTTTTAAT AAATCTAATA 1500
ATTATTCATC TAATGTATTA TGAGCCAAAA TGGTTAATTT TTCCTGCATG TTCTGTGACT 1560
GAAGAAGATG AGCCTTGCAG ATATCTGCAT GTGTCATGAA GAATGTTTCT GGAATTCTTC 1620
ACTTGCTTTT GAATTGCACT GAACAGAATT AAGAAATACT CATGTGCAAT AGGTGAGAGA 1680
ATGTATTTTC ATAGATGTGT TATTACTTCC TCAATAAAAA GTTTTATTTT GGGCCTGTTC 1740
CTT

Seq ID NO: 78 Protein sequence;
Protein Accession #: NP_002416

1 11 21 31 41 51
MHLAPLVLLC LPVCSAYPLS GAAKEEDSNK DLAQQYLEKY YNLEKDVKQF RRKDSNLIVK 60
KIQGMQKPLG LEVTGKLDTD TLEVMRKPRC GVPDVGIGFS FPGMPKWRKT HLTYRIVNYT 120
PDLPRDAVDS AIEKALKVWE EVTPLTFSRL YEGEADIMIS FAVKEHGDFY SFDGPGHSLA 180
HAYPPGPGLY GDIHFDDDEK WTEDASGTNL FLVAAHELGH SLGLFHSANT EALMYPLYNS 240
FTELAQFRLS QDDVNGIQSL YGPPPASTEE PLVPTKSVPS GSEMPAKCDP ALSFDAISTL 300
RGEYLFFKDR YFWRRSHWNP EPEFHLISAF WPSLPSYLDA AYEVNSRDTV FIFKGNEFWA 360
IRGNEVQAGY PRGIHTLGFP PTIRKIDAAV SDKEKKKTYF FAADKYWRFD ENSQSMEQGF 420
PRLIADDFPG VEPKVDAVLQ AFGFFYFFSG SSQFEFDPNA RMVTHILKSN SWLHC

Seq ID NO: 79 DNA sequence
Nucleic Acid Accession #: NM_000493.1
Coding sequence: 1-2043 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
ATGCTCCCAC AAATACCCTT TTTGCTGCTA GTATCCTTGA ACTTGGTTCA TGGAGTGTTT 60
TACGCTGAAC GATACCAAAC GCCCACAGGC ATAAAAGGCC CACTACCCAA CACCAAGACA 120

CAGTTCTTCA TTCCCTACAC CATAAAGAGT AAAGGTATAG CAGTAAGAGG AGAGCAAGGT 180
ACTCCTGGTC CACCAGGCCC TGCTGGACCT CGAGGGCACC CAGGTCCTTC TGGACCACCA 240
GGAAAACCAG GCTACGGAAG TCCTGGACTC CAAGGAGAGC CAGGGTTGCC AGGACCACCG 300
GGACCATCAG CTGTAGGGAA ACCAGGTGTG CCAGGACTCC CAGGAAAACC AGGAGAGAGA 360
GGACCATATG GACCAAAAGG AGATGTTGGA CCAGCTGGCC TACCAGGACC CCGGGGCCCA 420
CCAGGACCAC CTGGAATCCC TGGACCGGCT GGAATTTCTG TGCCAGGAAA ACCTGGACAA 480
CAGGGACCCA CAGGAGCCCC AGGACCCAGG GGCTTTCCTG GAGAAAAGGG TGCACCAGGA 540
GTCCCTGGTA TGAATGGACA GAAAGGGGAA ATGGGATATG GTGCTCCTGG TCGTCCAGGT 600
GAGAGGGGTC TTCCAGGCCC TCAGGGTCCC ACAGGACCAT CTGGCCCTCC TGGAGTGGGA 660
AAAAGAGGTG AAAATGGGGT TCCAGGACAG CCAGGCATCA AAGGTGATAG AGGTTTTCCG 720
GGAGAAATGG GACCAATTGG CCCACCAGGT CCCCAAGGCC CTCCTGGGGA ACGAGGGCCA 780
GAAGGCATTG GAAAGCCAGG AGCTGCTGGA GCCCCAGGCC AGCCAGGGAT TCCAGGAACA 840
AAAGGTCTCC CTGGGCCTCC AGGAATAGCT GGGCCCCCAG GGCCTCCTGG CTTTGGGAAA 900
CCAGGCTTGC CAGGCCTGAA GGGAGAAAGA GGACCTGCTG GCCTTCCTGG GGGTCCAGGT 960
GCCAAAGGGG AACAAGGGCC AGCAGGTCTT CCTGGGAAGC CAGGTCTGAC TGGACCCCCT 1020
GGGAATATGG GACCCCAAGG ACCAAAAGGC ATCCCGGGTA GCCATGGTCT CCCAGGCCCT 1080
AAAGGTGAGA CAGGGCCAGC TGGCCTGCA GGATACCCTG GGGCTAAGGG TGAAAGGGGT 1140
TCCCCTGGGT CAGATGGAAA ACCAGGGTAC CCAGGAAAAC CAGGTCTCGA TGGTCCTAAG 1200
GGTAACCCAG GGTTACCAGG TCCAAAAGGT GATCCTGGAG TTGGAGGACC TCCTGGTCTC 1260
CCAGGCCCTG TGGGCCCAGC AGGAGCAAAG GGAATGCCCG GACACAATGG AGAGGCTGGC 1320
CCAAGAGGTG CCCCTGGAAT ACCAGGTACT AGAGGCCCTA TTGGGCCACC AGGCATTCCA 1380
GGATTCCCTG GGTCTAAAGG GGATCCAGGA AGTCCCGGTC CTCCTGGCCC AGCTGGCATA 1440
GCAACTAAGG GCCTCAATGG ACCCACCGGG CCACCAGGGC CTCCAGGTCC AAGAGGCCCC 1500
TCTGGAGAGC CTGGTCTTCC AGGGCCCCCT GGGCCTCCAG GCCCACCAGG TCAAGCAGTC 1560
ATGCCTGAGG GTTTTATAAA GGCAGGCCAA AGGCCCAGTC TTTCTGGGAC CCCTCTTGTT 1620
AGTGCCAACC AGGGGGTAAC AGGAATGCCT GTGTCTGCTT TTACTGTTAT TCTCTCCAAA 1680
GCTTACCCAG CAATAGGAAC TCCCATACCA TTTGATAAAA TTTTGTATAA CAGGCAACAG 1740
CATTATGACC CAAGGACTGG AATCTTTACT TGTCAGATAC CAGGAATATA CTATTTTTCA 1800
TACCACGTGC ATGTGAAAGG GACTCATGTT TGGGTAGGCC TGTATAAGAA TGGCACCCCT 1860
GTAATGTACA CCTATGATGA ATACACCAAA GGCTACCTGG ATCAGGCTTC AGGGAGTGCC 1920
ATCATCGATC TCACAGAAAA TGACCAGGTG TGGCTCCAGC TTCCCAATGC CGAGTCAAAT 1980
GGCCTATACT CCTCTGAGTA TGTCCACTCC TCTTTCTCAG GATTCCTAGT GGCTCCAATG 2040
TGAGTACACC CCACAGAGCT AATCTAAATC TTGTGCTAGA AAAAGCATTC TCTAACTCTA 2100
CCCCACCCTA CAAAATGCAT ATGGAGGTAG GCTGAAAAGA ATGTAATTTT TATTTCTGA 2160
AATACAGATT TGAGCTATCA GACCAACAAA CCTTCCCCCT GAAAAGTGAG CAGCAACGTA 2220
AAAACGTATG TGAAGCCTCT CTTGAATTTC TAGTTAGCAA TCTTAAGGCT CTTTAAGGTT 2280
TTCTCCAATA TTAAAAAATA TCACCAAAGA AGTCCTGCTA TGTTAAAAAC AAACAACAAA 2340
AAACAAAGCA ACAAAAAAAA AAATTAAAAA AAAAAACAGA AATAGAGCTC TAAGTTATGT 2400
GAAATTTGAT TTGAGAAACT CGGCATTTCC TTTTTAAAAA AGCCTGTTTC TAACTATGAA 2460
TATGAGAACT TCTAGGAAAC ATCCAGGAGG TATCATATAA CTTTGTAGAA CTTAAATACT 2520
TGAATATTCA AATTTAAAAG ACACTGTATC CCCTAAAATA TTTCTGATGG TGCACTACTC 2580
TGAGGCCTGT ATGGCCCCTT TCATCAATAT CTATTCAAAT ATACAGGTGC ATATATACTT 2640
GTTAAAGCTC TTATATAAAA AAGCCCCAAA ATATTGAAGT TCATCTGAAA TGCAAGGTGC 2700
TTTCATCAAT GAACCTTTTC AAAACTTTTC TATGATTGCA GAGAAGCTTT TTATATAGCC 2760
AGCATAACTT GGAAACAGGT ATCTGACCTA TTCTTATTTA GTTAACACAA GTGTGATTAA 2820
TTTGATTTCT TTAATTCCTT ATTGAATCTT ATGTGATATG ATTTTCTGGA TTTACAGAAC 2880
ATTAGCACAT GTACCTTGTG CCTCCCATTC AAGTGAAGTT ATAATTTACA CTGAGGGTTT 2940
CAAAATTCGA CTAGAAGTGG AGATATATTA TTTATTTATG CACTGTACTG TATTTTTATA 3000
TTGCTGTTTA AAACTTTTAA GCTGTGCCTC ACTTATTAAA GCACAAAATG TTTTACCTAC 3060
TCCTTATTTA CGACACAATA AAATAACATC AATAGATTTT TAGGCTGAAT TAATTTGAAA 3120
GCAGCAATTT GCTGTTCTCA ACCATTCTTT CAAGGCTTTT CATTCGACAC AATAAAATAA 3180
CATCAATAGA TTTTTAGG

Seq ID NO: 80 Protein sequence;
Protein Accession #: NP_000484.1

1 11 21 31 41 51
MLPQIPFLLL VSLNLVHGVP YAERYQTPTG IKGPLPNTKT QPFIPYTDKS KGIAVRQEQG 60
TPGPPGPAGP RGHPGPSGPP GKPGYGSPGL QGEPGLPGPP GPSAVGKPGV PGLPGKPGER 120
GPVGPKGDVG PAGLPGPRGP PGPPGIPGPA GISVPGKPGQ QGPTGAPGPR GFPGEKGAPG 180
VPGMNGQKGE MGYGAPGRPG ERGLPGPQGP TGPSGPPGVG KRGENGVPGQ PGIKGDRGFP 240
GEMGPIGPPG PQGPPGERGP EGIGKPGAAG APQQPGIPGT KGLPGAPGIA GPPGPPGFGK 300
PGLPGLKGER GPAGLPGIPG AKGEQGPAGL PGKPGLTGPP GNMGPQGPKG EPGSHGLPGP 360
KGETGPAGPA GYPGAKGERG SPGSDGKPGY PGKPGLDGPK GNPGLPGPKG DPGVGGPPGL 420
PGPVGPAGAK GMPGHNGEAG PRGAPGIPGT RGPIGPPGIP GFPGSKGDPG SPGPPGPAGI 480
ATKGLNGPTG PPGPPGPRGP SGEPGLPGPP GPPGPPGQAV MPEGFIKAQQ RPSLSGTPLV 540
SANQGVTGMP VSAFTVILSK AYPAIGTPIP FDKILYNRQQ HVDPRTGFT CQIPGIYYFS 600
YHVHVKGTHV WVGLYKNGTP VMYTYDEYTK GYLDQASGSA IIDLTENDQV WLQLPNAESN 660
GLYSSEYVHS SFSGFLVAPM .

Seq ID NO: 81 DNA sequence
Nucleic Acid Accession #: NM_000786
Coding sequence: 332-1861 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51

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CGCGATTCTC AGGGATTGAT CCGCCTCTTC AGGTAAGTTA TCTTCCGGCC CCGTACCACT  60
GTGCCACAGG CGCAGCCCGC TTCCTCAGGT GCCCTATCCC GCGCAGAAGA CCACGGCTTC  120
ACAGAGTGTT ATTTAAGGGC GTGGCCAGCG GAACATCCCG CCCCATTCTG TGACGCACGG  180
GGTGGCGCGC GTGGGACCCG AGGGGTGGGG CTGGGTTTAG TAGGAGACCT GGGGCAAGGC  240
CCCCTGTGGA CGACCATCTG CCAGCTTCTC TCGTTCCGTC GATTGGGAGG AGCGGTGGCG  300
ACCTCGGCCT TCAGTGTTTC CGACGGAGTG AATGCGGCCG GCGGCTGGGA TGCTGCTGCT  360
GGGCTTGCTG CAGGCGGGTG GGTCGGTGCT GGGCCAGGCG ATGGAGAAGG TGACAGGCGG  420
CAACCTCTTG TCCATGCTGC TGATCGCCTG CGCCTTCACC CTCAGCCTGG TCTACCTGAT  480
CGGTCTGGCC GCCGGCCACC TGGTCCAGCT GCCCGCAGGG GTGAAAAGTC CTCCATACAT  540
TTTCTCCCCA ATTCCATTCC TTGGGCATGC CATAGCATTT GGGAAAAGTC CAATTGAATT  600
TCTAGAAAAT GCATATGAGA AGTATGGACC TGTATTTAGT TTTACCATGG TAGGCAAGAC  660
ATTTACTTAC CTTCTGGGGA GTGATGCTGC TGCACTGCTT TTTAATAGTA AAAATGAAGA  720
CCTGAATGCA GAAGATGTCT ACAGTCGCCT GACAACACCT GTGTTTGGGA AGGGAGTTGC  780
ATACGATGTG CCTAATCCAG TTTTCTTGGA GCAGAAGAAA ATGTTAAAAA GTGGCCTTAA  840
CATAGCCCAC TTTAAACAGC ATGTTTCTAT AATTGAAAAA GAAACAAAGG AATACTTTGA  900
GAGTTGGGGA GAAAGTGGAG AAAAAAATGT GTTTGAAGCT CTTTCTGAGC TCATAATTTT  960
AACAGCTAGC CATTGTTTGC ATGGAAAGGA AATCAGAAGT CAACTCAATG AAAAGGTAGC  1020
ACAGCTGTAT GCAGATTTGG ATGGAGGTTT CAGCCATGCA GCCTGGCTCT TACCAGGTTG  1080
GCTGCCTTTG CCTAGTTTCA GACGCAGGGA CAGAGCTCAT CGGGAAATCA AGGATATTTT  1140
CTATAAGGCA ATCCAGAAAC GCAGACAGTC TCAAGAAAAA ATTGATGACA TTCTCCAAAC  1200
TTTACTAGAT GCTACATACA AGGATGGGCG TCCTTTGACT GATGATGAAG TAGCAGGGAT  1260
GCTTATTGGA TTACTCTTGG CAGGGCAGCA TACATCCTCA ACTACTAGTG CTTGGATGGG  1320
CTTCTTTTTG GCCAGAGACA AAACACTTCA AAAAAAATGT TATTTAGAAC AGAAAACAGT  1380
CTGTGGAGAG AATCTGCCTC CTTTAACTTA TGACCAGCTC AAGGATCTAA ATTTACTTGA  1440
TCGCTGTATA AAAGAAACAT TAAGACTTAG ACCTCCTATA ATGATCATGA TGAGAATGGC  1500
CAGAACTCCT CAGACTGTGG CAGGGTATAC CATTCCTCCA GGACATCAGG TGTGTGTTTC  1560
TCCCACTGTC AATCAAAGAC TTAAAGACTC ATGGGTAGAA CGCCTGGACT TTAATCCTGA  1620
TCGCTACTTA CAGGATAACC CAGCATCAGG GGAAAAGTTT GCCTATGTGC CATTTGGAGC  1680
TGGGCGTCAT CGTTGTATTG GGGAAAATTT TGCCTATGTT CAAATTAAGA CAATTTGGTC  1740
CACTATGCTT CGTTTATATG AATTTGATCT CATTGATGGA TACTTTCCCA CTGTGAATTA  1800
TACAACTATG ATTCACACCC CTGAGAACCC AGTTATCCGT TACAAACGAA GATCAAAATG  1860
AAAAAGGTTG CAAGGAACGA ATATATGTGA TTATCACTGT AAGCCACAAA GGCATTCGAA  1920
GAGAATGAAG TGTACAAAAC AACTCTTGTA GTTTACTGTT TTTTTAAGTG TGTAATTCTA  1980
AAAGCCAGTT TATGATTTAG GATTTTGTTA ACTGAATGGT TCTATCAAAT ATAATAGCAT  2040
TTGACACATT TTCTAATAGT TATGATACTT ATACATGTGC TTTCAGGAAG TTCCTTGGTG  2100
AAACAATTGT TGAGGGGGGA TCTAGGTAAT TGGCAGATTC TAAATAATAT AATTTCCAGA  2160
TAGTAATTTT AAGAGTACTC ATCGCTCTTG CCAAATAAGT TCAGGGTATT CAAATCTTGG  2220
ACTAGTCCTG CAAGGTATAA AGAATAAAAA TCCCAGTGAG ATACTTGGAA ACCACAGTTT  2280
ATTATTATTT ATCTGGGCAA TTATTGTGTG TGTGAGGATG GAAGGGTAGG GAATAATCGA  2340
ACATCTAAAG CCTTGAATAA GAGAATACTA ATTGTTTTGG TATGATGATA CTCAGAAATG  2400
GAGATATTAT AGGAAAAAGA AATCCTTTGG AATTTTAACT AAAATCACTG CATATGGGAA  2460
ATTAAGAGAT CCAGGACCAT ATTTGATAAG AGTTCCTAAA AATAATGTAA TTATTAATGC  2520
TAAAGACTGC TCATGTATCT TGATCTAATT ACTAAATAAA TTACATATTT ATTTACCTGA  2580
TAAATATGTA TCTAGTTCTA CAAGGTCACA TTTATGTGGA AGTCCAAAGT CAAGTCCTTA  2640
GGGGATAATT TTGTTTTGGG CTCAGTTGTT CCCTGCTTCC TTTTTTTTTT TTTTTTTTTT  2700
TTGAGATGGA GTCTCGCTCT GTTGCCCAGG CTGGAGTGCA GTGGTGCGAT CTCAGCTCAC  2760
TGCATCCTCT GCCTCCCGGG TTCAAGCAAT TCTCTGCCTC AGCCTCCCAA GTAGTTGGGA  2820
TTACAGGCAC CTGCCACCAT GCCTGGCTAA TTTTTTGTAT TTTTAGTAGA GACGGGGTTT  2880
TCACTATGTT GGCTAGGCTG GTCTTGAACT CCTGAGCCTC GTGAGTCCAC CCGCCTTGGC  2940
CTCCCAAAGT GCTGGGATTA CAGGCATGAG CCACCGCACC TGGCCTTCCC TGCTTCCTCT  3000
CTAGAATCCA ATTAGGGATG TTTGTTACTA CTCATATTGA TTAAAACAGT TAACAAACTT  3060
TTTTCTTTTT AAAATGTGAG ATCAGTGAAC TCTGGTTTTA AGATAATCTG AAACAAGGTC  3120
CTTGGGAGTA ATAAAATTGG TCACATTCTG TAAAGCACAT TCTGTTTAGG AATCAACTTA  3180
TCTCAAATTG TAACTCGGGG CCTAACTATA TGAGATGGCT GAAAAAATAC CACATCGTCT  3240
GTTTTCACTA GGTGATGCCA AAATATTTTG CTTTATGTAT ATTACAGTTC TTTTTAAAAC  3300
ACTGGAAGAC TCATGTTAAA CTCTAATTGT GAAGGCAGAA TCTCTGCTAA TTTTTCAGAT  3360
TAAAATTCTC TTTGAAAAAA T
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Seq ID NO: 82 Protein sequence:
Protein Accession #: NP_000777

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1    11   21   31   41   51
|    |    |    |    |    |
MAAAAGMLLL GLLQAGGSVL GQAMEKVTGG NLLSMLLIAC AFTLSLVYLI RLAAGHLVQL  60
PAQVKSPPYI FSPIPFLGHA IAFGKSPIEF LENAYEKYGP VFSFTMVGKT FTYLLGSDAA  120
ALLFNSKNED LNARDVYSRL TTPVFGKGVA YDVPNPVFLE QKKMLKSGLN IAHFKQHVSI  180
IEKETKEYFE SWGESGEKNV FEALSELIIL TASICLHGKE IRSQLNEKVA QLYADLDGGF  240
SHAAWLLPGW LPLPSFRRRD RAHREIKDIF YKAIQKRRQS QEKIDDILQT LLDATYKDGR  300
PLTDDEVAGM LIGLLLAGQH TSSTTSAWMG FFLARDKTLQ KKCYLEQKTV CGENLPPLTY  360
DQLKDLNLLD RCIKETLRLR PPIMIMMRMA RTPQTVAGYT IPPGHQVCVS PTVNQRLKDS  420
WVERLDFNPD RYLQDNPASG EKFAYVPFGA GRHRCIGENF AYVQIKTIWS TMLRLYEFDL  480
IDGYFPTVNY TTMIHTPENP VIRYKRRSK
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Seq ID NO: 83 DNA sequence
Nucleic Acid Accession #: NM_006551.2
Coding sequence: 64-336 (underlined sequences correspond to start and stop codons)


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1    11   21   31   41   51
|    |    |    |    |    |
AATTCTAGAA GTCCAAATCA CTCATTGTTT GTGAAAGCTG AGCTCACAGC AAAACAAGCC  60
ACCATGAAGC TGTCGGTGTG TCTCCTGCTG GTCACGCTGG CCCTCTGCTG CTACCAGGGC  120
AATGCCGAGT TCTGCCCAGC TCTTGTTTCT GAGCTGTTAG ACTTCTTCTT CATTAGTGAA  180
CCTCTGTTCA AGTTAAGTCT TGCCAAATTT GATGCCCCTC CGGAAGCTGT TGCAGCCAAG  240
TTAGGAGTGA AGAGATGCAC GGATCAGATG TCCCTTCAGA AACGAAGCCT CATTGCGGAA  300
GTCCTGGTGA AAATATTGAA GAAATGTAGT GTGTGACATG TAAAAACTTT CATCCTGGTT  360
TCCACTGTCT TTCAATGACA CCCTGATCTT CACTGCAGAA TGTAAAGGTT TCAACGTCTT  420
GCTTTAATAA ATCACTTGCT CTAC
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Seq ID NO: 84 Protein sequence:
Protein Accession #: NP_006542.1

```
1    11   21   31   41   51
|    |    |    |    |    |
MKLSVCLLLV TLALCCYQAN AEFCPALVSE LLDFFFISEP LFKLSLAKFD APPEAVAAKL  60
GVKRCTDQMS LQKRSLIAEV LVKILKKCSV
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Seq ID NO: 85 DNA sequence
Nucleic Acid Accession #: NM_002317.1
Coding sequence: 231-1484 (underlined sequences correspond to start and stop codons)

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1    11   21   31   41   51
|    |    |    |    |    |
GGGCCAGGAC TGAGAAAGGG GAAAGGGAAG GGTGCCACGT CCGAGCAGCC GCCTTGACTG  60
GGGAAGGGTC TGAATCCCAC CCTTGGCATT GCTTGGTGGA GACTGAGATA CCCGTGCTCC  120
GCTCGCCTCC TTGGTTGAAG ATTTCTCCTT CCCTCACGTG ATTTGAGCCC CGTTTTTATT  180
TTCTGTGAGC CACGTCCTCC TCGAGCGGGG TCAATCTGGC AAAAGGAGTG ATGCGCTTCG  240
CCTGGACCGT GCTCCTGCTC GGGCCTTTGC AGCTCTGCGC GCTAGTGCAC TGCGCCCCTC  300
CCGCCGCCGG CCAACAGCAG CCCCCGCGCG AGCCGCCGGC GGCTCCGGGC GCCTGGCGCC  360
AGCAGATCCA ATGGGAGAAC AACGGCAGG TGTTCAGCTT GCTGAGCCTG GGCTCACAGT  420
ACCAGCCTCA GCGCCGCCGG GACCCGGGCG CCGCCGTCCC TGGTGCAGCC AACGCCTCCG  480
CCCAGCAGCC CCGCACTCCG ATCCTGCTGA TCCGCGACAA CCGCACCGCC GCGGGGCGAA  540
CGCGGACGGC CGGCTCATCT GGAGTCACCG CTGGCCGCCC CAGGCCCACC GCCCGTCACT  600
GGTTCCAAGC TGGCTACTCG ACATCTAGAG CCCGCGAAGC TGGGCCCTCG CGCGCGGAGA  660
ACCAGACAGC GCCGGGAGAA GTTCCTGCTC TCAGTAACCT GCGGCCGCCC AGCCGCGTGG  720
ACGGCATGGT GGGCGACGAC CCTTACAACC CCTACAAGTA CTCTGACGAC AACCCTTATT  780
ACAACTACTA CGATACTTAT GAAAGGCCCA GACCTGGGGG CAGGTACCGG CCCGGATACG  840
GCACTGGCTA CTTCCAGTAC GGTCTCCCAG ACCTGGTGGC CGACCCCTAC TACATCCAGG  900
CGTCCACGTA CGTGCAGAAG ATGTCCATGT ACAACCTGAG ATGCGCGGCG GAGGAAAACT  960
GTCTGGCCAG TACAGCATAC AGGGCAGATG TCAGAGATTA TGATCACAGG GTGCTGCTCA  1020
GATTTCCCCA AAGAGTGAAA AACCAAGGGA CATCAGATTT CTTACCCAGC CGACCAAGAT  1080
ATTCCTGGGA ATGGCACAGT TGTCATCAAC ATTACCACAG TATGGATGAG TTTAGCCACT  1140
TGTACCTGCT TGATGCCAAC ACCCAGAGGA GATGGGCTGA AGGCCACAAA GCAAGTTTCT  1200
GTCTTGAAGA CACATCCTGT GACTATGGCT ACCACAGGCG ATTTGCATGT ACTGCACACA  1260
CACAGGGATT GAGTCCTGGC TGTTATGATA CCTATGGTGC AGACATAGAC TGCCAGTGGA  1320
TTGATATTAC AGATGTAAAA CCTGGAAACT ATATCCTAAA GGTCAGTGTA AACCCCAGCT  1380
ACCTGGTTCC TGAATCTGAC TATACCAACA ATGTTGTGCG CTGTGACATT CGCTACACAG  1440
GACATCATGC GTATGCCTCA GGCTGCACAA TTTCACCGTA TTAGAAGGCA AAGCAAAACT  1500
CCCAATGGAT AAATCAGTGC CTGGTGTTCT GAAGTGGGAA AAAATAGACT AACTTCAGTA  1560
GGATTTATGT ATTTTGAAAA AGAGAACAGA AAACAACAAA AGAATTTTTG TTTGGACTGT  1620
TTTCAATAAC AAAGCACATA ACTGGATTTT GAACGCTTAA GTCATCATTA CTTGGGAAAT  1680
TTTTAATGTT TATTATTTAC ATCACTTTGT GAATTAACAC AGTGTTTCAA TTCTGTAATT  1740
ACATATTTGA CTCTTTCAAA AAAAAAAAAA AAAAAAAAAA
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Seq ID NO: 86 Protein sequence:
Protein Accession #: NP_002308.1

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1    11   21   31   41   51
|    |    |    |    |    |
MRFAWTVLLL GPLQLCALVH CAPPAAGQQQ PPREPPAAPG AWRQQIQWEN NGQVFSLLSL  60
GSQYQPQRRR DPGAAVPGAA NASAQQPRTP ILLIRDNRTA AGRTRTAGSS GVTAGRPRPT  120
ARHWFQAGYS TSRAREAGPS RAENQTAPGE VPALSNLRPP SRVDGMVGDD PYNPYKYSDD  180
NPYYNYYDTY ERPRPGGRYR PGYGTGYFQY GLPDLVADPY YIQASTYVQK MSMYNLRCAA  240
EENCLASTAY RADVRDYDHR VLLRFPQRVK NQGTSDFLPS RPRYSWEWHS CHQHYHSMDE  300
PSHLVLLDAN TQRRWAEGHK ASPCLEDTSC DYGVHRRFAC TAHTQGLSPG CYDTYGADID  360
CQWIDITDVK PGNYILKVSV NPSYLVPESD YTNNVVRCDI RYTGHHAYAS GCTISPY
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Seq ID NO: 87 DNA sequence
Nucleic Acid Accession #: NM_006419.1
Coding sequence: 91-420 (underlined sequences correspond to start and stop codons)

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1    11   21   31   41   51
|    |    |    |    |    |
TTCGGCACTT GGGAGAAGAT GTTTGAAAAA ACTGACTCTG CTAATGAGCC TGGACTCAGA  60
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GCTCAAGTCT GAACTCTACC TCCAGACAGA ATGAAGTTCA TCTCGACATC TCTGCTTCTC 120
ATGCTGCTGG TCAGCAGCCT CTCTCCAGTC CAAGGTGTTC TGGAGGTCTA TTACACAAGC 180
TTGAGGTGTA GATGTGTCCA AGAGAGCTCA GTCTTTATCC CTAGACGCTT CATTGATCGA 240
ATTCAAATCT TGCCCCGTGG GAATGGTTGT CCAAGAAAAG AAATCATAGT CTGGAAGAAG 300
AACAAGTCAA TTGTGTGTGT GGACCCTCAA GCTGAATGGA TACAAAGAAT GATGGAAGTA 360
TTGAGAAAAA GAAGTTCTTC AACTCTACCA GTTCCAGTGT TTAAGAGAAA GATTCCCTGA 420
TGCTGATATT TCCACTAAGA ACACCTGCAT TCTTCCCTTA TCCCTGCTCT GGATTTTAGT 480
TTTGTGCTTA GTTAAATCTT TTCCAGGGAG AAAGAACTTC CCCATACAAA TAAGGCATGA 540
GGACTATGTG AAAAATAACC TTGCAGGAGC TGATGGGGCA AACTCAAGCT TCTTCACTCA 600
CAGCACCCTA TATACACTTG GAGTTTGCAT TCTTATTCAT CAGGGAGGAA AGTTTCTTTG 660
AAAATAGTTA TTCAGTTATA AGTAATACAG GATTATTTTG ATTATATACT TGTTGTTTAA 720
TGTTTAAAAT TTCTTAGAAA ACAATGGAAT GAGAATTTAA GCCTCAAATT TGAACATGTG 780
GCTTGAATTA AGAAGAAAAT TATGGCATAT ATTAAAAGCA GGCTTCTATG AAAGACTCAA 840
AAAGCTGCCT GGGAGGCAGA TGGAACTTGA GCCTGTCAAG AGGCAAAGGA ATCCATGTAG 900
TAGATATCCT CTGCTTAAAA ACTCACTACG GAGGAGAATT AAGTCCTACT TTTAAAGAAT 960
TTCTTTATAA AATTTACTGT CTAAGATTAA TAGCATTCGA AGATCCCCAG ACTTCATAGA 1020
ATACTCAGGG AAAGCATTTA AAGGGTGATG TACACATGTA TCCTTTCACA CATTTGCCTT 1080
GACAAACTTC TTTCACTCAC ATCTTTTTCA CTGACTTTTT TTGTGGGGGC GGGGCCGGGG 1140
GGACTCTGGT ATCTAATTCT TTAATGATTC CTATAAATCT AATGACATTC AATAAAGTTG 1200
AGCAAACATT TTACTT

Seq ID NO: 88 Protein sequence:
Protein Accession #: NP_006410.1

1 11 21 31 41 51
MKFISTSLLL MLLVSSLSPV QGVLEVYYTS LRCRCVQESS VFIPRRFIDR IQILPRGNGC 60
PRKEIIVWKK NKSIVCVDPQ AEWIQRMMEV LRKRSSSTLP VPVFKRKIP

Seq ID NO: 89 DNA sequence
Nucleic Acid Accession #: NM_002652
Coding sequence: 37-477 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
CTTCTCTGGG ACACATTGCC TTCTGTTTTC TCCAGCATGC GCTTGCTCCA GCTCCTGTTC 60
AGGGCCAGCC CTGCCACCCT GCTCCTGGTT CTCTGCCTGC AGTTGGGGGC CAACAAAGCT 120
CAGGACAACA CTCGGAAGAT CATAATAAAG AATTTTGACA TTCCCAAGTC AGTACGTCCA 180
AATGACGAAG TCACTGCAGT GCTTGCAGTT CAAACAGAAT TGAAAGAATG CATGGTGGTT 240
AAAACTTACC TCATTAGCAG CATCCCTCTA CAAGGTGCAT TTAACTATAA GTATACTGCC 300
TGCCTATGTG ACGACAATCC AAAAACCTTC TACTGGGACT TTTACACCAA CAGAACTGTG 360
CAAATTGCAG CCGTCGTTGA TGTTATTCGG GAATTAGGCA TCTGCCCTGA TGATGCTGCT 420
GTAATCCCCA TCAAAAACAA CCGGTTTTAT ACTATTGAAA TCCTAAAGGT AGAATAATGG 480
AAGCCCTGTC TGTTTGCCAC ACCCAGGTGA TTTCCTCTAA AGAAACTTGG CTGGAATTTC 540
TGCTGTGGTC TATAAAATAA ACTTCTTAAC ATGCTT

Seq ID NO: 90 Protein sequence:
Protein Accession #: NP_002643.1

1 11 21 31 41 51
MRLLQLLFRA SPATLLLVLC LQLGANKAQD NTRKIIIKNF DIPKSVRPND EVTAVLAVQT 60
ELKECMVVKT YLISSIPLQG AFNYKYTACL CDDNPKTFYW DFYTNRTVQI AAVVDVIREL 120
GICPDDAAVI PIKNNRFYTI EILKV

Seq ID NO: 91 DNA sequence
Nucleic Acid Accession #: AK000341
Coding sequence: 85-975 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
GATAGCGCCG GGCAGAGGGA CCCGGCTACC CTGGACAGCG CATCGCCGCC CGCCCGGGTC 60
GCCGCGCCAC AGCCGCTGCG GATCATGGAA CATCTAAAGG CCTTTGATGA TGAAATCAAT 120
GCTTTTTTGG ACAATATGTT TGGACCGCGA GATTCTCGAG TCAGAGGGTG GTTCACGTTG 180
GACTCTTACC TTCCTACCTT TTTTCTTACT GTCATGTATC TGCTCTCAAT ATGGCTGGGT 240
AACAAGTATA TGAAGAACAG ACCTGCTCTT TCTCTCAGGG GTATCCTCAC CTTGTATAAT 300
CTTGGAATCA CACTTCTCTC CGCGTACATG CTGGCAGAGC TCATTCTCTC CACTTGGGAA 360
GGAGGCTACA ACTTACAGTG TCAAGATCTT ACCAGCGCAG GGGAAGCTGA CATCCGGGTA 420
GCCAAGGTGC TTTGGTGGTA CTATTTCTCC AAATCAGTAG AGTTCCTGGA CACAATTTTC 480
TTCGTTTTGC GGAAAAAAAC GAGTCAGATT ACTTTTCTTC ATGTATATCA TCATGCTTCT 540
ATGTTTAACA TCTGGTGGTG TGTCTTGAAC TGGATACCTT GTGGACAAAG TTTCTTTGGA 600
CCAACACTGA ACAGTTTTGT CCACATTCTT ATGTACTCCT ACTATGGACT TTCTGTGTTT 660
CCATCTATGC ACAAGTATCT TTGGTGGAAG AAATATCTCA CACAGGCTCA GCTGGTGCAG 720
TTCGTGCTCA CCATCACGCA CACCATGAGC GCCGTCGTGA AACCGTGTGG CTTCCCCTTC 780
GGTTGTCTCA TCTTCCAGTC ATCTTATATG CTAACGTTAG TCATCCTCTT CTTAAATTTT 840
TATGTTCAGA CATACCGAAA AAAGCCAATG AAGAAAGATA TGCAAGAGCC ACCTGCAGGG 900
AAAGAAGTGA AGAATGGTTT TTCCAAAGCC TACTTCACTG CAGCAAATGG AGTGATGAAC 960

AAGAAAGCAC AATAAAAATG AGTAACAGAA AAAGCACATA TACTAGCCTA ACAGATTGGC 1020
TTGTTTTAAA GCAAAGACTG AATTGAAGGT TACATGTTTT AGGATAAACT AATTTCTTTT 1080
GAGTTCATAA ATCATTTGTA CCCAGAATGT ATTAATATAT TGCTATTAGG TTAATCTGTT 1140
AACTGAATGC TTTGATCAGC ATTGAGGTGA TGCTCACCTC CGAGGACCTC AGAACTGGTG 1200
CAGCTTCTCT CTCCCTCCCT CCCACAGACT GAACCTTTCG CCAGAAGCTG TCCTTATAAC 1260
GCCTTATACG CATACACAGC CAGGAAACGT GGAGCATTGT TTCTCACAGA GAGTCTCCAA 1320
ATAAAAAGGG TTTTGTTCAG ATTAAAATGT TTACAACAAA ATGTTAATTA TATTCTAAAT 1380
ACAGGGTATG TTCTAATCTA TATTAAGCAA TAATGCCAGT GCATAATCAT TCCATTTGTT 1440
CCTTTAGCAA TCAACCCCAG AAAATATTAA AATGGGATCA TACACAGAAG ATAGAAAAAT 1500
CTAGCAAAAC TTCTCTTTCT GTAAGCCAGA GTCTTGTCTA TCAGATTCCC ACAACCACTC 1560
CTGATTCTAA ATTTAGTGAT ATGGTAATGA AATTGGTATT TATTTTAAAT ATTAGTTATT 1620
CTAAGGAGAA AAAAATGCTT CTGCAAGATT TTCATAATTC AGGGGCTGTG GATAGGATTG 1680
TTCCTCTGTT TCCCTAATCA TTCATCTGTT CATGTCTCCC TCTTGTGCCA GTCAGCCTAG 1740
GTTATACAGA TGCCATGCTC CACACCACGA GCAGTGTACA AATCTGGCTG CCCGTTTACT 1800
TTCTGAGCAA GCACTGGAGT CCACTCCGAC CTTTTTCTTT GAACATGCAT GCTGCTGCAA 1860
TATGTATAAA TCAGAACTAG CAGAAGTAGC AGAGTGATGG GAGCAAAATA GGCACTGAAT 1920
TCGTCAACTC TTTTTTGTGA GCCTACTTGT GAATATTACC TCAGATACCT GTTGTCACTC 1980
TTCACAGGTT ATTTAAGTTC TTGAAGCTGG GAGGAAAAAG ATGGAGTAGC TTGGAAAGAT 2040
TCCAGCACTG AGCCGTGAGC CGGTCATGAG CCACGATAAA AAATGCCAGT TTGGCAAACT 2100
CAGCACTCCT GTTCCCTGCT CAGGTATATG CGATCTCTAC TGAGAAGCAA GCACAAAAGT 2160
AGACCAAAGT ATTAATGAGT ATTTCCTTTC TCCATAAGTG CAGGACTGTT ACTCACTACT 2220
AAACTCTACC AAGAATGGAA ACCAAGAATA TTTTCTGAAG ATTTTTTTGA AGATTAATTT 2280
ATACCCTATA AAATAAAACT TGTTAGCTTC GATGAAGTCA AAAAAAAAAA AAAAAAAAAA

Seq ID NO: 92 Protein sequence:
Protein Accession #: BAA91096.1

1 11 21 31 41 51
MEHLKAFDDB INAFLDNMFG PRDSRVRGWF TLDSYLPTFF LTVMYLLSIW LGNKYMKNRP 60
ALSLRGILTL YNLGITLLSA YMLAELILST WEGGYNLQCQ DLTSAGBADI RVAKVLWWYY 120
FSKSVEFLDT IFFVLRKKTS QITFLHVYHH ASMFNIWWCV LNWIPCGQSF FGPTLNSFVH 180
ILMYSYYGLS VFPSMHKYLW WKKYLTQAQL VQFVLTTHHT MSAVVKPCGF FPGCLIPQSS 240
YMLTLVILFL NFYVQTYRKK PMKKDMQEPP AGKEVKNGFS KAYFTAANGV MNKKAQ

Seq ID NO: 93 DNA sequence
Nucleic Acid Accession #: NM_000044
Coding sequence: 1115-3874 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
CGAGATCCCG GGGAGCCAGC TTGCTGGGAG AGCGGGACGG TCCGGAGCAA GCCCACAGGC 60
AGAGGAGGCG ACAGAGGGAA AAAGGGCCGA GCTAGCCGCT CCAGTGCTGT ACAGGAGCCG 120
AAGGGACGCA CCACGCCAGC CCCAGCCCGG CTCCAGCGAC AGCCAACGCC TCTTGCAGCG 180
CGGCGGCTTC GAAGCCGCCG CCCGCAGCTG CCCTTTCCTC TTCGTGAAG TTTTTAAAAG 240
CTGCTAAAGA CTCGGAGGAA GCAAGGAAAG TCCCTGGTAG GACTGACGGC TGCCTTTGTC 300
CTCCTCCTCT CCACCCCGCC TCCCCCCACC CTGCCTTCCC CCCCTCCCCC GTCTTCTCTC 360
CCGCAGCTGC CTCAGTCGGC TACTCTCAGC CAACCCCCCT CACCACCCTT CTCCCCACCC 420
GCCCCCCCGC CCCCGTCGGC CCAGCGCTGC CAGCCCGAGT TTGCAGAGAG GTAACTCCCT 480
TTGGCTGCGA GCGGGCGAGC TAGCTGCACA TTGCAAAGAA GGCTCTTAGG AGCCAGGCGA 540
CTGGGGAGCG GCTTCAGCAC TGCAGCCACG ACCCGCCTGG TTAGAATTCC GGCGGAGAGA 600
ACCCTCTGTT TTCCCCCACT CTCTCTCCAC CTCCTCCTGC CTTCCCCACC CCGAGTGCGG 660
AGCAGAGATC AAAAGATGAA AAGGCAGTCA GGTCTTCAGT AGCCAAAAAA CAAAACAAAC 720
AAAAACAAAA AAGCCGAAAT AAAAGAAAAA GATAATAACT CAGTTCTTAT TTUCACCTAC 780
TTCAGTGGAC ACTGAATTTG GAAGGTGGAG GATTTTGTTT TTTTCTTTTA AGATCTGGGC 840
ATCTTTTGAA TCTACCCTTC AAGTATTAAG AGACAGACTG TGAGCCTAGC AGGGCAGATC 900
TTGTCCACCG TGTGTCTTCT TCTGCACGAG ACTTTGAGGC TGTCAGAGCG CTTTTTGCGT 960
GGTTGCTCCC GCAAGTTTCC TTCTCTGGAG CTTCCCGCAG GTGGGCAGCT AGCTGCAGCG 1020
ACTACCGCAT CATCACAGCC TGTTGAACTC TTCTGAGCAA GAGAAGGGGA GGCGGGGTAA 1080
GGGAAGTAGG TGGAAGATTC AGCCAAGCTC AAGGATTGAA GTGCAGTTAG GGCTGGGAAG 1140
GGTCTACCCT CGGCCGCCGT CCAAGACCTA CCGAGGAGCT TTCCAGAATC TGTTCCAGAG 1200
CGTGCGCGAA GTGATCCAGA ACCCGGGCCC CAGGCACCCA GAGGCCGCGA GCGCAGCACC 1260
TCCCGGCGCC AGTTTGCTGC TGCTGCAGCA GCAGCAGCAG CAGCAGCAGC AGCAGCAGCA 1320
GCAGCAGCAG CAGCAGCAGC AGCAGCAAGA GACTAGCCCC AGGCAGCAGC AGCAGCAGCA 1380
GGGTGAGGAT GGTTCTCCCC AAGCCCATCG TAGAGGCCCC ACAGGCTACC TGGTCCTGGA 1440
TGAGGAACAG CAACCTTCAC AGCCGCAGTC GGCCCTGGAG TGCCACCCCG AGAGAGGTTG 1500
CGTCCCAGAG CCTGGAGCCG CCGTGGCCGC CAGCAAGGGG CTGCCCAGAC AGCTCCCAGC 1560
ACCTCCGGAC GAGGATGACT CAGCTGCCCC ATCCACGTTG TCCCTGCTGG GCCCCACTTT 1620
CCCCGGCTTA AGCAGCTGCT CCGCTGACCT TAAAGACATC CTGAGCGAGG CCAGCACCAT 1680
GCAACTCCTT CAGCAACAGC AGCAGGAAGC AGTATCCGAA GGCAGCAGCA GCGGGAGAGC 1740
GAGGGAGGCC TCGGGGGCTC CCACTTCCTC CAAGGACAAT TACTTAGGGG GCACTTCGAC 1800
CATTTCTGAC AACGCCAAGG AGTTGTGTAA GGCAGTGTCG GTGTCCATGG GCCTGGGTGT 1860
GGAGGCGTTG GAGCATCTGA GTCCAGGGGA ACAGCTTCGG GGGGATTGCA TGTACGCCCC 1920
ACTTTTGGGA GTTCCACCCG CTGTGCGTCC CACTCCTTGT GCCCCATTGG CCGAATGCAA 1980
AGGTTCTCTG CTAGACGACA GCGCAGGCAA GAGCACTGAA GATACTGCTG AGTATTCCCC 2040
TTTCAAGGGA GGTTACACCA AAGGGCTAGA AGGCGAGAGC CTAGGCTGCT CTGGCAGCGC 2100
TGCAGCAGGG AGCTCCGGGA CACTTGAACT GCCGTCTACC CTGTCTCTCT ACAAGTCCGG 2160

AGCACTGGAC GAGGCAGCTG CGTACCAGAG TCGCGACTAC TACAACTTTC CACTGGCTCT 2220
GGCCGGACCG CCGCCCCCTC CGCCGCCTCC CCATCCCCAC GCTCGCATCA AGCTGGAGAA 2280
CCCCGCTGAC TACGGCAGCG CCTGGGCGGC TGCGGCGGCG CAGTGCCGCT ATGGGGACCT 2340
GGCGAGCCTG CATGGCGCGG GTGCAGCGGG ACCCGGTTCT GGGTCACCCT CAGCCGCCGC 2400
TTCCTCATCC TGGCACACTC TCTTCACAGC CGAAGAAGGC CAGTTGTATG GACCGTGTGG 2460
TGGTGGTGGG GGTGGTGGCG GCGGCGGCGG CGGCGGCGGC GGCGGCGGCG GCGGCGGCGG 2520
CGGCGGCGGC GAGGCGGGAG CTGTAGCCCC CTACGGCTAC ACTCGGCCCC CTCAGGGGCT 2580
GGCGGGCCAG GAAAGCGACT TCACCGCACC TGATGTGTGG TACCCTGGCG GCATGGTGAG 2640
CAGAGTGCCC TATCCCAGTC CCACTTGTGT CAAAAGCGAA ATGGGCCCCT GGATGGATAG 2700
CTACTCCGGA CCTTACGGGG ACATGCGTTT GGAGACTGCC AGGGACCATG TTTTGCCCAT 2760
TGACTATTAC TTTCCACCCC AGAAGACCTG CCTGATCTGT GGAGATGAAG CTTCTGGGTG 2820
TCACTATGGA GCTCTCACAT GTGGAAGCTG CAAGGTCTTC TTCAAAAGAG CCGCTGAAGG 2880
GAAACAGAAG TACCTGTGCG CCAGCAGAAA TGATTGCACT ATTGATAAAT TCCGAAGGAA 2940
AAATTGTCCA TCTTGTCGTC TTCGGAAATG TTATGAAGCA GGGATGACTC TGGGAGCCCG 3000
GAAGCTGAAG AAACTTGGTA ATCTGAAACT ACAGGAGGAA GGAGAGGCTT CCAGCACCAC 3060
CAGCCCCACT GAGGAGACAA CCCAGAAGCT GACAGTGTCA CACATTGAAG GCTATGAATG 3120
TCAGCCCATC TTTCTGAATG TCCTGGAAGC CATTGAGCCA GGTGTAGTGT GTGCTGGACA 3180
CGACAACAAC CAGCCCGACT CCTTTGCAGC CTTGCTCTCT AGCCTCAATG AACTGGGAGA 3240
GAGACAGCTT GTACACGTGG TCAAGTGGGC CAAGGCCTTG CCTGGCTTCC GCAACTTACA 3300
CGTGGACGAC CAGATGGCTG TCATTCAGTA CTCCTGGATG GGGCTCATGG TGTTTGCCAT 3360
GGGCTGGCGA TCCTTCACCA ATGTCAACTC CAGGATGCTC TACTTCGCCC CTGATCTGGT 3420
TTTCAATGAG TACCGCATGC ACAAGTCCCG GATGTACAGC CAGTGTGTCC GAATGAGGCA 3480
CCTCTCTCAA GAGTTTGGAT GGCTCCAAAT CACCCCCCAG GAATTCCTGT GCATGAAAGC 3540
ACTGCTACTC TTCAGCATTA TTCCAGTGGA TGGGCTGAAA AATCAAAAAT TCTTTGATGA 3600
ACTTCGAATG AACTACATCA AGGAACTCGA TCGTATCATT GCATGCAAAA GAAAAAATCC 3660
CACATCCTGC TCAAGACGCT TCTACCAGCT CACCAAGCTC CTGGACTCCG TGCAGCCTAT 3720
TGCGAGAGAG CTGCATCAGT TCACTTTTGA CCTGCTAATC AAGTCACACA TGGTGAGCGT 3780
GGACTTTCCG GAAATGATGG CAGAGATCAT CTCTGTGCAA GTGCCCAAGA TCCTTTCTGG 3840
GAAAGTCAAG CCCATCTATT TCCACACCCA GTGAAGCATT GGAAACCCTA TTTCCCCACC 3900
CCAGCTCATG CCCCCTTTCA GATGTCTTCT GCCTGTTATA ACTCTGCACT ACTCCTCTGC 3960
AGTGCCTTGG GGAATTTCCT CTATTGATGT ACAGTCTGTC ATGAACATGT TCCTGAATTC 4020
TATTTGCTGG GCTTTTTTTT TCTCTTTCTC TCCTTTCTTT TTCTTCTTCC CTCCCTATCT 4080
AACCCTCCCA TGGCACCTTC AGACTTTGCT TCCCATTGTG GCTCCTATCT GTGTTTTGAA 4140
TGGTGTTGTA TGCCTTTAAA TCTGTGATGA TCCTCATATG GCCCAGTGTC AAGTTGTGCT 4200
TGTTTACAGC ACTACTCTGT GCCAGGCACA CAAACGTTTA CTTATCTTAT GCCACGGGAA 4260
GTTTAGAGAG CTAAGATTAT CTGGGGAAAT CAAAACAAAA AACAAGCAAA CAAAAAAAAA 4320
A

Seq ID NO: 94 Protein sequence:
Protein Accession #: NP_000035.1

1 11 21 31 41 51
MEVQLGLGRV YPRPPSKTYR GAFQNLFQSV REVIQNPGPR HPEAASAAPP GASLLLLQQQ 60
QQQQQQQQQQ QQQQQQQQET SPRQQQQQQQ EDGSPQAHRR GPTGYLVLDE EQQPSQPQSA 120
LECHPERGCV PEPQAAVAAS KGLPQQLPAP PDEDDSAAPS TLSLLGPTFP GLSSCSADLK 180
DILSEASTMQ LLQQQQQEAV SEGSSSGRAR EASGAPTSSK DNYLGGTSTI SDNAKELCKA 240
VSVSMGLGVE ALEHLSPGEQ LRGDCMYAPL LGVPPAVRPT PCAPLAECKG SLLDDSAGKS 300
TEDTAEYSPF KGGYTKGLEG ESLGCSGSAA AGSSGTLELP STLSLYKSGA LDEAAAYQSR 360
DYYNFPLALA GPPPPPPPPH PHARIKLENP LDYGSAWAAA AAQCRYGDLA SLHGAGAAGP 420
GSGSPSAAAS SSWHTLFTAE EGQLYGPCGG GGGGGGGGG GGGGGGGGG GGEAGAVAPY 480
GYTRPPQGLA GQESDFTAPD VWYPGGMVSR VPYPSPTCVK SEMGPWMDSY SGPYGDMRLE 540
TARDHVLPID YYFPPQKTCL ICGDEASGCH YGALTCGSCK VFFKRAAEGK QKYLCASRND 600
CTIDKFRKKN CPSCRLRKCY EAGMTLGARK LKKLGNLKLQ EEGEASSTTS PTEETTQKLT 660
VSHIEGYECQ PIFLNVLEAI EPGVVCAGHD NNQPDSFAAL LSSLNELGER QLVHVVKWAK 720
ALPGFRNLHV DDQMAVIQYS WMGLMVFAMG WRSFTNVNSR MLYFAPDLVF NEYRMHKSRM 780
YSQCVRMRHL SQEFGWLQIT PQEFLCMKAL LLFSIIPVDG LKNQKFFDEL RMNYIKELDR 840
IIACKRKNPT SCSRRFYQLT KLLDSVQPIA RELHQFTFDL LIKSHMVSVD FPEMMAEIIS 900
VQVPKILSGK VKPIYFHTQ

Seq ID NO: 95 DNA sequence
Nucleic Acid Accession #: NM_002497
Coding sequence: 135-1472 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
GGCACGAGTA GGGGTGGCGG GTCAGTGCTG CTCGGGGGCT TCTCCATCCA GGTCCCTGGA 60
GTTCCTGGTC CCTGGAGCTC CGCACTTGGC GCGCAACCTG CGTGAGGCAG CGCCACTCTG 120
GCGACTGGCC GGCCATGCCT TCCCGGGCTG AGGACTATGA AGTGTTTGTC ACCATTGGCA 180
CAGGCTCCTA CGGCCGCTGC CAGAAGATCC GGAGGAAGAG TGATGGCAAG ATATTAGTTT 240
GGAAAGAACT TGACTATGGC TCCATGACAG AAGCTGAGAA ACAGATGCTT GTTTCTGAAG 300
TGAATTTGCT TCGTGAACTG AAACATCCAA ACATCGTTCG TTACTATGAT CGGATTATTG 360
ACCGGACCAA TACAACACTG TACATTGTAA TGGAATATTG TGAAGGAGGG GATCTTGCTA 420
GTGTAATTAC AAAGGGAACC AAGGAAAGGC AATACTTAGA TGAAGAGTTT GTTCTTCGAG 480
TGATGACTCA GTTGACTCTG GCCCTGAAGG AATGCCACAG ACGAAGTGAT GGTGGTCATA 540
CCGTATTGCA TCGGGATCTT AAACCAGCCA ATGTTTTCCT GGATGGCAAG CAAAACGTCA 600
AGCTTGGAGA CTTTGGGCTA GCTAGAATAT TAAACCATGA CACGAGTTTT GCAAAAACAT 660

TTGTTGGCAC ACCTTATTAC ATGTCTCCTG AACAAATGAA TCGCATGTCC TACAATGAGA 720
AATCAGATAT CTGGTCATTG GGCTGCTTGC TGTATGAGTT ATGTGCATTA ATGCCTCCAT 780
TTACAGCTTT TAGCCAGAAA GAACTCGCTG GGAAAATCAG AGAAGGCAAA TTCAGGCGAA 840
TTCCATACGG TTACTCTGAT GAATTGAATG AAATTATTAC GAGGATGTTA AACTTAAAGG 900
ATTACCATCG ACCTTCTGTT GAAGAAATTC TTGAGAACCC TTTAATAGCA GATTTGGTTG 960
CAGACGAGCA AAGAAGAAAT CTTGAGAGAA GAGGGCGACA ATTAGGAGAG CCAGAAAAAT 1020
CGCAGGATTC CAGCCCTGTA TTGAGTGAGC TGAAACTGAA GGAAATTCAG TTACAGGAGC 1080
GAGAGCGAGC TCTCAAAGCA AGAGAAGAAA GATTGGAGCA GAAAGAACAG GAGCTTTGTG 1140
TTCGTGAGAG ACTAGCAGAG GACAAACTGG CTAGAGCAGA AAATCTGTTG AAGAACTACA 1200
GCTTGCTAAA GGAACGGAAG TTCCTGTCTC TGGCAAGTAA TCCAGAACTT CTTAATCTTC 1260
CATCCTCAGT AATTAAGAAG AAAGTTCATT TCAGTGGGGA AAGTAAAGAG AACATCATGA 1320
GGAGTGAGAA TTCTGAGAGT CAGCTCACAT CTAAGTCCAA GTGCAAGGAC CTGAAGAAAA 1380
GGCTTCACGC TGCCCAGCTG CGGGCTCAAG CCCTGTCAGA TATTGAGAAA AATTACCAAC 1440
TGAAAAGCAG ACAGATCCTG GGCATGCGCT AGCCAGGTAG AGAGACACAG AGCTGTGTAC 1500
AGGATGTAAT ATTACCAACC TTTAAAGACT GATATTCAAA TGCTGTAGTG TTGAATACTT 1560
GGCCCCATGA GCCATGCCTT TCTGTATAGT ACACATGATA TTTCGGAATT GGTTTTACTG 1620
TTCTTCAGCA ACTATTGTAC AAAATGTTCA CATTTAATTT TTCTTTCTTC TTTTAAGAAC 1680
ATATTATAAA AAGAATACTT TCTTGGTTGG GCTTTTAATC CTGTGTGTGA TTACTAGTAG 1740
GAACATGAGA TGTGACATTC TAAATCTTGG GAGAAAAAAT AATATTAGGA AAAAAATATT 1800
TATGCAGGAA GAGTAGCACT CACTGAATAG TTTTAAATGA CTGAGTGGTA TGCTTACAAT 1860
TGTCATGTCT AGATTTAAAT TTTAAGTCTG AGATTTTAAA TGTTTTTGAG CTTAGAAAAC 1920
CCAGTTAGAT GCAATTTGGT CATTAATACC ATGACATCTT GCTTATAAAT ATTCCATTGC 1980
TCTGTAGTTC AAATCTGTTA GCTTTGTGAA AATTCATCAC TGTGATGTTT GTATTCTTTT 2040
TTTTTTTCTG TTTAACAGAA TATGAGCTGT CTGTCATTTA CCTACTTCTT TCCCACTAAA 2100
TAAAAGAATT CTTCAGTTA

Seq ID NO: 96 Protein sequence:
Protein Accession #: NP_002488

1 11 21 31 41 51
GIREFNPNIM ANEVERJNMI TOSISGRNEA RELATEDKIN ASEHOMOSAP IRNSMPSRAE 60
DYEVLYTIOT GSYGRCQKIR RKSDGKILVW KELDYGSMTE AEKQMLVSEV NLLRELKHPN 120
IVRYYDRIID RTNTTLYIVM EYCEGGDLAS VITKGTKERQ YLDEEFVLRV MTQLTLALKE 180
CHRRSDGGHT VLHRDLKPAN VFLDGKQNVK LGDFGLARIL NHDTSFAKTF VGTPYYMSPE 240
QMNRMSYNEK SDIWSLGCLL YELCALMPPF TAFSQKELAG KIREGKFRRI PYRYSDELNE 300
IITRMLNLKD YHRPSVEEIL ENPLIADLVA DEQRRNLERR GRQLGEPEKS QDSSPVLSEL 360
KLKEIQLQER ERALKAREER LEQKEQELCV RERLAEDKLA RAENLLKNYS LLKERKPLSL 420
ASNPELLNLP SSVIKKKVHF SQESKENDMR SENSESQLTS KSKCKDLKKR LHAAQLRAQA 480
LSDIEKNYQL KSRQILQMR

Seq ID NO: 97 DNA sequence
Nucleic Acid Accession #: NM_007050.2
Coding sequence: 185-4576 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
CCTCCCGCCT CAGTTCGCGC CGCGCCTCGG CTTGGAACGC AGGAGCGCCG GCTCCGGGAG 60
CCCGAGCGGA GCCAGCGGCG CGCACAGCCA GCGGCCGCGC CGGCGATGCG GGGCCACCCC 120
GCGCCCGCCC CAGTCCCGGC CCCGGCCCCC GCGGGAAGGG GCTGAGCTGC CCGCCGCCGC 180
CCGGATGGCG AGCCTCGCCG CGCTCGCCCT CAGCCTGCTC CTGAGGCTGC AGCTGCCGCC 240
ACTGCCCGGC GCCCGGGCTC AGAGCGCCCC AGGTGGCTGT TCCTTCATGA AGCACTACAG 300
CAACTGTGGT TATAGTGTGG CTCTAGGGAC CAATGGGTTC ACCTGGGAGC AGATTAACAC 360
AACGGAGAAA CCAATGCTGG ACCAGGCAGT GCCCACAGGA TCTTTCATGA TGGTGAACAG 420
CTCTGGGAGA GCCTCTGGCC AGAAGGCCCA CCTTCTCCTG CCAACCCTGA AGGAGAATGA 480
CACCCACTGC ATCGACTTCC ATTACTACTT CTCCAGCCGT GACAGGTCCA GCCCAGGGGC 540
CTTGAACGTC TACGTGAAGG TGAATGGTGG CCCCCAAGGG AACCCTGTGT GGAATGTGTC 600
CGGGGTCGTC ACTGAGGGCT GGGTGAAGGC AGAGCTCGCC ATCAGCACTT TCTGGCCACA 660
TTTCTATCAG GTGTATATTG AATCCGTCTC ATTGAAGGGT CATCCTGGCT ACATCGCCGT 720
GGACGAGGTC CGGGTCCTTG CTCATCCATG CAGAAAAGCA CCTCATTTTC TGCGACTCCA 780
AAACGTGGAG GTGAATGTGG GGCAGAATGC CACATTTCAG TGCATTGCTG GTGGGAAGTG 840
GTCTCAGCAT GACAAGCTTT GGCTCCAGCA ATGGAATGGC AGGGACACGG CCCTCATGGT 900
CACCCCGTGT GTCAACCACA GGCGCTTCTC AGCCACAGTC AGTGTGGCAG ACACTGCCCA 960
GCGGAGCGTC AGCAAGTACC GCTGTGTGAT CCGCTCTGAT GGTGGGTCTG GTGTGTCCAA 1020
CTACGGGGAG CTGATCGTGA AAGAGCCTCC CACGCCCATT GCTCCCCCAG AGCTGCTGGC 1080
TGTGGGGGCC ACATACCTGT GGATCAAGCC AAATGCCAAC TCCATCATCG GGGATGGCCC 1140
CATCATCCTG AAGGAAGTGG AATATCGCAC CACCACAGGC AGTGGGCAG AGACCCACAT 1200
AGTCGACTCT CCCAACTATA AGCTGTGGCA TCTGGACCCC GATGTTGAGT ATGAGATCCG 1260
AGTGCTCCTC ACACGACCAG GTGAGGGGGG TACGGGACCG CCAGGGGCTC CCCTCACCAC 1320
CAGGACCAAG TGTGCAGATC CGGTACATGG CCCACAGAAC GTGGAAATCG TAGACATCAG 1380
AGCCCGGCAG CTGACCCTGC AGTGGGAGCC CTTCGGCTAC GCGGTGACCC GCTGCCATAG 1440
CTACAACCTC ACCGTGCAGT ACCAGTATGT GTTCAACCAG CAGCAGTACG AGCCCGAGGA 1500
GGTCATCCAG ACCTCCTCCC ACTACACCCT GCGAGGCCTG CGCCCCTTCA TGACCATCGG 1560
GCTGCGACTC TTGCTGTCTA ACCCCGAGGG CCGAATGGAG AGCGAGGAGC TGGTGGTGCA 1620
GACTGAGGAA GACGTTCCAG GAGCTGTTCC TCTAGAATCC ATCCAAGGGG GGCCCTTTGA 1680
GGAGAAGATC TACATCCAGT GGAAACCTCC CAATGAGACC AATGGGGTCA TCACGCTCTA 1740
CGAGATCAAC TACAAGGCTG TCGGCTCGCT GGACCCAAGT GCTGACCTCT CGAGCCAGAG 1800

WO 02/059377 PCT/US02/02242

TTAATGTAGT TCATGGTTCC TTAGTGAGCA GGACTCTTGG ATGTGGAGGA GAAAGGGTCA 11100
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CACCCTGTCC CTGTATCTCC CATGGAAGAT GAATAATGTC AGGTGTTCTT TGGGTCAAAG 11280
GCCCCAGGGC AGTCTGGAGG CTTAGAGGGC AGAGTGGTGT CATTCCATGT AAAGTTAGGC 11340
TTCTGAGGGG TCAGGCAGAA TATGGTGTCC ATATCTTCCA TAGCTCTGCA GATTCTTGGA 11400
TGAAGTCAAG CACAGTTTGC TAGACCCAGG TCACTCCTCT GAGTATAACT AGGACCCATG 11460
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CTGCTTTGCC ATAGACCCAA TACCCATGTA GATCTCTCAT GAGAGCAGCC ATAACTCAGA 11880
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ATTATAATCA TTTCCAGTGC ACACATTTCA TCACCAGGTG GATCCTGAGC TAGCCCATGT 12120
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CTAGCCAATC AAAGACAAAG AGTTGTGGCC TCTACCATTG CCTTGGCTTC TGGACACCCT 12240
CACAAGCTAT CCCAAGGTTC CCGCTCAACT CCAGGGAGGC TGACATCTTC ACATCCACTG 12300
GGCATATAAT ATTGCATGAG ACCAAAGTCT CCACACTCTT TGCAGCCTCC TCCATGAATC 12360
CCAATGGCCT GCACTTGTAC AGTTTGGGTG TTTGATAGAT AAAGCACGTA TGAGAAGAGA 12420
AAACAAAATA AATCAACTTT TTAAAAAAGC CAGCACTGTG CTGTCAATGT TTTTTTTTC 12480
TTTTCAATTC TAGCTCAGAA AAGCAGAAGG TAAATAATGT CAGGTCAATG AATATCAGAT 12540
ATATTTTTTG ACTGTACATT ACAGTGAAGT GTAATCTTTT TACACCTGCA AGTCCATCTT 12600
ATTTATTCTT GTAAATGTTC CCTGACAATG TTTGTAATAT GGCTGTGTTA AAAAATCTAT 12660
ACAATAAAGC TGTGACCCTG

Seq ID NO: 98 Protein sequence:
Protein Accession #: NP_008981.1

1 11 21 31 41 51
| | | | | |
GIREFNPPRO TEINTYROSI NEPHOSPHAT ASERECEPTO RTYPETHOMO SAPIENSMAS 60
LAALALSLLL RLQLPPLPGA RAQSAPGGCS PDEHYSNCGY SVALGTNGFT WEQINTTEKP 120
MLDQAVPTGS FMMVNSSGRA SGQKAHLLLP TLKENDTHCI DFHYYFSSRD RSSPGALNVY 180
VKVNGGPQGN PVWNVSGVVT EGWVKAELAI STFWPHFYQV IFESVSLKGH PGYIAVDEVR 240
VLAHPCRKAP HFLRLQNVEV NVGQNATFQC IAGGKWSQHD KLWLQQWNGR DTALMVTRVV 300
NHRRFSATVS VADTAQRSVS KYRCVIRSDG GSGVSNYAEL IVKEPPTPIA PPELLAVQAT 360
YLWIKPNANS IIGDGPIILK EVEYRTTTGT WAETHIVDSP NYKLWHLDPD VEYEIRVLLT 420
RPGEGGTGPP GAPLTTRTKC ADPVHGPQNV EIVDIRARQL TLQWEPFGYA VTRCHSYNLT 480
VQYQYVFNQQ QYEAEEVIQT SSHYTLRGLR PFMTIRLRLL LSNPEGRMES EELVVQTEED 540
VPGAVPLESI QGGPFEEKIY IQWKPPNETN GVITLYEINY KAVGSLDPSA DLSSQRGKVP 600
KLRNETHHLP VGLYPGTTYS FTIKASTAKG PGPPVTTRIA TKISAPSMPE YDTDTPLNET 660
DTTITVMLKP AQSRGAPVSV YQLVVKEERL QKSRRAADII ECPSVPVSYR NASSLDSLHY 720
FAABLKPANL PVTQPFTVGD NKTYNGYWNP PLSPLKSYSI YPQALSKANG ETKINCVRLA 780
TKAPMGSAQV TPGTPLCLLT TGASTQNSNT VEPEKQVDNT VKMAGVIAGL LMFIIILLGV 840
MLTIKRRRNA YSYSYYLSQR KLAKKQKETQ SGAQREMGPV ASADKPTTKL SASRNDEGPS 900
SSSQDVNGFT DGSRGELSQP TLTIQTHPYR TCDPVEMSYP RDQFQLAIRV ADLLQHTTQM 960
KRGGQYGFKE EYEALPEGQT ASWDTAKEDE NRNKNRYGNI ISYDHSRVRL LVLDGDPHSD 1020
YINANYIDGY HRPRHYIATQ GPMQETVKDF WRMIWQENSA SIVMVTNLVE VGRVKCVRYW 1080
PDDTEVYGDI KVTLIETEPL AEYVIRTFTV QKKGYHEIRB LRLFHFTSWP DHGVPCYATG 1140
LLGFVRQVKF LNPPEAGPIV VHCSAGAURT GCFIAIDTML DMAENEGVVD IFNCVRELRA 1200
QRVNLVQTEE QYVFVHDAIL EACLCGNTAI PVCEFRSLYY NISRLDFQTN SSQIKDEFQT 1260
LNIVTPRVRP EDCSIGLLPR NHDKNRSMDV LPLDRCLPFL ISVDGESSNY INAALMDSHK 1320
QPAAFVVTQH PLPNTVADFW RLVFDYNCSS VVMLNEMDTA QFCMQYWPEK TSGCYGPIQV 1380
EFVSADIDED IIHRIFRICN MARPQDGYRI VQHLQYIGWP AYRDTPPSKR SLLKVVRRLE 1440
KWQEQYDGRE GRTVVHCLNG GGRSGTFCAI CSVCEMIQQQ NIIDVFHIVK TLRNNKSNMV 1500
GTLEQYKFVY EVALBYLSSF

Seq ID NO: 99 DNA sequence
Nucleic Acid Accession #: NM_002988.1
Coding sequence: 71-340 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
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GCCCAGCATC ATGAAGGGCC TTGCAGCTGC CCTCCTTGTC CTCGTCTGCA CCATGGCCCT 120
CTGCTCCTGT GCACAAGTTG GTACCAACAA AGAGCTCTGC TGCCTCGTCT ATACCTCCTG 180
GCAGATTCCA CAAAAGTTCA TAGTTGACTA TTCTGAAACC AGCCCCCAGT GCCCCAAGCC 240
AGGTGTCATC CTCCTAACCA AGAGAGCCCG GCAGATCTGT GCTGACCCCA ATAAGAAGTG 300
GGTCCAGAAA TACATCAGCG ACCTGAAGCT GAATGCCTGA GGGGCCTGGA AGCTGCAGG 360
GCCCAGTGAA CTTGGTGGGC CCAGGAGGGA ACAGGAGCCT GAGCCAGGGC AATGGCCCTG 420
CCACCCTGGA GGCCACCTCT TCTAAGAGTC CCATCTGCTA TGCCCAGCCA CATTAACTAA 480
CTTTAATCTT AGTTTATGCA TCATATTTCA TTTTGAAATT GATTTCTATT GTTGAGCTGC 540
ATTATGAAAT TAGTATTTTC TCTGACATCT CATGACATTG TCTTTATCAT CCTTCCCCT 600

TTCCCTTCAA CTCTTGGTAC ATTCAATGCA TGGATCAATC AGTGTGATTA GCTTTCTCAG 660
CAGACATTGT GCCATATGTA TCAAATGACA AATCTTTATT GAATGGTTTT GCTCAGCACC 720
ACCTTTTAAT ATATTGGCAG TACTTATTAT ATAAAAGGTA AACCAGCATT CTCACTGTGA 780
AAAAAAAAAA AAAAAAAAAA AAA

Seq ID NO: 100 Protein sequence:
Protein Accession #: NP_002979.1

1 11 21 31 41 51
| | | | | |
MKGLAAALLV LVCTMALCSC AQVGTNKELC CLVYTSWQIP QKFIVDYSET SPQCPKPGVI 60
LLTKRGRQIC ADPNKKWVQK YISDLKLNA

Seq ID NO: 101 DNA sequence
Nucleic Acid Accession #: NM_015507.2
Coding sequence: 241-1902 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
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CCGCCAGAGGA GCCTCGGCCA GGCTAGCCAG GGCGCCCCCA GCCCCTCCCC AGGCCGCGAG 60
CGCCCCTGCC GCGGTGCCTG GCCTCCCCTC CCAGACTGCA GGGACAGCAC CCGGTAACTG 120
CGAGTGGAGC GGAGGACCCG AGCGGCTGAG GAGAGAGGAG GCGGCGGCTT AGCTGCTACG 180
GGGTCCGGCC GGCGCCCTCC CGAGGGGGGC TCAGGAGGAG GAAGGAGGAC CCGTGCGAGA 240
ATGCCTCTGC CCTGGAGCCT TGCGCTCCCG CTGCTGCTCT CCTGGGTGGC AGGTGGTTTC 300
GGGAACGCGG CCAGTGCAAG GCATCACGGG TTGTTAGCAT CGGCACGTCA GCCTGGGGTC 360
TGTCACTATG GAACTAAACT GGCCTGCTGC TACGGCTGGA GAAGAAACAG CAAGGGAGTC 420
TGTGAAGCTA CATGCGAACC TGGATGTAAG TTTGGTGAGT GCGTGGGACC AAACAAATGC 480
AGATGCTTTC CAGGATACAC CGGGAAAACC TGCAGTCAAG ATGTGAATGA GTGTGGAATG 540
AAACCCCGGC CATGCCAACA CAGATGTGTG AATACACACG GAAGCTACAA GTGCTTTTGC 600
CTCAGTGGCC ACATGCTCAT GCCAGATGCT ACGTGTGTGA ACTCTAGGAC ATGTGCCATG 660
ATAAACTGTC AGTACAGCTG TGAAGACACA GAAGAAGGGC CACAGTGCCT GTGTCCATCC 720
TCAGGACTCC GCCTGGCCCC AAATGGAAGA GACTGTCTAG ATATTGATGA ATGTGCCTCT 780
GGTAAAGTCA TCTGTCCCTA CAATCGAAGA TGTGTGAACA CATTTGGAAG CTACTACTGC 840
AAATGTCACA TTGGTTTCGA ACTGCAATAT ATCAGTGGAC GATATGACTG TATAGATATA 900
AATGAATGTA CTATGGATAG CCATACGTGC AGCCACCATG CCAATTGCTT CAATACCCAA 960
GGGTCCTTCA AGTGTAAATG CAAGCAGGGA TATAAAGGCA ATGGACTTCG GTGTTCTGCT 1020
ATCCCTGAAA ATTCTGTGAA GGAAGTCCTC AGAGCACCTG GTACCATCAA AGACAGAATC 1080
AAGAAGTTGC TTGCTCACAA AAACAGCATG AAAAAGAAGG CAAAAATTAA AAATGTTACC 1140
CCAGAACCCA CCAGGACTCC TACCCCTAAG GTGAACTTGC AGCCCTTCAA CTATGAAGAG 1200
ATAGTTTCCA GAGGCGGGAA CTCTCATGGA GGTAAAAAAG GGAATGAAGA GAAAATGAAA 1260
GAGGGGCTTG AGGATGAGAA AAGAGAAGAG AAAGCCCTGA AGAATGACAT AGAGGAGCGA 1320
AGCCTGCGAG GAGATGTGTT TTTCCCTAAG GTGAATGAAG CAGGTGAATT CGGCCTGATT 1380
CTGGTCCAAA GGAAAGCGCT AACTTCCAAA CTGGAACATA AAGATTTAAA TATCTCGGTT 1440
GACTGCAGCT TCAATCATGG GATCTGTGAC TGGAAACAGG ATAGAGAAGA TGATTTTGAC 1500
TGGAATCCTG CTGATCGAGA TAATGCTATT GGCTTCTATA TGGCAGTTCC GGCCTTGGCA 1560
GGTCACAAGA AAGACATTGG CCGATTGAAA CTTCTCCTAC CTGACCTGCA ACCCCAAAGC 1620
AACTTCTGTT TGCTCTTTGA TTACCGGCTG GCCGGAGACA AAGTCGGCAA ACTTCGAGTG 1680
TTTGTGAAAA ACAGTAACAA TGCCCTGGCA TGGGAGAAGA CCACGAGTGA GGATGAAAAG 1740
TGGAAGACAG GGAAAATTCA GTTGTATCAA GGAACTGATG CTACCAAAAG CATCATTTTT 1800
GAAGCAGAAC GTGGCAAGGG CAAAACCGGC GAAATCGCAG TGGATGGCGT CTTGCTTGTT 1860
TCAGGCTTAT GTCCAGATAG CCTTTTATCT GTGGATGACT GAATGTTACT ATCTTTATAT 1920
TTGACTTTGT ATGTCAGTTC CCTGGTTTTT TTGATATTGC ATCATAGGAC CTCTGGCATT 1980
TTAGAATTAC TAGCTGAAAA ATTGTAATGT ACCAACAGAA ATATTATTGT AAGATGCCTT 2040
TCTTGTATAA GATATGCCAA TATTTGCTTT AAATATCATA TCACTGTATC TTCTCAGTCA 2100
TTTCTGAATC TTTCCACATT ATATTATAAA ATATGGAAAT GTCAGTTTAT CTCCCCTCCT 2160
CAGTATATCT GATTTGTATA AGTAAGTTGA TGAGCTTCTC TCTACAACAT TTCTAGAAAA 2220
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TATGACATCA AAGATAGACT TTTGCCTAAG TGGCTTAGCT GGGTCTTTCA TAGCCAAACT 2340
TGTATATTTA AATTCTTTGT AATAATAATA TCCAAATCAT CAAAAAAAAA AAAAAAAA

Seq ID NO: 102 Protein sequence:
Protein Accession #: NP_056322.2

1 11 21 31 41 51
| | | | | |
MPLPWSLALP LLLSWVAGGF GNAASARHHG LLASARQPGV CHYGTKLACC YGWRRNSKGV 60
CBATCEPGCK FGBCVGPNKC RCFPGYTGKT CSQDVNECOM KPRPCQHRCV NTHGSYKCFC 120
LSGHMLMPDA TCVNSRTCAM INCQYSCEDT EEGPQCLCPS SGLRLAPNGR DCLDIDECAS 180
GKVICPYNRR CVNTPGSYYC KCHGGFELQY ISGRYDCIDI NECTMDSHTC SHHANCFNTQ 240
OSFKCKCKQG YKGNGLRCSA IPENSVKEVL RAPGTIKDRI KKLLAHKNSM KKKAKIKNVT 300
PEPTRTPTPK VNLQPFNYEE IVSRGGNSHG GKKGNEEKMK EGLEDEKREE KALKNDIEER 360
SLRGDVFFPK VNEAGEFGLI LVQRKALTSK LEHKDLNISV DCSFNHGICD WKQDREDDFD 420
WNPADRDNAI GFYMAVPALA GHKKDIGRLK LLLPDLQPQS NFCLLFDYRL AGDKVGKLRV 480
FVKNSNNALA WEKTTSEDEK WKTGKIQLYQ GTDATKSIIF EAERGKGKTG EIAVDGVLLV 540
SGLCPDSLLS VDD

Seq ID NO: 103 DNA sequence

Nucleic Acid Accession #: NM_001565.1
Coding sequence: 67-363 (underlined sequences correspond to start and stop codons)

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GAGACATTCC TCAATTGCTT AGACATATTC TGAGCCTACA GCAGAGGAAC CTCCAGTCTC  60
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ATTCAAGGAG TACCTCTCTC TAGAACCGTA CGCTGTACCT GCATCAGCAT TAGTAATCAA  180
CCTGTTAATC CAAGGTCTTT AGAAAAACTT GAAATTATTC CTGCAAGCCA ATTTTGTCCA  240
CGTGTTGAGA TCATTGCTAC AATGAAAAAG AAGGGTGAGA AGAGATGTCT GAATCCAGAA  300
TCGAAGGCCA TCAAGAATTT ACTGAAAGCA GTTAGCAAGG AAATGTCTAA AAGATCTCCT  360
TAAAACCAGA GGGGAGCAAA ATCGATGCAG TGCTTCCAAG GATGGACCAC ACAGAGGCTG  420
CCTCTCCCAT CACTTCCCTA CATGGAGTAT ATGTCAAGCC ATAATTGTTC TTAGTTTGCA  480
GTTACACTAA AAGGTGACCA ATGATGGTCA CCAAATCAGC TGCTACTACT CCTGTAGGAA  540
GGTTAATGTT CATCATCCTA AGCTATTCAG TAATAACTCT ACCCTGGCAC TATAATGTAA  600
GCTCTACTGA GGTGCTATGT TCTTAGTGGA TGTTCTGACC CTGCTTCAAA TATTTCCCTC  660
ACCTTTCCCA TCTTCCAAGG GTACTAAGGA ATCTTTCTGC TTTGGGGTTT ATCAGAATTC  720
TCAGAATCTC AAATAACTAA AAGGTATGCA ATCAAATCTG CTTTTTAAAG AATGCTCTTT  780
ACTTCATGGA CTTCCACTGC CATCCTCCCA AGGGGCCCAA ATTCTTTCAG TGGCTACCTA  840
CATACAATTC CAAACACATA CAGGAAGGTA GAAATATCTG AAAATGTATG TGTAAGTATT  900
CTTATTTAAT GAAAGACTGT ACAAAGTATA AGTCTTAGAT GTATATATTT CCTATATTGT  960
TTTCAGTGTA CATGGAATAA CATGTAATTA AGTACTATGT ATCAATGAGT AACAGGAAAA  1020
TTTTAAAAAT ACAGATAGAT ATATGCTCTG CATGTTACAT AAGATAAATG TGCTGAATGG  1080
TTTTCAAATA AAAATGAGGT ACTCTCCTGG AAATATTAAG
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Seq ID NO: 104 Protein sequence:
Protein Accession #: NP_001556.1

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1   11   21   31   41   51
|    |    |    |    |    |
MNQTAILICC LIFLTLSGIQ GVPLSRTVRC TCISISNQPV NPRSLEKLEI IPASQFCPRV  60
EIIATMKKKG EKKCLNPESK AIKNLLKAVS KEMSKRSP
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Seq ID NO: 105 DNA sequence
Nucleic Acid Accession #: NM_015068.1
Coding sequence: 1170-2243 (underlined sequences correspond to start and stop codons)

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1   11   21   31   41   51
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GTAACAACCG TCACCCTGGG TCCCGACTGC CCACCTCCTC CTCCTCCCCC TCCCCCCAAC  60
AACAACAACA ACAACAACTC CAAGCACACC GGCCATAAGA GTGCGTGTGT CCCCAACATG  120
ACCGAACGAA GAAGGGACGA GCTCTCTGAA GAGATCAACA ACTTAAGAGA GAAGGTCATG  180
AAGCAGTCGG AGGAGAACAA CAACCTGCAG AGCCAGGTGC AGAAGCTCAC AGAGGAGAAC  240
ACCACCCTTC GAGAGCAAGT GGAACCCACC CCTGAGGATG AGGATGATGA CATCGAGCTC  300
CGCGGTGCTG CAGCAGCTGC TGCCCCACCC CCTCCAATAG AGGAAGAGTG CCCAGAAGAC  360
CTCCCAGAGA AGTTCGATGG CAACCCAGAC ATGCTGGCTC CTTTCATGGC CCAGTGCCAG  420
ATCTTCATGG AAAAGAGCAC CAGGGATTTC TCAGTTGATC GTGTCCGTGT CTGCTTCGTG  480
ACAAGCATGA TGACCGGCCG TGCTGCCCGT TGGGCCTCAG CAAAGCTGGA GCGCTCCCAC  540
TACCTGATGC ACAACTACCC AGCTTTCATG ATGGAAATGA AGCATGTCTT TGAAGACCCT  600
CAGAGCGCAG AGGTTGCCAA ACGCAAGATC AGACGCCTGC GCCAAGGCAT GGGGTCTGTC  660
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ATTGCAAGCC ACCACCAGGT AGATCCAACC GAGCCGGTGG GAGGTGCCCG CATGCGCCTG  960
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GGTCACTACG CTGACAATTG TCCTGCCAAG GCCTCAAAGT CTTCGCCGGC GGGAAACTCC  1080
CCGGCCCCGC TGTAGAGGGA CCTTCAGCGA CCGGGCCAGA AATAATAAGG TCCCCACAAG  1140
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CCCTGTTCGT CCGAGCCATG ATCGATTCTG GTGCTTCTGG CAACTTCATT GATCACGAAT  1260
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TTGATGGGCG CCCCATAGCA TCGGGCCCAG TTGTCCACGA AACTCACGAC CTGATAGTTG  1380
ACCTGGGAGA TCACCGAGAG GTGCTGTCAT TTGATGTGAC TCAGTCTCCA TTCTTCCCTG  1440
TCGTCCTAGG GGTTCGCTGG CTGAGCACAC ATGATCCCAA TATCACATGG AGCACTCCAT  1500
CTATCGTCTT TGATTCTGAA TACTGCCGCT ACCACTGCGG GATGTATTCT CCAATACCAC  1560
CATCGCTCCC ACCACCAGCA CCACAACCGC CACTCTATTA TCCAGTAGAT GGATACAGAG  1620
TTTACCAACC AGTGAGGTAT TACTATGTCC AGAATGTGTA CACTCCAGTA GATGAGCACG  1680
TCTACCCAGA TCACCGCCTG GTTGACCCTC ACATAGAAAT GATACCTGGA GCACACAGTA  1740
TTCCCAGTGG ACATGTGTAT TCACTGTCCG AACCTGAAAT GGCAGCTCTT CGAGATTTTG  1800
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ATTTTACTAT CCAGAATCAG TATCCTCGCC TATCTATTCC AAATTTAGAA GACCAAGCAC  1980
ACCTGGCAAC GTACACTGAA TTCGTACCTC AAATACCTGG ATACCAAACA TACCCCACAT  2040
ATGCCGCGTA CCCGACCTAC CCAGTAGGAT TCGCCTGGTA CCCAGTGGGA CGAGACGGAC  2100
AAGGAAGATC ACTATATGTA CCTGTGATGA TCACTTGGAA TCCACACTGG TACCGCCAGC  2160
CTCCGGTACC ACAGTACCCG CCGCCACAGC CGCCGCCTCC ACCACCACCA CCGCCGCCGC  2220
CTCCATCTTA CAGTACCCTG TAAATACCTG TCATGTCCTT CAGGATCTCT GCCCTCAAAA  2280
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TTTATTCCTG TTCAGCTTCT CAATCAGTGA CTGTGTGCTA AATTTTAGGC TACTGTATCT  2340
TCAGGCCACC TGAGGCACAT CCTCTCTGAA ACGGCTATGG AAGGTTAGGG CCACTCTGGA  2400
CTGGCACACA TCCTAAAGCA CCAAAAGACC TTCAACATTT TCTGAGAGCA ACAGAGTATT  2460
TGCCAATAAA TGATCTCTCA TTTTTCCACC TTGACTGCCA ATCTAACTAA AATAATTAAT  2520
AAGTTTACTT TCCAGCCAGT CCTGGAAGTC TGGGTTTTAC CTGCCAAAAC CTCCATCACC  2580
ATCTAAATTA TAGGCTGCCA AATTTGCTGT TTAACATTTA CAGAGAAGCT GATACAAACG  2640
CAGGAAATGC TGATTTCTTT ATGGAGGGGG AGACGAGGAG GAGGAGGACA TGACTTTTCT  2700
TGCGGTTTCG GTACCCTCTT TTTAAATCAC TGGAGGACTG AGGCCTTATT AAGGAAGCCA  2760
AAATTATCGG TGCAGTGTGG AAAGGCTTCC GTGATCCTCT CGCTGCACCC TTAGAAACTT  2820
CACCGTCTTC AAACTCCATT TCCATGGTTC TGTTAATTCT CAAGGAGCAG CAACTCGACT  2880
GGTTCTCCCA GGAGCAGGAA AAACCCTTGT GACATGAAAC ATCTCAGGCC TGAAAAGAAA  2940
GTGCTCTCTC AGATGGACTC TTGCATGTTA AGACTATGTC TTCACATCAT GGTGCAAATC  3000
ACATGTACCC AATGACTCCG GCTTTGACAC AACACCTTAC CATCATCATG CCATGATGGC  3060
TTCCACAAAG CATTAAACCT GGTAACCAGA GATTACTGGT GGCTCCAGCG TTGTTAGATG  3120
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GACTCCAAAA TCCCATACCC AACTCTTAAG AGATTTGTCC TGGTACTTCA GAAAGAATTT  3240
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TGTGTCTGCC TCCATATGCA TCTGGCATTT TCATCTTCAG TCCCCTCATT AGACTGTAGC  3360
ATTAGGATGT GTGGAGAGAG GAGAAATGAT TTAGCACCCA GATTCACACT CCTATGCCTG  3420
GAAGGGGGAC ATCTTTGAAG AAGAGGAATT AGGGCTGTGG ACACTGTCTT GAGGATGTGG  3480
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Seq ID NO: 106 Protein sequence:
Protein Accession #: NP_055883.1

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VIDYSNAFQM IAQDLDWNEP ALIDQYHEGL SDHIQEELSH LEVAKSLSAL IQQCIHERR  240
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Seq ID NO: 107 DNA sequence
Nucleic Acid Accession #: NM_003679.1
Coding sequence: 47-1507(underlined sequences correspond to start and stop codons)

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Seq ID NO: 108 Protein sequence:
Protein Accession #: NP_003670.1

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FEEFEKLLTS NDVVDFFQKY FPDAPLIGE KLLVQDFFLL PAQPMISVKC SSFHFKSHCV 300
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MYNYIEMRAH VNSSWFIFQK NMERFLHAIM PSTFIPLYTM VTPSRIRYHE AVQRWHWQRK 420
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Seq ID NO: 109 DNA sequence
Nucleic Acid Accession #: NM_006115.1
Coding sequence: 236-1765 (underlined sequences correspond to start and stop codons)

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Protein Accession #: NP_006106.1

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Seq ID NO: 111 DNA sequence
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Coding sequence: 8-2452 (underlined sequences correspond to start and stop codons)

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TCCCCTACCA TGACTGAAGG CGCCAGAGAC TGGCGGTGTC TTAAGACTCC GGGCACCGCC  2580
ACGCGCTGTC AAGCAACACT CTGCGGACCT GCCGGCGTAG TTGCAGCGGG GGCTTGGGGA  2640
GGGGCTGGGG GTTGGACGGG ATTGAGGAAG GTCCGCACAG CCTGTCTCTG CTCAGTTGCA  2700
ATAAACGTGA CATCTTGGGA GCGTTAAAAA AAAAAAAAAA
```

Seq ID NO: 112 Protein sequence:
Protein Accession #: NP_003806.2

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1    11    21    31    41    51
|    |     |     |     |     |
MRLALLWALG LLGAGSPLPS WPLPNIGGTB EQQAESEKAP REPLEPQVLQ DDLPISLKKV  60
LQTSLPEPLR IKLELDGDSH ILELLQNREL VPGRPTLVWY QPDGTRVVSE GHTLENCCYQ  120
ORVRGYAGSW VSICTCSGLR GLVVLTPERS YTLEQGPGDL QGPPIISRIQ DLHLPGHTCA  180
LSWRESVHTQ TPPEHIPLGQR HRRRRDVVT ETKTVELVIV ADHSEAQKYR DFQHLLNRTL  240
EVALLLDTFP RPLNVRVALV GLEAWTQRDL VEISPNPAVT LENFLHWRRA HLLPRLPHDS  300
```



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AQLVTGTSPS GPTVGMAIQN SICSPDPSGG VNMDHSTSIL GVASSIAHEL QHSLGLDHDL  360
PGNSCPCPGP APAKTCIMBA STDFLPGLNF SNCSRRALBK ALLDGMGSCL FERLPSLPPM  420
AAFCGNMFVE PGEQCDCGFL DDCVDPCCDS LTCQLRPGAQ CASDGPCCQN CQLRPSGWQC  480
RPTRGDCDLP EPCPGDSSQC PPDVSLGDGE PCAGGQAVCM HGRCASYAQQ CQSLWGPGAQ  540
PAAPLCLQTA NTRGNAFGSC GRNPSGSYVS CTPRDAICGQ LQCQTGRTQP LLGSIRDLLW  600
ETIDVNGTEL NCSWVHLDLG SDVAQPLLTL PGTACGPGLV CIDHRCQRVD LLGAQECRSK  660
CHGHGVCDSN RHCYCBEGWA PPDCTTQLKA TSSLTTGLLL SLLVLLVLVM LGAGYWYRAR  720
LHQRLCQLKG PTCQYRAAQS GPSERPGPPQ RALLARGTKS QGPAKPPPPR KPLPADPQGR  780
CPSGDLPGPG AGIPPLVVPS RPAPPPPTVS SLYL
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Seq ID NO: 113 DNA sequence
Nucleic Acid Accession #: NM_002416
Coding sequence: 40-417 (underlined sequences correspond to start and stop codons)

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1    11    21    31    41    51
|    |     |     |     |     |
ATCCAATACA GGAGTGACTT GGAACTCCAT TCTATCACTA TGAAGAAAAG TGGTGTTCTT  60
TTCCTCTTGG GCATCATCTT GCTGGTTCTG ATTGGAGTGC AAGGAACCCC AGTAGTGAGA  120
AAGGGTCGCT GTTCCTGCAT CAGCACCAAC CAAGGGACTA TCCACCTACA ATCCTTGAAA  180
GACCTTAAAC AATTTCCCCC AAGCCCTTCC TGCCAGAAAA TTGAAATCAT TGCTACACTG  240
AAGAATGGAG TTCAAACATG TCTAAACCCA GATTCAGCAG ATGTGAAGGA ACTGATTAAA  300
AAGTGGGAGA AACAGGTCAG CCAAAAGAAA AAGCAAAAGA ATGGGAAAAA ACATCAAAAA  360
AAGAAAGTTC TGAAAGTTCG AAAATCTCAA CGTTCTCGTC AAAAGAAGAC TACATAAGAG  420
ACCACTTCAC CAATAAGTAT TCTGTGTTAA AAATGTTCTA TTTTAATTAT ACCGCTATCA  480
TTCCAAAGGA GGATGGCATA TAATACAAAG GCTTATTAAT TTGACTAGAA AATTTAAAAC  540
ATTACTCTGA AATTGTAACT AAAGTTAGAA AGTTGATTTT AAGAATCCAA ACGTTAAGAA  600
TTGTTAAAGG CTATGATTGT CTTTGTTCTT CTACCACCCA CCAGTTGAAT TTCATCATGC  660
TTAAGGCCAT GATTTTAGCA ATACCCATGT CTACACAGAT GTTCACCCAA CCACATCCCA  720
CTCACAACAG CTGCCTGGAA GAGCAGCCCT AGGCTTCCAC GTACTGCAGC CTCCAGAGAG  780
TATCTGAGGC ACATGTCAGC AAGTCCTAAG CCTGTTAGCA TGCTGGTGAG CCAAGCAGTT  840
TGAAATTGAG CTGGACCTCA CCAAGCTGCT GTGGCCATCA ACCTCTGTAT TTGAATCAGC  900
CTACAGGCCT CACACACAAT GTGTCTGAGA GATTCATGCT GATTGTTATT GGGTATCACC  960
ACTGGAGATC ACCAGTGTGT GGCTTTCAGA GCCTCCTTTC TGGCTTTGGA AGCCATGTGA  1020
TTCCATCTTG CCCGCTCAGG CTGACCACTT TATTTCTTTT TGTTCCCCTT TGCTTCATTC  1080
AAGTCAGCTC TTCTCCATCC TACCACAATG CAGTGCCTTT CTTCTCTCCA GTGCACCTGT  1140
CATATGCTCT GATTTATCTG AGTCAACTCC TTTCTCATCT TGTCCCCAAC ACCCCACAGA  1200
AGTGCTTTCT TCTCCCAATT CATCCTCACT CAGTCCAGCT TAGTTCAAGT CCTGCCTCTT  1260
AAATAAACCT TTTTGGACAC ACAAATTATC TTAAAACTCC TGTTTCACTT GGTTCAGTAC  1320
CACATGGGTG AACACTCAAT GGTTAACTAA TTCTTGGGTG TTTATCCTAT CTCTCCAACC  1380
AGATTGTCAG CTCCTTGAGG GCAAGAGCCA CAGTATATTT CCCTGTTTCT TCCACAGTGC  1440
CTAATAATAC TGTGGAACTA GGTTTTAATA ATTTTTTAAT TGATGTTGTT ATGGGCAGGA  1500
TGGCAACCAG ACCATTGTCT CAGAGCAGGT GCTGGCTCTT TCCTGGCTAC TCCATGTTGG  1560
CTAGCCTCTG GTAACCTCTT ACTTATTATC TTCAGGACAC TCACTACAGG GACCAGGGAT  1620
GATGCAACAT CCTTGTCTTT TTATGACAGG ATGTTTGCTC AGCTTCTCCA ACAATAAGAA  1680
GCACGTGGTA AAACACTTGC GGATATTCTG GACTGTTTTT AAAAAATATA CAGTTTACCG  1740
AAAATCATAT AATCTTACAA TGAAAAGGAC TTTATAGATC AGCCAGTGAC CAACCTTTTC  1800
CCAACCATAC AAAAATTCCT TTTCCCGAAG GAAAAGGGCT TTCTCAATAA GCCTCAGCTT  1860
TCTAAGATCT AACAAGATAG CCACCGAUAT CCTTATCGAA ACTCATTTTA GGCAAATATG  1920
AGTTTTATTG TCCGTTTACT TGTTTCAGAG TTTGTATTGT GATTATCAAT TACCACACCA  1980
TCTCCCATGA AGAAAGGGAA CGGTGAAGTA CTAAGCGCTA GAGGAAGCAG CCAAGTCCTT  2040
TAGTGGAAGC ATGATTGGTG CCCAGTTAGC CTCTGCAGGA TGTGGAAACC TCCTTCCAGG  2100
GGAGGTTCAG TGAATTGTGT AGGAGAGGTT GTCTGTGGCC AGAATTCAAC CCTATACTCA  2160
CTTTCCCAAA TTGAATCACT GCTCACACTG CTGATGATTT AGAGTGCTGT CCGGTGGAGA  2220
TCCCACCCGA ACGTCTTATC TAATCATGAA ACTCCCTAGT TCCTTCATGT AACTTCCCTG  2280
AAAAATCTAA GTGTTTCATA AATTTGAGAG TCTGTGACCC ACTTACCTTG CATCTCACAG  2340
GTAGACAGTA TATAACTAAC AACCAAAGAC TACATATTGT CACTGACACA CACGTTATAA  2400
TCATTTATCA TATATATACA TACATGCATA CACTCTCAAA GCAAATAATT TTTCACTTCA  2460
AAACAGTATT GACTTGTATA CCTTGTAATT TGAAATATTT TCTTTGTTAA AATAGAATGG  2520
TATCAATAAA TAGACCATTA ATCAG
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Seq ID NO: 114 Protein sequence:
Protein Accession #: NP_002407

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1    11    21    31    41    51
|    |     |     |     |     |
MKKSGVLFLL GIILLVLIGV QGTPVVRKGR CSCISTNQGT IHLQSLKDLK QFAPSPSCEK  60
IEIIATLKNG VQTCLNPDSA DVKELIKKWE KQVSQKKKQK NGKKHQKKKV LKVRKSQRSR  120
QKKTT
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Seq ID NO: 115 DNA sequence
Nucleic Acid Accession #: NM_003238.1
Coding sequence: 182-1426 (underlined sequences correspond to start and stop codons)

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1    11    21    31    41    51
|    |     |     |     |     |
CAAGCAGGAT ACGTTTTTCT GTTGGGCATT GACTAGATTG TTTGCAAAAG TTTCGCATCA  60
AAAACAAACA ACAACAACAA AAAACCAAAC AACTCTCCTT GATCTATACT TTGAGAATTG  120
```

TTGATTTCTT TTTTTTTATT CTGACTTTTA AAAACAACTT TTTTTTCCAC TTTTTTAAAA 180
AATGCACTAC TGTGTGCTGA GCGCTTTTCT GATCCTGCAT CTGGTCACGG TCGCGCTCAG 240
CCTGTCTACC TGCAGCACAC TCGATATGGA CCAGTTCATG CGCAAGAGGA TCGAGGCGAT 300
CCGCCGGCAG ATCCTGAGCA AGCTGAAGCT CACCAGTCCC CCAGAAGACT ATCCTGAGCC 360
CGAGGAAGTC CCCCCGGAGG TGATTTCCAT CTACAACAGC ACCAGGGACT TGCTCCAGGA 420
GAAGGCGAGC CGGAGGGCGG CCGCCTGCGA GCGCGAGAGG AGCGACGAAG AGTACTACGC 480
CAAGGAGGTT TACAAAATAG ACATGCCGCC CTTCTTCCCC TCCGAAAATG CCATCCCGCC 540
CACTTTCTAC AGACCCTACT TCAGAATTGT TCGATTTGAC GTCTCAGCAA TGGAGAAGAA 600
TGCTTCCAAT TTGGTGAAAG CAGAGTTCAG AGTCTTTCGT TTGCAGAACC CAAAAGCCAG 660
AGTGCCTGAA CAACGGATTG AGCTATATCA GATTCTCAAG TCCAAAGATT TAACATCTCC 720
AACCCAGCGC TACATCGACA GCAAAGTTGT GAAAACAAGA GCAGAAGGCG AATGGCTCTC 780
CTTCGATGTA ACTGATGCTG TTCATGAATG GCTTCACCAT AAAGACAGGA ACCTGGGATT 840
TAAAATAAGC TTACACTGTC CCTGCTGCAC TTTTGTACCA TCTAATAATT ACATCATCCC 900
AAATAAAAGT GAAGAACTAG AAGCAAGATT TGCAGGTATT GATGGCACCT CCACATATAC 960
CAGTGGTGAT CAGAAAACTA TAAAGTCCAC TAGGAAAAAA AACAGTGGGA AGACCCCACA 1020
TCTCCTGCTA ATGTTATTGC CCTCCTACAG ACTTGAGTCA CAACAGACCA ACCGGCGGAA 1080
GAAGCGTGCT TTGGATGCGG CCTATTGCTT TAGAAATGTG CAGGATAATT GCTGCCTACG 1140
TCCACTTTAC ATTGATTTCA AGAGGGATCT ACGGTGGAAA TGGATACACG AACCCAAAGG 1200
GTACAATGCC AACTTCTGTG CTGGAGCATG CCCGTATTTA TGGAGTTCAG ACACTCAGCA 1260
CAGCAGGGTC CTGAGCTTAT ATAATACCAT AAATCCAGAA GCATCTGCTT CTCCTTGCTG 1320
CGTGTCCCAA GATTTAGAAC CTCTAACCAT TCTCTACTAC ATTGGCAAAA CACCCAAGAT 1380
TGAACAGCTT TCTAATATGA TTGTAAAGTC TTGCAAATGC AGCTAAAATT CTTGGAAAAG 1440
TGGCAAGACC AAAATGACAA TGATGATGAT AATGATGATG ACGACGACAA CGATGATGCT 1500
TGTAACAAGA AAACATAAGA GAGCCTTGGT TCATCAGTGT TAAAAAATTT TTGAAAAGGC 1560
GGTACTAGTT CAGACACTTT GGAAGTTTGT GTTCTGTTTG TTAAAACTGG CATCTGACAC 1620
AAAAAAAGTT GAAGGCCTTA TTCTACATTT CACCTACTTT GTAAGTGAGA GAGACAAGAA 1680
GCAAATTTTT TTAAA

Seq ID NO: 116 Protein sequence:
Protein Accession #: NP_003229.1

1 11 21 31 41 51
MHYCVLSAFL ILHLVTVALS LSTCSTLDMD QFMRKRIBAI RQQILSKLKL TSPPEDVPEP 60
EEVPPEVISI VNSTRDLLQB KASRRAAACB RERSDEEYYA KEVYKIDMPP FFPSENAIPP 120
TFVRPYFRIV RFDVSAMEKN ASNLVKAEFR VFRLQNPKAR VPEQRIELYQ ILKSKDLTSP 180
TQRVIDSKVV KTRAEGEWLS FDVTDAVHEW LHHKDRNLGF KISLHCPCCT PVPSNNVIP 240
NKSEEILEARF AGIDGTSTYT SGDQKTIKST RKKNSGKTPH LLLMLLPSYR LESQQTNRRK 300
KRALDAAYCF RNVQDNCCLR PLYIDFKRDL GWKWIHEPKG YNANFCAGAC PYLWSSDTQH 360
SRVLSLYNTI NPEASASPCC VSQDLEPLTI LYYIGKTPKI EQLSNMIVKS CKCS

Seq ID NO: 117 DNA sequence
Nucleic Acid Accession #: NM_000095.1
Coding sequence: 26-2299 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
CAGCACCCAG CTCCCCGCCA CCGCCATGGT CCCCGACACC GCCTGCGTTC TTCTGCTCAC 60
CCTGGCTGCC CTCGGCGCGT CCGGACAGGG CCAGAGCCCG TTGGGCTCAG ACCTGGGCCC 120
GCAGATGCTT CGGGAACTGC AGGAAACCAA CGCGGCGCTG CAGGACGTGC GGGACTGGCT 180
GCGGCAGCAG GTCAGGGAGA TCACGTTCCT GAAAAACACG GTGATGGAGT GTGACGCGTG 240
CGGGATGCAG CAGTCAGTAC GCACCGGCCT ACCCAGCGTG CGGCCCCTGC TCCACTCGGC 300
GCCCGGCTTC TGCTTCCCCG GCGTGGCCTG CATCCAGACG GAGAGCGGCG GCGGCTGCGG 360
CCCCTGCCCC GCGGGCTTCA CGGGCAACGG CTCGCACTGC ACCGACGTCA ACGAGTGCAA 420
CGCCCACCCC TGCTTCCCCC GAGTCCGCTG TATCAACACC AGCCCGGGGT TCCGCTGCGA 480
GGCTTGCCCG CCGGGGTACA GCGGCCCCAC CCACCAGGGC GTGGGGCTGG CTTTCGCCAA 540
GGCCAACAAG CAGGTTTGCA CGGACATCAA CGAGTGTGAG ACCGGGCAAC ATAACTGCGT 600
CCCCAACTGC GTGTGCATCA ACACCCGGGG CTCCTTCCAG TGCGGCCCGT GCGACCCCGG 660
CTTCGTGGGC GACCAGGCGT CCGGCTGCCA GCGCGGCGCA CAGCGCTTCT GCCCCGACGG 720
CTCCCCCAGC GAGTGCCACG AGCATGCAGA CTGCGTCCTA GAGCGCGATG GCTCGCGGTC 780
GTGCGTGTGT CGCGTTGGCT GGGCGGCAA CGGGATCCTC TGTGGTCGCG ACACTGACCT 840
AGACGGCTTC CCGGACGAGA AGCTGCGCTG CCCGGAGCCG CAGTGCCGTA AGGACAACTG 900
CGTGACTGTG CCCAACTCAG GGCAGGAGGA TGTGGACCGC GATGGCATCG GAGACGCCTG 960
CGATCCGGAT GCCGACGGGG ACGGGGTCCC CAATGAAAAG GACAACTGCC CGCTGGTGCG 1020
GAACCCAGAC CAGCGCAACA CGGACGAGGA CAAGTGGGGC GATGCGTGCG ACAACTGCCG 1080
GTCCCAGAAG AACGACGACC AAAAGGACAC AGACCAGGAC GCCCGGGGCG ATGCGTGCGA 1140
CGACGACATC GACGGCGACC GGATCCGCAA CCAGGCCGAC AACTGCCCTA GGGTACCCAA 1200
CTCAGACCAG AAGGACAGTG ATGGCGATGG TATAGGGGAT GCCTGTGACA ACTGTCCCCA 1260
GAAGAGCAAC CCGGATCAGG CGGATGTGGA CCACGACTTT GTGGGAGATG CTTGTGACAG 1320
CGATCAAGAC CAGGATGGAG ACGGACATCA GGACTCTCGG GACAACTGTC CCACGGTGCC 1380
TAACAGTGCC CAGGAGGACT CAGACCACGA TGGCCAGGGT GATGCCTGCG ACGACGACGA 1440
CGACAATGAC GGAGTCCCTG ACAGTCGGGA CAACTGCCGC CTGGTGCCTA ACCCCGGCCA 1500
GGAGGACGCG GACAGGGACG GCGTGGGCTA CGTGTGCCAG GACGACTTTG ATGCAGACAA 1560
GGTGGTAGAC AAGATCGACG TGTGTCCGGA GAACGCTGAA GTCACGCTCA CCGACTTCAG 1620
GGCCTTCCAG ACAGTCGTGC TGGACCCGGA GGGTGACGCG CAGATTGACC CCAACTGGGT 1680
GGTGCTCAAC CAGGGAAGGG AGATCGTGCA GACAATGAAC AGCGACCCAG GCCTGGCTGT 1740
GGGTTACACT GCCTTCAATG GCGTGGACTT CGAGGGCACG TTCCATGTGA ACACGGTCAC 1800

GGATGACGAC TATGCGGGCT TCATCTTTGG CTACCAGGAC AGCTCCAGCT TCTACGTGGT 1860
CATGTGGAAG CAGATGGAGC AAACGTATTG GCAGGCGAAC CCCTTCCGTG CTGTGGCCGA 1920
GCCTGGCATC CAACTCAAGG CTGTGAAGTC TTCCACAGGC CCCGGGGAAC AGCTGCGGAA 1980
CGCTCTGTGG CATACAGGAG ACACAGAGTC CCAGGTGCGG CTGCTGTGGA AGGACCCGCG 2040
AAACGTGGGT TGGAAGGACA AGAAGTCCTA TCGTTGGTTC CTGCAGCACC GGCCCCAAGT 2100
GGGCTACATC AGGGTGCGAT TCTATGAGGG CCCTGAGCTG GTGGCCGACA GCAACGTGGT 2160
CTTGGACACA ACCATGCGGG GTGGCCGCCT GGGGGTCTTC TGCTTCTCCC AGGAGAACAT 2220
CATCTGGGCC AACCTGCGTT ACCGCTGCAA TGACACCATC CCAGAGGACT ATGAGACCCA 2280
TCAGCTGCGG CAAGCCTAGG GACCAGGGTG AGGACCCGCC GGATGACAGC CACCCTCACC 2340
GCGGCTGGAT GGGGGCTCTG CACCCAGCCC AAGGGGTGGC CGTCCTGAGG GGGAAGTGAG 2400
AAGGGCTCAG AGAGGACAAA ATAAAGTGTG TGTGCAGGG

Seq ID NO: 118 Protein sequence:
Protein Accession #: NP_000086.1

1 11 21 31 41 51
MVPDTACVLL LTLAALGASQ QGQSPLGSDL GPQMLRELQE TNAALQDVRD WLRQQVREIT 60
FLKNTVMECD ACGMQQSVRT GLPSVRPLLH CAPGFCFPGV ACIQTESGGR CGPCPAGFTG 120
NGSHCTDVNE CNAHPCFPRV RCINTSPGFR CEACPPGYSG PTHQGVGLAF AKANKQVCTD 180
INECETGQHN CVPNSVCINT RGSFQCGPCQ PGFVGDQASG CQRGAQRFCP DGSPSECHEH 240
ADCVLERDGS RSCVCRVGWA GNGILCGRDT DLDGFPDEKL RCPEPQCRKD NCVTVPNSGQ 300
EDVDRDGIGD ACDPDADGDG VPNEKDNCPL VRNPDQRNTD EDKWGDACDN CRSQKNDDQK 360
DTDQDGRGDA CDDDIDGDRI RNQADNCPRV PNSDQKDSDG DGIGDACDNC PQKSNPDQAD 420
VDHDFVGDAC DSDQDQDGDG HQDSRDNCPT VPNSAQEDSD HDQQGDACDD DDDNDGVPDS 480
RDNCRLVPNP QQEDADRDGV GDVCQDDFDA DKVVDKIDVC PENAEVTLTD FRAFQTVVLD 540
PEGDAQIDPN WVVLNQGREI VQTMNSDPGL AVGYTAFNGV DFEGTFHVNT VTDDDYAGFI 600
FGYQDSSSFY VVMWKQMEQT YWQANPFRAV ABPGIQLKAV KSSTGPGEQL RNALWHTGDT 660
ESQVRLLWKD PRNVGWKDKK SYRWFLQHRP QVGYIRVRFY EGPELVADSN VVLDTTMRGG 720
RLGVFCFSQE NIIWANLRYR CNDTIPEDYE THQLRQA

Seq ID NO: 119 DNA sequence
Nucleic Acid Accession #: NM_014211
Coding sequence: 157-1479 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
GGGACAGGGC TGAGGATGAG GAGAACCCTG GGGACCCAGA AGACCGTGCC TTGCCCGGAA 60
GTCCTGCCTG TAGGCCTGAA GGACTTGCCC TAACAGAGCC TCAACAACTA CCTGGTGATT 120
CCTACTTCAG CCCCTTGGTG TGAGCAGCTT CTCAACATGA ACTACAGCCT CCACTTGGCC 180
TTCGTGTGTC TGAGTCTCTT CACTGAGAGG ATGTGCATCC AGGGGAGTCA GTTCAACGTC 240
GAGGTCGGCA GAAGTGACAA GCTTTCCCTG CCTGGCTTTG AGAACCTCAC AGCAGGATAT 300
AACAAATTTC TCAGGCCCAA TTTTGGTGGA GAACCCGTAC AGATAGCGCT GACTCTGGAC 360
ATTGCAAGTA TCTCTAGCAT TTCAGAGAGT AACATGGACT ACACAGCCAC CATATACGTC 420
CGACAGCGCT GGATGGACCA GCGGCTGGTG TTTGAAGGCA ACAAGAGCTT CACTCTGGAT 480
GCCCGCCTCG TGGAGTTCCT CTGGGTGCCA GATACTTACA TTGTGGAGTC CAAGAAGTCC 540
TTCCTCCATG AAGTCACTGT GGGAAACAGG CTCATCCGCC TCTTCTCCAA TGGCACGGTC 600
CTGTATGCCC TCAGAATCAC GACAACTGTT GCATGTAACA TGGATCTGTC TAAATACCCC 660
ATGGACACAC AGACATCCAA GTTGCAGCTG GAAAGCTGGG GCTATGATGG AAATGATGTG 720
GAGTTCACCT GGCTGAGAGG GAACGACTCT GTGCGTGGAC TGGAACACCT GCGGCTTGCT 780
CAGTACACCA TAGAGCGGTA TTTCACCTTA GTCACCAGAT CGCAGCAGGA GACAGGAAAT 840
TACACTAGAT TGGTCTTACA GTTTGAGCTT CGGAGGAATG TTCTGTATTT CATTTTGGAA 900
ACCTACGTTC CTTCCACTTT CCTGGTGGTG TTGTCCTGGG TTTCATTTTG GATCTCTCTC 960
GATTCAGTCC CTGCAAGAAC CTGCATTGGA GTGACGACCG TGTTATCAAT GACCACACTG 1020
ATGATCGGGT CCCGCACTTC TCTTCCCAAC ACCAACTGCT TCATCAAGGC CATCGATGTG 1080
TACCTGGGGA TCTGCTTTAG CTTTGTGTTT GGGGCCTTGC TAGAATATGC AGTTGCTCAC 1140
TACAGTTCCT TACAGCAGAT GGCAGCCAAA GATAGGGGGA CAACAAAGGA AGTAGAAGAA 1200
GTCAGTATTA CTAATATCAT CAACAGCTCC ATCTCCAGCT TTAAACGGAA GATCAGCTTT 1260
GCCAGCATTG AAATTTCCAG CGACAACGTT GACTACAGTG ACTTGACAAT GAAAACCAGC 1320
GACAAGTTCA AGTTTGTCTT CCGAGAAAAG ATGGGCAGGA TTGTTGATTA TTTCACAATT 1380
CAAAACCCCA GTAATGTTGA TCACTATTCC AAACTACTGT TTCCTTTGAT TTTTATGCTA 1440
GCCAATGTAT TTTACTGGGC ATACTACATG TATTTTTGAG TCAATGTTAA ATTTCTTTCA 1500
TGCCATAGGT CTTCAACAGG ACAAGATAAT GATGTAAATG GTATTTTAGG CCAAGTGTGC 1560
ACCCACATCC AATGGTGCTA CAAGTGACTG AAATAATATT TGAGTCTTTC TGCTCAAAGA 1620
ATGAAGCTCC AACCATTGTT CTAAGCTGTG TAGAAGTCCT AGCATTATAG GATCTTGTAA 1680
TAGAAACATC AGTCCATTCC TCTTTCATCT TAATCAAGGA CATTCCCATG GAGCCCAAGA 1740
TTACAAATGT ACTCAGGGCT GTTTATTCGG TGGCTCCCTG GTTTGCATTT ACCTCATATA 1800
AAGAATGGGA AGGAGACCAT TGGGTAACCC TCAAGTGTCA GAAGTTGTTT CTAAAGTAAC 1860
TATACATGTT TTTTACTAAA TCTCTGCAGT GCTTATAAAA TACATTGTTG CCTATTTAGG 1920
GAGTAACATT TTCTAGTTTT TGTTTCTGGT TAAAATGAAA TATGGGCTTA TGTCAATTCA 1980
TTGGAAGTCA ATGCACTAAC TCAATACCAA GATGAGTTTT TAAATAATGA ATATTATTTA 2040
ATACCACAAC AGAATTATCC CCAATTTCCA ATAAGTCCTA TCATTGAAAA TTCAAATATA 2100
AGTGAAGAAA AAATTAGTAG ATCAACAATC TAAACAAATC CCTCGGTTCT AAGATACAAT 2160
GGATTCCCCA TACTGGAAGG ACTCTGAGGC TTTATTCCCC CACTATGCAT ATCTTATCAT 2220
TTTATTATTA TACACACATC CATCCTAAAC TATACTAAAG CCCTTTTCCC ATGCATGGAT 2280
GGAAATGGAA GATTTTTTTG TAACTTGTTC TAGAAGTCTT AATATGGGCT GTTCCCATGA 2340
AGGCTTGCAG AATTGAGTCC ATTTTCTAGC TGCCTTTATT CACATAGTGA TGGGGTACTA 2400

AAAGTACTGG GTTGACTCAG AGAGTCGCTG TCATTCTGTC ATTGCTGCTA CTCTAACACT 2460
GAGCAACACT CTCCCAGTGG CAGATCCCCT GTATCATTCC AAGAGGAGCA TTCATCCCTT 2520
TGCTCTAATG ATCAGGAATG ATGCTTATTA GAAAACAAAC TGCTTGACCC AGGAACAAGT 2580
GGCTTAGCTT AAGTAAACTT GGCTTTGCTC AGATCCCTGA TCCTTCCAGC TGGTCTGCTC 2640
TGAGTGGCTT ATCCCGCATG AGCAGGAGCG TGCTGGCCCT GAGTACTGAA CTTTCTGAGT 2700
AACAATGAGA CACGTTACAG AACCTATGTT CAGGTTGCGG GTGAGCTGCC CTCTCCAAAT 2760
CCAGCCAGAG ATGCACATTC CTCGGCCAGT CTCAGCCAAC AGTACCAAAA GTGATTTTTG 2820
AGTGTGCCAG GGTAAAGGCT TCCAGTTCAG CCTCAGTTAT TTTAGACAAT CTCGCCATCT 2880
TTAATTTCTT AGCTTCCTGT TCTAATAAAT GCACGGCTTT ACCTTTCCTG TCAGAAATAA 2940
ACCAAGGCTC TAAAAGATGA TTTCCCTTCT GTAACTCCCT AGAGCCACAG GTTCTCATTC 3000
CTTTTCCCAT TATACTTCTC ACAATTCAGT TTCTATGAGT TTGATCACCT GATTTTTTTA 3060
ACAAAATATT TCTAACGGGA ATGGGTGGGA GTGCTGGTGA AAAGAGATGA AATGTGGTTG 3120
TATGAGCCAA TCATATTTGT GATTTTTTAA AAAAAGTTTA AAAGGAAATA TCTGTTCTGA 3180
AACCCCACTT AAGCATTGTT TTTATATAAA AACAATGATA AAGATGTGAA CTGTGAAATA 3240
AATATACCAT ATTAGCTACC CACC

Seq ID NO: 120 Protein sequence:
Protein Accession #: NP_055026.1

1 11 21 31 41 51
MNYSLHLAPV CLSLFTERMC IQQSQFNVEV GRSDKLSLPG FENLTAGYNK FLRPNFGGEP 60
VQIALTLDIA SISSISESNM DYTATIYLRQ RWMDQRLVFE GNKSFTLDAR LVEFLWVPDT 120
YIVESKKSFL HEVTVGNRLI RLFSNGTVLY ALRITTTVAC NMDLSKYPMD TQTCKLQLES 180
WGYDGNDVEF TWLRGNDSVR GLEHLRLAQY TIERYFTLVT RSQQETGNYT RLVLQFELRR 240
NVLYFILETY VPSTFLVVLS WVSFWISLDS VPARTCIGVT TVLSMTTLMI GSRTSLPNTN 300
CFIKAIDVYL GICFSFVFGA LLEYAVAHYS SLQQMAAKDR GTTKEVEEVS ITNIINSSIS 360
SFKRRISFAS IEISSDNVDY SDLTMKTSDK FKFVFREKMG RIVDYFTIQN PSNVDHYSKL 420
LFPLIFMLAN VFYWAYYMYF

Seq ID NO: 121 DNA sequence
Nucleic Acid Accession #: NM_001854
Coding sequence: 163-5582 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
AACCATCAAA TTTAGAAGAA AAAGCCCTTT GACTTTTTCC CCCTCTCCCT CCCCAATGGC 60
TGTGTAGCAA ACATCCCTGG CGATACCTTG GAAAGGACGA AGTTGGTCTG CAGTCGCAAT 120
TTCGTGGGTT GAGTTCACAG TTGTGAGTGC GGGGCTCGGA GATGGAGCCG TGGTCCTCTA 180
GGTGGAAAAC GAAACGGTGG CTCTGGGATT TCACCGTAAC AACCCTCGCA TTGACCTTCC 240
TCTTCCAAGC TAGAGAGGTC AGAGGAGCTG CTCCAGTTGA TGTACTAAAA GCACTAGATT 300
TTCACAATTC TCCAGAGGGA ATATCAAAAA CAACGGGATT TTGCACAAAC AGAAAGAATT 360
CTAAAGGCTC AGATACTGCT TACAGAGTTT CAAAGCAAGC ACAACTCAGT GCCCCAACAA 420
AACAGTTATT TCCAGGTGGA ACTTTCCCAG AAGACTTTTC AATACTATTT ACAGTAAAAC 480
CAAAAAAAGG AATTCAGTCT TTCCTTTTAT CTATATATAA TGAGCATGGT ATTCAGCAAA 540
TTGGTGTTGA GGTTGGGAGA TCACCTGTTT TTCTGTTTGA AGACCACACT GGAAAACCTG 600
CCCCAGAAGA CTATCCCCTC TTCAGAACTG TTAACATCGC TGACGGGAAG TGGCATCGGG 660
TAGCAATCAG CGTGGAGAAG AAAACTGTGA CAATGATTGT TGATTGTAAG AAGAAAACCA 720
CGAAACCACT TGATAGAAGT GAGAGAGCAA TTGTTGATAC CAATGGAATC ACGGTTTTTG 780
GAACAAGGAT TTTGGATGAA GAAGTTTTTG AGGGGACAT TCAGCAGTTT TTGATCACAG 840
GTGATCCCAA GGCAGCATAT GACTACTGTG AGCATTATAG TCCAGACTGT GACTCTTCAG 900
CACCCAAGGC TGCTCAAGCT CAGGAACCTC AGATAGATGA GTATGCACCA GAGGATATAA 960
TCGAATATGA CTATGAGTAT GGGGAAGCAG AGTATAAAGA GGCTGAAAGT GTAACAGAGG 1020
GACCCACTGT AACTGAGGAG ACAATAGCAC AGACGGAGGC AAACATCGTT GATGATTTTC 1080
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GGACAAATGA GCCAAATCCA GTTGAAGAAA TATTTACTGA AGAATATCTA ACGGAGAGG 1200
ATTATGATTC CCAGAGGAAA AATTCTGAGG ATACACTATA TGAAAACAAA GAAATAGACG 1260
GCAGGGATTC TGATCTTCTG GTAGATGGAG ATTTAGGCGA ATATGATTTT TATGAATATA 1320
AAGAATATGA AGATAAACCA ACAAGCCCCC CTAATGAAGA ATTTGGTCCA GGTGTACCAG 1380
CAGAAACTGA TATTACAGAA ACAAGCATAA ATGGCCATGG TGCATATGGA GAGAAAGGAC 1440
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CAGGACCTGC AGGTATTATG GGTCCTCCAG GTCTACAAGG CCCCACTGGA CCCCCTGGTG 1560
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GTTCATCTGG GGCCAAAGGT GAGAGTGGTG ATCCAGGTCC TCAGGGCCCT CGAGGCGTCC 1860
AGGGTCCCCC TGGTCCAACG GGAAAACCTG GAAAAAGGGG TCGTCCAGGT GCAGATGGAG 1920
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CAATTGGTCC TCCTGGTGAA AAAGGACCAC AAGGAAAACC AGGACTTGCT GGACTTCCTG 2340
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TTCTCAACTC TCCTTTTCCT ATTTGAATTT CTTTGGTGCT GTAGAAAACA AAAAAGAAAA 5880
AATATATATT CATAAAAAAT ATGGTGCTCA TTCTCATCCA TCCAGGATGT ACTAAAACAG 5940
TGTGTTTAAT AAATTGTAAT TATTTTGTGT ACAGTTCTAT ACTGTTATCT GTGTCCATTT 6000
CCAAAACTTG CACGTGTCCC TGAATTCCGC TGACTCTAAT TTATGAGGAT GCCGAACTCT 6060
GATGGCAATA ATATATGTAT TATGAAAATG AAGTTATGAT TTCCGATGAC CCTAAGTCCC 6120
TTTCTTTGGT TAATGATGAA ATTCCTTTGT GTGTGTTT

Seq ID NO: 122 Protein sequence:
Protein Accession #: NP_001845

1 11 21 31 41 51
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CTNRKNSKGS DTAYRVSKQA QLSAPTKQLF PGGTFPEDFS ILFTVKPKKG IQSFLLSIYN 120
EHGIQQIGVE VGRSPVFLFB DHTGKPAPED YPLFRTVNIA DGKWHRVAIS VEKKTVTMIV 180
DCKKKTTKPL DRSERAIVDT NGITVFGTRI LDEEVFEGDI QQFLITGDPK AAYDYCEHYS 240
PDCDSSAPKA AQAQEPQIDE YAPEDIEEYD YEYGEAEVKE AESVTEGPTV TEETIAQTEA 300
NIVDDFQEYN YGTMESYQTE APRHVSGTNE PNPVEEGPTE EYLTGEDYDS QRKNSEDTLY 360
ENKEIDGRDS DLLVDGDLGE YDPYEYKEYE DKPTSPPNEE FGPGVPAETD ITETSINGHG 420
AYQEKGQKGE PAVVEPGMLV EGPPGPAGPA GIMGPPGLQG PTGPPGDPGD RGPPGRPGLP 480

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GPVGGPGSSG AKGESGDPGP QGPRGVQGPP GPTGKPGKRG RPGADGGRGM PGEPGAKGDR 600
GFDGLPGLPG DKGHRGERGP QGPPGPPGDD GMRGEDGEIG PRGLPGEAGP RGLLGPRGTP 660
GAPGQPGMAG VDGPPGPKGN MGPQGEPGPP GQQGNPGPQG LPGPQGPIGP PGEKGPQGKP 720
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GPKGTSGGDG PPGPPGERGP QGPQGPVGPP GPKGPPGPPG RMGCPGHPGQ RGETGFQGKT 960
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GPPGPAGEKG APGEKGPQGP AGRDGVQGPV GLPGPAGPAG SPGEDGDKGE IGEPGQKGSK 1140
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GLPGPPGEKG ENGDVGPWGP PGPPGPRGPQ GPNGADGPQG PPGSVGSVGG VGEKGEPGEA 1260
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EYWIDPNQGC SGDSFKVYCN FTSGGETCIY PDKKSEGVRV SSWPKEKPGS WFSEFKRGKL 1680
LSYLDVEGNS INMVQMTFLK LLTASARQNF TYHCHQSAAW YDVSSGSYDK ALRFLGSNDE 1740
EMSYDNNPFI KTLYDGCTSR KGYEKTVIEI NTPKIDQVPI VDVMISDFGD QNQKFGFEVG 1800
PVCPLG

Seq ID NO: 123 DNA sequence
Nucleic Acid Accession #: NM_015886
Coding sequence: 485-1261 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51

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TGAAAATTTC CCACTGAAAA TATGCAGTAA TATATTTTGT GGTTCAGACA TTTGGGGCAA 180
ATGGTTCACA TTCATTTTAG GGTTAGTGGT CATGCTGTTT ATTTTTCTCT GCTATACAAA 240
GTTCCTCTTA GGGGTCTGCC TCATGACACT AAAAAATGAA TAGAGATTCT ACTGTAGGTT 300
ATCTCCTAGG CTTGAGTTCA ACATTTGTTT GGATTTTTGA AGAAAGTCAA ATCAAGCAAT 360
GCTCCCAAAT GATGTCTTTG TAAATTCATA CCCTCTGGCC CTATTTTTTT TCATAGACCC 420
TAACTCTACC TTTCTGCTTT AAAGCAAAGT AAACTCGGTG GCCTCTTCTT CTCCACCCCT 480
CAAAATGATA GCAATCTCTG CCGTCAGCAG TGCACTCCTG TTCTCCCTTC TCTGTGAAGC 540
AAGTACCGTC GTCCTACTCA ATTCCACTGA CTCATCCCCG CCAACCAATA ATTTCACTGA 600
TATTGAAGCA GCTCTGAAAG CACAATTAGA TTCAGCGGAT ATCCCCAAAG CCAGGCGGAA 660
GCGCTACATT TCGCAGAATG ACATGATCGC CATTCTTGAT TATCATAATC AAGTTCGGGG 720
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TGTGTGGCGA CGTGCAGTTT ACTTGGTATG CAACTATGCC CCAAAGGGCA ATTGGATTGG 1140
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AGTTTACCTT TTCCTCCAGG AAATATAATG ATTTCTGGGA ACATGGGCAT GTATATATAT 1320
ATATGGAGAG AGAATTTTGC ACATATTATA CATATTTTGT GCTAATCTTG TTTTCCTCTT 1380
AGTATTCCTT TGTATAAATT AGTGTTTGTC TAGCATGTTT GTTTAATCCT TTGGGAATTC

Seq ID NO: 124 Protein sequence:
Protein Accession #: NP_056970.1

1 11 21 31 41 51

MIAISAVSSA LLFSLLCEAS TVVLLNSTDS SPPTNNPTDI EAALKAQLDS ADIPKARRKR 60
YISQNDMIAI LDYHNQVRGK VFPPAANMEY MVWDENLAKS ABAWAATCIW DHGPSYLLRF 120
LQQNLSVRTG RYRSILQLVK PWYDEVKDYA FPYPQDCNPR CPMRCFGPMC TIVTQMVWAT 180
SNRIGCAIHA CQNMNVWGSV WRRAVYLVCN YAPKGNWIGE APYKVGVPCS SCPPSYGGSC 240
TDNLCPPGVT SNYLYWFK

Seq ID NO: 125 DNA sequence
Nucleic Acid Accession #: NM_001793
Coding sequence: 54-2543 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51

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CCTCCGAGCC GTGCCGGGCG GTCTTCAGGG AGGCTGAAGT GACCTTGGAG GCGGGAGGCG 180
CGGAGCAGGA GCCCGGCCAG GCGCTGGGGA AAGTATTCAT GGGCTGCCCT GGGCAAGAGC 240

CAGCTCTGTT TAGCACTGAT AATGATGACT TCACTGTGCG GAATGGCGAG ACAGTCCAGG 300
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Seq ID NO: 126 Protein sequence:
Protein Accession #: NP_001784

1 11 21 31 41 51

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KGPFPQRLNQ LKSNKDRDTK IFYSITGPGA DSPPEGVFAV EKETGWLLLN KPLDREEIAK 180
YELFGHAVSB NGASVEDPMN ISIIVTDQND HKPKFTQDTF RGSVLEGVLP GTSVMQVTAT 240
DEDDAIYTYN GVVAYSIHSQ EPKDPHDLMF TIHRSTGTIS VISSGLDREK VPEYTLTIQA 300
TDMDGDGSTT TAVAVVEILD ANDNAPMFDP QKYEAHVPEN AVGHEVQRLT VTDLDAPNSP 360
AWRATYLIMG GDGGDHFTIT THPESNQGIL TTRKGLDFEA KNQHTLYVEV TNEAPFVLKL 420
PTSTATIVVH VEDVNEAPVF VPPSKVVEVQ EGIPTGEPVC VYTAEDPDKE NQKISYRILR 480
DPAGWLAMDP DSGQVTAVGT LDREDEQFVR NNIYEVMVLA MDNGSPPTTG TGTLLLTLID 540
VNDHGPVPEP RQITICNQSP VRHVLNITDK DLSPHTSPFQ AQLTDDSDIY WTAEVNEEGD 600
TVVLSLKKFL KQDTYDVHLS LSDHGNKEQL TVIRATVCDC HGHVETCPGP WKGGFILPVL 660
GAVLALLFLI LVLLLLVRKK RKIKEPLLLP EDDTRDNVFY YGEEGGGRED QDYDITQLHR 720
GLEARPEVVL RNDVAPTIIP TPMYRPRPAN PDEIGNFIIE NLKAANTDPT APPYDTLLVF 780
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Seq ID NO: 127 DNA sequence
Nucleic Acid Accession #: NM_003256.1
Coding sequence: 60-734 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51

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GGCTGTTGGA ACGAAAGCTC TATGGTTACC AGGCTCAGCA TTATGTCTGT ATGAAGCATG 660
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ATAAGAAGTG CCAAGTGGAC AGTCTGGCCA CTGTCAAGGC AGGGAAGGGG CCATGACTTT 900
TCTGCCCTGC CCTCAGCCTG TTGCCCTGCC TCCCAAACCC CATTAGTCTA GCCTTGTAGC 960
TGTTACTGCA AGTGTTTCTT CTGGCTTAGT CTGTTTTCTA AAGCCAGGAC TATTCCCTTT 1020
CCTCCCCAGG AATATGTGTT TTCCTTTGTC TTAATCGATC TGGTAGGGGA GAAATGGCGA 1080
ATGTCATACA CATGAGATGG TATATCCTTG CGATGTACAG AATCAGAAGG TGTTTTGACA 1140
GCATCATAAA CAGGCTGACT GGCAGGAATG AAAAAAAAAA AAAAAAAAA

Seq ID NO: 128 Protein sequence:
Protein Accession #: NP_003247.1

1 11 21 31 41 51
| | | | | |
MPGSPRPAPS WVLLLRLLAL LRPPGLGEAC SCAPAHPQQH ICHSALVIRA KISSEKVVPA 60
SADPADTEKM LRVEIKQIKM FKGFEKVKDV QYIYTPFDSS LCGVKLEANS QKQYLLTGQV 120
LSDGKVFIHL CNYIEPWEDL SLVQRESLNH HYHLNCGCQI TTCYTVPCTI SAPNECLWTD 180
WLLERKLYGY QAQHYVCMKH VDGTCSWYRG HLPLRKEFVD IVQP

Seq ID NO: 129 DNA sequence
Nucleic Acid Accession #: NM_007207.2
Coding sequence: 143-1591 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
| | | | | |
CCACGCGTCC GCAATGAAGC CGAGTGAATG GGGGCTGAAT GTGCGAGTCC ATAGCTGAAG 60
AGGAGCGCCA GATGGTGGAG GAATACACTT ATTTATGAAA CTGTCTTGAG TTCTTCTTGA 120
ATTGCCAGTT TTCAGCCTCC TCATGCCTCC GTCTCCTTTA GACGACAGGG TAGTAGTGGC 180
ACTATCTAGG CCCGTCCGAC CTCAGGATCT CAACCTTTGT TTAGACTCTA GTTACCTTGG 240
CTCTGCCAAC CCAGGCAGTA ACAGCCACCC TCCTGTCATC GCCACCACCG TTGTGTCCCT 300
CAAGGCTGCG AATCTGACGT ATATGCCCTC ATCCAGCGGC TCTGCCCGCT CGCTGAATTG 360
TGGATGCAGC AGTGCCAGCT GCTGCACTGT GGCAACCTAC GACAAGGACA ATCAGGCCCA 420
AACCCAAGCC ATTGCCGCTG GCACCACCAC CACTGCCATC GGAACCTCTA CCACCTGCCC 480
TGCTAACCAG ATGGTCAACA ATAATGAGAA TACAGGCTCT CTAAGTCCAT CAAGTGGGGT 540
GGGCAGCCCT GTGTCAGGGA CCCCCAAGCA GCTAGCCAGC ATCAAAATAA TCTACCCCAA 600
TGACTTGGCA AAGAAGATGA CCAAATGCAG CAAGAGTCAC CTGCCGAGTC AGGGCCCTGT 660
CATCATTGAC TGCAGGCCCT TCATGGAGTA CAACAAGAGT CACATCCAAG GAGCTGTCCA 720
CATTAACTGT GCCGATAAGA TCAGCCGGCG GAGACTGCAG CAGGGCAAGA TCACTGTCCT 780
AGACTTGATT TCCTGTAGGG AAGGCAAGGA CTCTTTCAAG AGGATCTTTT CCAAAGAAAT 840
TATAGTTTAT GATGAGAATA CCAATGAACC AAGCCGAGTG ATGCCCTCCC AGCCACTTCA 900
CATAGTCCTC GAGTCCCTGA AGAGAGAAGG CAAAGAACCT CTGGTGTTGA AAGGTGGACT 960
TAGTAGTTTT AAGCAGAACC ATGAAAACCT CTGTGACAAC TCCCTCCAGC TCCAAGAGTG 1020
CCGGGAGGTG GGGGCCGCCA CATCCGCGGC CTCGAGCTTG CTACCTCAGC CCATCCCCAC 1080
CACCCCTGAC ATCGAGAACG CTGAGCTCAC CCCCATCTTG CCCTTCCTGT TCCTTGGCAA 1140
TGAGCAGGAT GCTCAGGACC TGGACACCAT GCAGCGGCTG AACATCGGCT ACGTCATCAA 1200
CGTCACCACT CATCTTCCCC TCTACCACTA TGAGAAAGGC CTGTTCAACT ACAAGCGGCT 1260
GCCAGCCACT GACAGCAACA AGCAGAACCT GCGGCAGTAC TTTGAAGAGG CTTTTGAGTT 1320
CATTGAGGAA GCTCACCAGT GTGGGAAGGG GCTTCTCATC CACTGCCAGG CTGGGGTGTC 1380
CCGCTCCGCC ACCATCGTCA TCGCTTACTT GATGAAGCAC ACTCGGATGA CCATGACTGA 1440
TGCTTATAAA TTTGTCAAAG GCAAACGACC AATTATCTCC CCAAACCTTA ACTTCATGGG 1500
GCAGTTGCTA GAGTTCGAGG AAGACCTAAA CAACGGTGTG ACACCGAGAA TCCTTACACC 1560
AAAGCTGATG GGCGTGGAGA CGGTTGTGTG ACAATGGTCT GGATGGAAAG GATTGCTGCT 1620
CTCCATTAGG AGACAATGAG GAAGGAGGAT GGATTCTGGT TTTTTTTCTT TCTTTTTTTT 1680
TTGTAGTTGG GAGTAAAGTT TGTGAATGGA AACAAACTTG GTTAAACACT TTATTTTTAA 1740
CAAGTGTAAG AAGACTATAC TTTTGATGCC ATTGAGATTC ACCTTCCACA AACTGGCCAA 1800
ATTAAGGAGG TTAAAGAAGT AATTTTTTTT AAGCCCAACC ATTAAAAATT TAATACAACT 1860
TGGTTTCTCC CCCTTTTTCC TTTAAAGCTA NTTTGTAAAA GTTTATGAG

Seq ID NO: 130 Protein sequence:
Protein Accession #: NP_009138.1

1 11 21 31 41 51
| | | | | |
MPPSPLDDRV VVALSRPVRP QDLNLCLDSS YLGSANPGSN SHPPVIATTV VSLKAANLTY 60
MPSSSGSARS LNCGCSSASC CTVATYDKDN QAQTQAIAAG TTTTAIGTST TCPANQMVNN 120
NENTGSLSPS SGVGSPVSGT PKQLASIKII YPNDLAKKMT KCSKSHLPSQ GPVIIDCRPP 180

MEYNKSHIQG AVHINCADKI SRRRLQQGKI TVLDLISCRE GKDSFKRIFS KEIIVYDENT 240
NEPSRVMPSQ PLHIVLESLK REGKEPLVLK GGLSSFKQNH ENLCDNSLQL QECREVGGGA 300
SAASSLLPQP IPTTPDIENA ELTPILPFLF LGNEQDAQDL DTMQRLNIGV VINVTTHLPL 360
YHYEKGLFNY KRLPATDSNK QNLRQYFEEA FEFIEEAHQC GKGLLIHCQA GVSRSATIVI 420
AYLMKHTRMT MTDAYKFVKG KRPIISPNLN FMGQLLEFEE DLNNGVTPRI LTPKLMGVET 480
VV

Seq ID NO: 131 DNA sequence
Nucleic Acid Accession #: NM_005409.3
Coding sequence: 94-378 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
| | | | | |
TTCCTTTCAT GTTCAGCATT TCTACTCCTT CCAAGAAGAG CAGCAAAGCT GAAGTAGCAG 60
CAACAGCACC AGCAGCAACA GCAAAAAACA AACATGAGTG TGAAGGGCAT GGCTATAGCC 120
TTGGCTGTGA TATTGTGTGC TACAGTTGTT CAAGGCTTCC CCATGTTCAA AAGAGGACGC 180
TGTCTTTGCA TAGGCCCTGG GGTAAAAGCA GTGAAAGTGG CAGATATTGA GAAAGCCTCC 240
ATAATGTACC CAAGTAACAA CTGTGACAAA ATAGAAGTGA TTATTACCCT GAAAGAAAAT 300
AAAGGACAAC GATGCCTAAA TCCCAAATCG AAGCAAGCAA GGCTTATAAT CAAAAAAGTT 360
GAAAGAAAGA ATTTTTAAAA ATATCAAAAC ATATGAAGTC CTGGAAAAGG GCATCTGAAA 420
AACCTAGAAC AAGTTTAACT GTGACTACTG AAATGACAAG AATTCTACAG TAGGAAACTG 480
AGACTTTTCT ATGGTTTTGT GACTTTCAAC TTTTGTACAG TTATGTGAAG GATGAAAGGT 540
GGGTGAAAGG ACCAAAAACA GAAATACAGT CTTCCTGAAT GAATGACAAT CAGAATTCCA 600
CTGCCCAAAG GAGTCCAGCA ATTAAATGGA TTTCTAGGAA AAGCTACCTT AAGAAAGGCT 660
GGTTACCATC GGAGTTTACA AAGTGCTTTC ACGTTCTTAC TTGTTGTATT ATACATTCAT 720
GCATTTCTAG GCTAGAGAAC CTTCTAGATT TGATGCTTAC AACTATTCTG TTGTGACTAT 780
GAGAACATTT CTGTCTCTAG AAGTTATCTG TCTGTATTGA TCTTTATGCT ATATTACTAT 840
CTGTGGTTAC AGTGGAGACA TTGACATTAT TACTGGAGTC AAGCCCTTAT AAGTCAAAAG 900
CATCTATGTG TCGTAAAGCA TTCCTCAAAC ATTTTTTCAT GCAAATACAC ACTTCTTTCC 960
CCAAATATCA TGTAGCACAT CAATATGTAG GGAAACATTC TTATGCATCA TTTGGTTTGT 1020
TTTATAACCA ATTCATTAAA TGTAATTCAT AAAATGTACT ATGAAAAAAA TTATACGCTA 1080
TGGGATACTG GCAACAGTGC ACATATTTCA TAACCAAATT AGCAGCACCG GTCTTAATTT 1140
GATGTTTTTC AACTTTTATT CATTGAGATG TTTTGAAGCA ATTAGGATAT GTGTGTTTAC 1200
TGTACTTTTT GTTTTGATCC GTTTGTATAA ATGATAGCAA TATCTTGGAC ACATTTGAAA 1260
TACAAAATGT TTTTGTCTAC CAAAGAAAAA TGTTGAAAAA TAAGCAAATG TATACCTAGC 1320
AATCACTTTT ACTTTTTGTA ATTCTGTCTC TTAGAAAAAT ACATAATCTA ATCAATTTCT 1380
TTGTTCATGC CTATATACTG TAAAATTTAG GTATACTCAA GACTAGTTTA AAGAATCAAA 1440
GTCATTTTTT TCTCTAATAA ACTACCACAA CCTTTCTTTT TTAAAAAAAA AAA

Seq ID NO: 132 Protein sequence:
Protein Accession #: NP_005400.1

1 11 21 31 41 51
| | | | | |
MSVKGMAIAL AVILCATVVQ GFPMFKRGRC LCIGPGVKAV KVADIEKASI MYPSNNCDKI 60
EVIITLKENK GQRCLNPKSK QARLIIKKVE RKNF

Seq ID NO: 133 DNA sequence
Nucleic Acid Accession #: NM_012342
Coding sequence: 373-1155 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
| | | | | |
CTGGCCGCGG CGGGAGCTGC GGCGGATACC CTTGCGTGCT GTGGAGACCC TACTCTCTTC 60
GCTGAGAACG GCCGCTAGCG GGGACTGAAG GCCGGGAGCC CACTCCCGAC CCGGGGCTAG 120
CGTGCGTCCC TAGAGTCGAG CGGGGCAAGG GAGCCAGTGG CCGCCGACGG GGGACCGGGA 180
AACTTTTCTG GGCTCCTGGA GAGCCCTGTA GCCGCGCTCC ATGCTCCGGC AGCGGCCCGA 240
AACCCAGCCC CGCCGCTGAC GGAGCCCGCC GCTCCGGGCA GGGCCCATGC CCTGCGCGCT 300
CCTGGGGTCG TAGCTGCCGC CGAGCCGGGG CTCCGGAAGC CGGCGGGGGC GCCGCGGCCG 360
TGCGGGGCGT CATGGATCG CCACTCCAGC TACATCTTCA TCTGGCTGCA GCTGGAGCTC 420
TGCGCCATGG CCGTGCTGCT CACCAAAGGT GAAATTCGAT GCTACTGTGA TGCTGCCCAC 480
TGTGTAGCCA CTGGTTATAT GTGTAAATCT GAGCTCAGCG CCTGCTTCTC TAGACTTCTT 540
GATCCTCAGA ACTCAAATTC CCCACTCACC CATGGCTGCC TGGACTCTCT TGCAAGCACG 600
ACAGACATCT GCCAAGCCAA ACAGGCCCCA AACCACTCTG GCACCACCAT ACCCACATTG 660
GAATGCTGTC ATGAAGACAT GTGCAATTAC AGAGGGCTGC ACGATGTTCT CTCTCCTCCC 720
AGGGGTGAGG CCTCAGGACA AGGAAACAGG TATCAGCATG ATGGTAGCAG AAACCTTATC 780
ACCAAGGTGC AGGAGCTGAC TTCTTCCAAA GAGTTGTGGT TCCGGGCAGC GGTCATTGCC 840
GTGCCCATTG CTGGAGGGCT GATTTTAGTG TTGCTTATTA TGTTGCCCCT GAGGATGCTT 900
CGAAGTGAAA ATAAGAGGCT GCAGGATCAG CGGCAACAGA TGCTCTCCCG TTTGCACTAC 960
AGCTTTCACG GACACCATTC CAAAAAGGGG CAGGTTGCAA AGTTAGACTT GGAATGCATG 1020
GTGCCGGTCA GTGGGCACGA GAACTGCTGT CTGACCTGTG ATAAAATGAG ACAAGCAGAC 1080
CTCAGCAACG ATAAGATCCT CTCGCTTGTT CACTGGGGCA TGTACAGTGG GCACGGGAAG 1140
CTGGAATTCG TATGACGGAG TCTTATCTGA ACTACACTTA CTGAACAGCT TGAAGGCCTT 1200
TTGAGTTCTG CTGGACAGGA GCACTTTATC TGAAGACAAA CTCATTTAAT CATCTTTGAG 1260
AGACAAAATG ACCTCTGCAA ACAGAATCTT GGATATTTCT TCTGAAGGAT TATTTGCACA 1320
GACTTAAATA CAGTTAAATG TGTTATTTGC TTTTAAAATT ATAAAAAGCA AAGAGAAGAC 1380
TTTGTACACA CTGTCACCAG GGTTATTTGC ATCCAAGGGA GCTGGAATTG AGTACCTAAA 1440

TAAACAAAAA TGTGCCCTAT GTAAGCTTCT ACATCTTGAT TTATTGTAAA GATTTAAAAG 1500
AAATATATAT ATTTTGTCTG A

Seq ID NO: 134 Protein sequence:
Protein Accession #: NP_036474.1

1 11 21 31 41 51
MDRHSSYIFI WLQLELCAMA VLLTKQEIRC YCDAAHCVAT GYMCKSELSA CFSRLLDPQN 60
SNSPLTHGCL DSLASTTDIC QAKQARNHSG TTIPTLECCH EDMCNYRGLH DVLSPPRGEA 120
SQQGNRYQHD GSRNLITKVQ ELTSSKELWP RAAVIAVPIA GGLILVLLIM LALRMLRSEN 180
KRLQDQRQQM LSRLHYSFHQ HHSKKGQVAK LDLECMVPVS GHENCCLTCD KMRQADLSND 240
KILSLVHWQM YSGHGKLEFV

Seq ID NO: 135 DNA sequence
Nucleic Acid Accession #: NM_001627.1
Coding sequence: 64-1815 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
CGGGACGACG CCCCCTCCTG CGGCGTGGAC TCCGTCAGTG GCCCACCAAG AAGGAGGAGG 60
AATATTGAAT CCAAGGGGGC CAGTTCCTGC CGTCTGCTCT TCTGCCTCTT GATCTCCGCC 120
ACCGTCTTCA GGCCAGGCCT TGGATGGTAT ACTGTAAATT CAGCATATGG AGATACCATT 180
ATCATACCTT GCCGACTTGA CGTACCTCAG AATCTCATGT TTGGCAAATG GAAATATGAA 240
AAGCCCGATG GCTCCCCAGT ATTTATTGCC TTCAGATCCT CTACAAAGAA AAGTGTGCAG 300
TACGACGATG TACCAGAATA CAAAGACAGA TTGAACCTCT CAGAAAACTA CACTTTGTCT 360
ATCAGTAATG CAAGGATCAG TGATGAAAAG AGATTTGTGT GCATGCTAGT AACTGAGGAC 420
AACGTGTTTG AGGCACCTAC AATAGTCAAG GTGTTCAAGC AACCATCTAA ACCTGAAATT 480
GTAAGCAAAG CACTGTTTCT CGAAACAGAG CAGCTAAAAA AGTTGGGTGA CTGCATTTCA 540
GAAGACAGTT ATCCAGATGG CAATATCACA TGGTACAGGA ATGGAAAAGT GCTACATCCC 600
CTTGAAGGAG CGGTGGTCAT AATTTTTAAA AAGGAAATGG ACCCAGTGAC TCAGCTCTAT 660
ACCATGACTT CCACCCTGGA GTACAAGACA ACCAAGGCTG ACATACAAAT GCCATTCACC 720
TGCTCGGTGA CATATTATGG ACCATCTGGC CAGAAAACAA TTCATTCTGA ACAGGCAGTA 780
TTTGATATTT ACTATCCTAC AGAGCAGGTG ACAATACAAG TGCTGCCACC AAAAAATGCC 840
ATCAAAGAAG GGGATAACAT CACTCTTAAA TGCTTAGGGA ATGGCAACCC TCCCCCAGAG 900
GAATTTTTGT TTTACTTACC AGGACAGCCC GAAGGAATAA GAAGCTCAAA TACTTACACA 960
CTGATGGATG TGAGGCGCAA TGCAACAGGA GACTACAAGT GTTCCCTGAT AGACAAAAAA 1020
AGCATGATTG CTTCAACAGC CATCACAGTT CACTATTTGG ATTGTCCTT AAACCCAAGT 1080
GGAGAAGTGA CTAGACAGAT TGGTGATGCC CTACCCGTGT CATGCACAAT ATCTGCTAGC 1140
AGGAATGCAA CTGTGGTATG GATGAAAGAT AACATCAGGC TTCGATCTAG CCCGTCATTT 1200
TCTAGTCTTC ATTATCAGGA TGCTGGAAAC TATGTCTGCG AAACTGCTCT GCAGGAGGTT 1260
GAAGGACTAA AGAAAAGAGA GTCATTGACT CTCATTGTAG AAGGCAAACC TCAAATAAAA 1320
ATGACAAAGA AAACTGATCC CAGTGGACTA TCTAAAACAA TAATCTGCCA TGTGGAAGGT 1380
TTTCCAAAGC CAGCCATTCA GTGGACAATT ACTGGCAGTG GAAGCGTCAT AAACCAAACA 1440
GAGGAATCTC CTTATATTAA TGGCAGGTAT TATAGTAAAA TTATCATTTC CCCTGAAGAG 1500
AATGTTACAT TAACTTGCAC AGCAGAAAAC CAACTGGAGA GAACAGTAAA CTCCTTGAAT 1560
GTCTCTGCTA TAAGTATTCC AGAACACGAT GAGGCAGACG AGATAAGTGA TGAAAACAGA 1620
GAAAAGGTGA ATGACCAGGC AAAACTAATT GTGGGAATCG TTGTTGGTCT CCTCCTTGCT 1680
GCCCTTGTTG CTGGTGTCGT CTACTGGCTG TACATGAAGA AGTCAAAGAC TGCATCAAAA 1740
CATGTAAACA AGGACCTCGG TAATATGGAA GAAAACAAAA AGTTAGAAGA AAACAATCAC 1800
AAAACTGAAG CCTAAGAGAG AAACTGTCCT AGTTGTCCAG AGATAAAAAT CATATAGACC 1860
AATTGAAGCA TGAACGTGGA TTGTATTTAA GACATAAACA AAGACATTGA CAGCAATTCA 1920
TGGTTCAAGT ATTAAGCAGT TCATTCTACC AAGCTGTCAC AGGTTTTCAG AGAATTATCT 1980
CAAGTAAAAC AAATGAAATT TAATTACAAA CAATAAGAAC AAGTTTTGGC AGCCATGATA 2040
ATAGGTCATA TGTTGTGTTT GGTTCAATTT TTTTTCCGTA AATGTCTGCA CTGAGGATTT 2100
CTTTTTGGTT TGCCTTTTAT GTAAATTTTT TACGTAGCTA TTTTTATACA CTGTAAGCTT 2160
TGTTCTGGGA GTTGCTGTTA ATCTGATGTA TAATGTAATG TTTTTATTTC AATTGTTTAT 2220
ATGGATAATC TGAGCAGGTA CATTTCTGAT TCTGATTGCT ATCAGCAATG CCCCAAACTT 2280
TCTCATAAGC ACCTAAAACC CAAAGGTGGC AGCTTGTGAA GATTGGGGAC ACTCATATTG 2340
CCCTAATTAA AAACTGTGAT TTTTATCACA AGGGAGGGGA GGCCGAGAGT CAGACTGATA 2400
GACACCATAG GAGCCGACTC TTTGATATGC CACCAGCGAA CTCTCAGAAA TAAATCACAG 2460
ATGCATATAG ACACACATAC ATAATGGTAC TCCCAAACTG ACAATTTTAC CTATTCTGAA 2520
AAAGACATAA AACAGAATT

Seq ID NO: 136 Protein sequence:
Protein Accession #: NP_001618.1

1 11 21 31 41 51
MESKGASSCR LLFCLLISAT VFRPGLGWYT VNSAYGDTII IPCRLDVPQN LMFGKWKYEK 60
PDGSPVFIAF RSSTKKSVQY DDVPEYKDRL NLSENYTLSI SNARISDEKR FVCMLVTEDN 120
VFEAPTIVKV FKQPSKPEIV SKALFLETEQ LKKLGDCISE DSYPDGNITW YRNGKVLHPL 180
EGAVVIIFKK EMDPVTQLYT MTSTLEYKTT KADIQMPFTC SVTYYGPSGQ KTIHSEQAVF 240
DIYYPTEQVT IQVLPPKNAI KEGDNITLKC LGNGNPPPEE FLFYLPGQPE GIRSSNTYTL 300
MDVRRNATGD YKCSLIDKKS MIASTAITVH YLDLSLNPSG EVTRQIGDAL PVSCTISASR 360
NATVVWMKDN IRLRSSPSPS SLHYQDAGNY VCETALQEVE GLKKRESLTL IVEGKPQIKM 420
TKKTDPSGLS KTIICHVEGF PKPAIQWTIT GSGSVINQTE ESPYINGRYY SKIIISPEEN 480

VTLTCTAENQ LERTVNSLNV SAISIPEHDE ADEISDENRE KVNDQAKLIV GIVVGLLLAA 540
LVAGVVYWLY MKKSKTASKH VNKDLGNMEE NKKLEENNHK TEA

Seq ID NO: 137 DNA sequence
Nucleic Acid Accession #: XM_030559
Coding sequence: 1-119 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
ATGAACCGCA GCCACCGGCA CGGGGCGGGC AGCGGCTGCC TGGGCACTAT GGAGGTGAAG 60
AGCAAGTTTG GAGCTGAATT TCGTCGGTTT TCGCTGGAAA GATCAAAACC TGGAAAATTT 120
GAGGAGTTTT ATGGATTACT ACAACATGTT CATAAGATCC CCAATGTTGA CGTTTTGGTA 180
GGCTATGCAG ACATCCATGG AGACTTACTA CCTATAAATA ATGATGATAA TTATCACAAA 240
GCTGTTTCAA CGGCCAATCC ACTGCTTAGG ATATTTATAC AAAAGAAGGA AGAAGCAGAC 300
TACAGTGCCT TTGGTACAGA CACGCTAATA AAGAAGAAGA ATGTTTTAAC CAACGTATTG 360
CGTCCTGACA ACCATAGAAA AAAGCCACAT ATAGTCATTA GTATGCCCCA AGACTTTAGA 420
CCTGTGTCTT CTATTATAGA CGTGGATATT CTCCCAGAAA CGCATCGTAG GGTACGTCTT 480
TACAAATACG GCACGGAGAA ACCCCTAGGA TTCTACATCC GGGATGUCTC CAGTGTCAGG 540
GTAACACCAC ATGGCTTAGA AAAGGTTCCA GGGATCTTTA TATCCAGGCT TGTCCCAGGA 600
GGTCTGGCTC AAAGTACAGG ACTATTAGCT GTTAATGATG AAGTTTTAGA AGTTAATGGC 660
ATAGAAGTTT CAGGGAAGAG CCTTGATCAA GTAACAGACA TGATGATTGC AAATAGCCGT 720
AACCTCATCA TAACAGTGAG ACCGGCAAAC CAGAGGAATA ATGTTGTGAG GAACAGTCGG 780
ACTTCTGGCA GTTCCGGTCA GTCTACTGAT AACAGCCTTC TTGGCTACCC ACAGCAGATT 840
GAACCAAGCT TTGAGCCAGA GGATGAAGAC AGCGAAGAAG ATGACATTAT CATTGAAGAC 900
AATGGAGTGC CACAGCAGAT TCCAAAAGCT GTTCCTAATA CTGAGAGCCT GGAGTCATTA 960
ACACAGATAG AGCTAAGCTT TGAGTCTGGA CAGAATGGCT TTATTCCCTC TAATGAAGTG 1020
AGCTTAGCAG CCATAGCAAG CAGCTCAAAC ACGGAATTTG AAACACATGC TCCAGATCAA 1080
AAACTCTTAG AAGAAGATGG AACAATCATA ACATTATGA

Seq ID NO: 138 Protein sequence:
Protein Accession #: XP_030559

1 11 21 31 41 51
MNRSHRHGAG SGCLGTMEVK SKFGAEFRRF SLERSKPGKF EEFYGLLQHV HKIPNVDVLV 60
GYADIHGDLL PINNDDNYHK AVSTANPLLR IFIQKKEEAD YSAFGTDTLI KKKNVLTNVL 120
RPDNHRKKPH IVISMPQDFR PVSSIIDVDI LFETHRRVRL YKYGTEKPLQ PVIRDGSSVR 180
VTPHQLEKVP GIFISRLVPG GLAQSTGLLA VNDEVLEVNG IEVSGKSLDQ VTDMMIANSR 240
NLIITVRPAN QRNNVVRNSR TSQSSGQSTD NSLLGYPQQI EPSTEPEDED SEEDDIIIED 300
NGVPQQIPKA VPNTESLESL TQIELSFESG QNGFIPSNEV SLAAIASSSN TEPETHAPDQ 360
KLLEEDGTII TL

It is understood that the examples described above in no way serve to limit the true scope of this invention, but rather are presented for illustrative purposes. All publications, sequences of accession numbers, and patent applications cited in this specification are herein incorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference.

WHAT IS CLAIMED IS:

1. A method of detecting a breast cancer-associated transcript in a cell from a patient, the method comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-25.

2. The method of claim 1, wherein the biological sample comprises isolated nucleic acids.

3. The method of claim 2, wherein the nucleic acids are mRNA.

4. The method of claim 2, further comprising the step of amplifying nucleic acids before the step of contacting the biological sample with the polynucleotide.

5. The method of claim 1, wherein the polynucleotide comprises a sequence as shown in Tables 1-25.

6. The method of claim 1, wherein the polynucleotide is immobilized on a solid surface.

7. The method of claim 1, wherein the patient is undergoing a therapeutic regimen to treat breast cancer.

8. The method of claim 1, wherein the patient is suspected of having breast cancer.

9. An isolated nucleic acid molecule consisting of a polynucleotide sequence as shown in Tables 1-25.

10. The nucleic acid molecule of claim 9, which is labeled.

11. An expression vector comprising the nucleic acid of claim 9.

12. A host cell comprising the expression vector of claim 11.

13. An isolated polypeptide which is encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1-25.

14. An antibody that specifically binds a polypeptide of claim 13.

15. The antibody of claim 14, further conjugated to an effector component.

16. The antibody of claim 15, wherein the effector component is a fluorescent label.

17. The antibody of claim 15, wherein the effector component is a radioisotope or a cytotoxic chemical.

18. The antibody of claim 15, which is an antibody fragment.

19. The antibody of claim 15, which is a humanized antibody

20. A method of detecting a breast cancer cell in a biological sample from a patient, the method comprising contacting the biological sample with an antibody of claim 14.

21. The method of claim 20, wherein the antibody is further conjugated to an effector component.

22. The method of claim 21, wherein the effector component is a fluorescent label.

23. A method for identifying a compound that modulates a breast cancer-associated polypeptide, the method comprising the steps of:

(i) contacting the compound with a breast cancer-associated polypeptide, the polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-25; and

(ii) determining the functional effect of the compound upon the polypeptide.

24. A drug screening assay comprising the steps of

(i) administering a test compound to a mammal having breast cancer or a cell isolated therefrom;

(ii) comparing the level of gene expression of a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-25 in a treated cell or mammal with the level of gene expression of the polynucleotide in a control cell or mammal, wherein a test compound that modulates the level of expression of the polynucleotide is a candidate for the treatment of breast cancer.